

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: April 14, 2006, 01:34:23 ; Search time 75 Seconds
(without alignments)
3848.671 Million cell updates/sec

Title: US-10-668-767-128_COPY_1_3000
Perfect score: 15748
Sequence: 1 MAEABGASBQDDVSFLRTE.....RLADNADIWAKKKEELVT 3000

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12295	78.1	5126	2 S40450	ryanodine receptor
2	6828	43.4	5107	2 T29144	partial CDS - Caen
3	6770.5	43.0	4969	2 A37113	ryanodine receptor
4	6769	43.0	4967	2 S72269	ryanodine receptor
5	6534.5	41.5	5037	1 A54161	ryanodine-binding
6	6453.5	41.0	5035	1 A56646	ryanodine receptor
7	6442.5	40.9	5032	1 A35041	ryanodine receptor
8	6439	40.9	5037	2 B35041	ryanodine receptor
9	6438.5	40.9	4859	2 S74173	ryanodine receptor
10	6423	40.8	4869	2 S66572	ryanodine receptor
11	6419	40.8	4868	2 B54161	ryanodine-binding
12	6413	40.7	4872	2 S27272	ryanodine receptor
13	538	3.4	163	2 I47214	probable brain rya
14	520	3.3	162	2 I47213	cardiac muscle rya
15	327	2.1	2783	2 T31431	inositol 1,4,5-tri
16	323	2.1	2701	2 S17796	inositol-trisphosp
17	296.5	1.9	2693	2 A40743	IP3 receptor, XIP3
18	292.5	1.9	2695	2 S54974	type 1 inositol 1,
19	290.5	1.8	2670	2 A46719	inositol 1,4,5-tri
20	289	1.8	2713	2 A55713	inositol 1,4,5-tri
21	286.5	1.8	2734	2 B36579	inositol 1,4,5-tri
22	285	1.8	2671	2 A49873	inositol 1,4,5-tri
23	284	1.8	1966	2 T32552	hypothetical prote
24	284	1.8	2848	2 T32550	hypothetical prote
25	279	1.8	2749	1 A6MSIT	inositol 1,4,5-tri
26	279	1.8	2749	2 A36579	inositol 1,4,5-tri
27	277.5	1.8	2833	2 A43360	inositol 1,4,5-tri
28	205	1.3	1676	2 E71410	probable centromer
29	203.5	1.3	2541	2 T29340	hypothetical prote

30	198	1.3	3259	1 A56539	giantin - human
31	198	1.3	5369	2 T44807	myosubtilin synth
32	197.5	1.3	2954	2 T14156	kinesin-related pr
33	196.5	1.2	2218	2 B84683	hypothetical prote
34	192	1.2	1727	2 T50073	myosin-like coiled
35	192	1.2	3225	2 T52300	giantin - human
36	191	1.2	1882	2 T00069	hypothetical prote
37	189.5	1.2	2663	1 S28261	centromere protein
38	188.5	1.2	1642	2 T08880	NMDA receptor-bind
39	188	1.2	4540	2 T30838	cytoplasmic dynein
40	182.5	1.2	2331	2 T25410	hypothetical prote
41	182.5	1.2	3187	2 UC5837	364k Golgi complex
42	180.5	1.1	2712	2 T05113	hypothetical prote
43	179	1.1	6669	2 S55024	nebulin, skeletal
44	178	1.1	4151	2 T13734	groovin gene prote
45	177	1.1	52	2 I46644	ryanodine receptor

ALIGNMENTS

RESULT 1					
S40450					
ryanodine receptor/calcium release channel - fruit fly (Drosophila melanogaster)					
C/Species: Drosophila melanogaster					
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 11-Jun-1999					
C/Accession: S40450					
R:Takehima, H.; Niehi, M.; Iwabe, N.; Miyata, T.; Hosoya, T.; Masai, I.; Hotta, Y.					
FEBS Lett. 337, 81-87, 1994					
A>Title: Isolation and characterization of a gene for a ryanodine receptor/calcium rele					
A/Reference number: S40450; MID:94102409; PMID:8276118					
A/Accession: S40450					
A>Status: preliminary					
A/Molecule type: DNA					
A/Residues: 1-5126 <PAK>					
A/Cross-references: UNIPARC:UPI000017CF36					
C/Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homol					
Query Match					
Best Local Similarity 77.5%; Pred. No. 0;					
Matches 2348; Conservative 275; Mismatches 338; Indels 68; Gaps 22;					
Qy	1	MAEABGASBQDDVSFLRTEDMVCLSTATGEBVCLAEFGNRRHCELENIAADKNIPDL	60		
Db	1	MAEABG-SQDDVSFLRTEDMVCLSTATGEBVCLAEFGNRRHCELENIAADKNIPDL	59		
Qy	61	SQCVFVEQALSVRALQELVTAAGSETGKSGHRTLLYGNAILLRHNSDWYLAQLST	120		
Db	60	SQCVFVEQALSVRALQELVTAAGSETGKSGHRTLLYGNAILLRHNSDWYLAQLST	119		
Qy	121	SSSODKALPVGIQHNSQSGACWMTLHPAKKSSSEKQKVPVGDLLIVSATERVLTHTK	180		
Db	120	SSSNDKLSFVGIQHSQSGACWMTVHPAKKSSSEKQKVPVGDLLIVSATERVLTHTK	179		
Qy	181	ENEVSIYNASFEHTYHNSVPGYGTGISPMKTVGVYFGDVARFPFGSGDECLTIPSTWKG	240		
Db	180	ENESIVNASFEHTYHNSVPGYGTGISPMKTVGVYFGDVARFPFGSGDECLTIPSTWREA	239		
Qy	241	GONIVVEGGSVNSQARSRLRLRLARTKMAAGFINMTPMRIRHTTTGRTLVGNDONELY	300		
Db	240	GONIVVEGGSVNSQARSRLRLRLARTKMAAGFINMTPMRIRHTTTGRTLVGNDONELY	299		
Qy	301	LVNREEXTTASCACLRQEDDDQVLEDDLVYGAPIIKYGDSTYIVGHSFGMLASTY	360		
Db	300	LVNREEXTTATTFSSW-QERDDEKVELDDLEVTGSPILKYGTIVIVGHSFGMLASTY	358		
Qy	361	KSYETKKKGKGVKYEKOAILHEBGKMDGDLDFRSQGEESRTAVIRKCSLFTKFINGL	420		
Db	359	KSYETKKKGKGVKYEKOAILHEBGKMDGDLDFRSQGEESRTAVIRKCSLFTKFINGL	418		
Qy	421	ETLOENRRHSMFPASVNLGEMVNCLEDLINYPAPDEDMHEBKONFRALRNQDLFOE	480		
Db	419	ETLOENRRHSMFPQKVLINEMVNCLEDLINYPAPDEDMHEBKONFRALRNQDLFOE	478		

Qy	481	GGI:NL:ILEA:IDK:IN:VTSOG:FLA:GDSGOS:MEM:ISGL:YOLLA:AI:KGN:TNCAQ	540
Db	479	EGV:LL:ILEA:IDK:IN:VTSOG:FLA:GDSGOS:WDL:STYL:YOLLA:AI:KGN:TNCAQ	538
Qy	541	FANS:RL:MWL:FS:RL:SG:QAS:GEGTGM:LDV:HCVL:ID:SP:EA:LN:MM:RDEH:KVII:SL:HEK:GR	600
Db	539	FANS:RL:MWL:FS:RL:SG:QAS:SEGS:GMLDV:HCVL:ID:SP:EA:LN:MM:RDEH:KVII:SL:HEK:GR	598
Qy	601	DPK:LDV:CS:LCV:GNGVA:VRSS:ONNIC:CYLL:LP:GR:KULL:Q:TA:LV:DV:VSSVR:PNI:FG:RV:G	660
Db	599	DPK:LDV:CS:LCV:GNGVA:VRSS:ONNIC:CPFL:PG:KULL:Q:TA:LV:DV:VSSVR:PNI:FG:RV:G	658
Qy	661	SAVY:KMY:FEY:TM:DH:IEK:TTMM:PH:RI:GM:ANTT:GYV:PY:PGGGE:KMG:NGV:DD:LY:SY:GF	720
Db	659	SSM:YQ:KMY:FEY:TM:DH:IEK:TTMM:PH:RI:GM:ANTT:GYV:PY:PGGGE:KMG:NGV:DD:LY:SY:GF	718
Qy	721	DG:AVI:WSG:GRKT:PVN:RT:HA:EE:PY:IR:KGDV:IG:CALD:LV:P:IN:FM:NGVR:VTS:GF:TN:MLE	780
Db	719	DG:AVI:WSG:GRKT:LV:DA:LP:EE:PF:IR:KGDV:IG:CALD:LV:P:IN:FM:NGVR:VTS:GF:TN:MLE	778
Qy	781	GM:FP:VUS:SCSS:KLS:RFL:GGEH:GL:RYA:AP:BG:V:PLVE:SL:LPQ:II:SL:EP:CY:GN:SK	840
Db	779	GM:FP:VUS:SCSS:KLS:RFL:GGEH:GL:RYA:AP:BG:V:PLVE:SL:LPQ:II:SL:EP:CY:GN:SK	838
Qy	841	RAL:AGP:LV:OD:DTA:V:FP:PT:VD:TL:Q:TL:TY:VEQ:ILDK:EA:ENI:HEM:AM:ANKI:EAG:MY:QDQ	900
Db	839	NVL:AGP:MW:IE:DD:TA:V:FP:PK:VD:TL:GT:V:TL:PS:VD:Q:IEK:EA:ENI:HEM:AL:INKI:EAG:MS:WEH	898
Qy	901	RED:HK:HP:CL:V:PP:ER:LP:PA:EK:RD:IO:LA:V:OT:KL:TL:AL:GY:II:SL:DK:PA:RI:RV:RL:NE	960
Db	899	RDD:HR:HP:CL:TH:HE:K:LP:PA:EK:RY:DN:O:LA:V:OT:KL:TL:IS:LY:IT:MD:K:PA:RI:RV:RL:NE	958
Qy	961	PF:MO:NG:K:PA:R:PL:DS:AT:V:LP:KMD:EL:VD:O:LA:EN:TH:MA:EB:RI:Q:OG:TY:GL:NE:DS:DM:R	1020
Db	959	IF:MO:NG:K:PA:R:PL:DS:AT:V:LP:KLE:EL:VD:O:LA:EN:TH:MA:EB:RI:Q:OG:TY:GL:NE:DS:EM:R	1018
Qy	1021	SP:HL:V:PY:PK:VD:AI:KK:AN:RD:TA:SE:TV:RT:LV:YGY:ML:DP:PT:SG:HE:ALL:LE:AS:K:Q:K:OD:R	1080
Db	1019	SP:HL:V:PY:AK:VD:EA:IK:KAN:RD:TA:SE:TS:ANA:PG:RL:CL:GS:DS:DR:RN:G:TS:GR:ET:TP:QV:RR:IP	1078
Qy	1081	TY:RA:EK:NY:AA:V:SG:KMY:FE:FE:IL:TL:PG:MM:VGN:HA:MD:MA:G:ML:GO:EN:MA:AD:G:NY:EE:KY	1140
Db	1079	TY:RE:BN:VA:V:TS:G:KMY:FE:FE:V:LT:SG:MM:VGN:AR:AD:CY:PA:ML:GS:ED:TS:MA:DG:SH:V:TV:DH	1138
Qy	1141	SG:NT:SE:FG:K:O:AV:GD:V:V:G:V:PL:DL:ID:KT:IS:FS:IN:GE:IL:MD:AL:G:SE:IT:TP:AD:V:--OG:DN:FP:YA	1198
Db	1139	AG:SI:IE:HF:CV:RY:EA:BG:VD:IS:CF:ID:V:KE:QT:IS:FS:IN:GE:IL:MD:AL:G:SE:IT:TP:AD:V:YA:BG:FP:YA	1198
Qy	1199	CTL:G:VG:K:AA:RL:TY:GD:V:V:NT:LK:FT:TC:GL:Q:EG:Y:EP:CV:MM:K:RD:V:Y:TT:TK:OD:PI:EN:TD:EM	1258
Db	1199	CTL:G:VG:O:AA:RL:TY:GD:V:V:DL:SK:FT:TC:GL:Q:EG:Y:EP:CV:MM:R:PP:V:Y:TT:MY:TK:OD:PI:EN:TD:EM	1258
Qy	1259	ID:TI:ID:V:TR:IP:AG:SD:TP:CL:K:IS:NT:FE:TM:KA:MM:FE:RL:SL:PV:CH:NE:FI:DE:AE:K:AR:W	1318
Db	1259	PD:CI:ID:V:TR:IP:IG:AD:TP:PH:LK:IS:NT:FE:TM:KA:MM:FE:RL:SL:PY:TC:ME:FI:SE:Q:EK:AR:W	1318
Qy	1319	VEI:K:O:Q:O:IL:ME:KA-VEA:Q:-----PAH:ID:IM:SG:FT:ND:IK:GL:AY:VE-DN:Q:EL:P:SS:K:W	1371
Db	1319	DEI:K:RO:Q:R:IL:RE:AE:IL:AA:Q:OV:OT:O:AA:IM:HD:ML:K:G:FM:ND:IK:GL:TR:FP:DE:HA:LA:EA:DM	1378
Qy	1372	KRL:PS:RP:K:GS:MT:RG:V:TI:Q:V:Y:NN:U:Q:PO:QV:GM:HR:STS:EA:MA:KY:DL:GA:Q:LT:JD:DD:K:DK	1431
Db	1379	MRG:EN:RP:K:RS:LT:RN:IT:-----F:ET:DM:SA:LD:EM:Q:IS:TS:-----V:ID:MM:GL:EE:MD:DK:K-K	1429
Qy	1432	RG:SP:PF:K:FS:K:G:SS:SD:RA:KS:KT:PD:PS:DT:EV:PS:ER:GA:RR:PN:PI:K:YS:Q:AN:Q:RY:NG	1491
Db	1430	RG:RP:PF:K:FS-SS:K:SD:GS:REK-MG:AR:TL:DT:LS:ER:NT:Y:AH:BR:NV:NN:Q:MT:RA:PT:LR:LN	1487
Qy	1492	MNA:PS:RT:NL:Y:GS:OV:GL:MA:TP:TD:RK:Q:MT:ST:LA:Q:AT:BF:V:GN:EI:PA:EL:CL:K:IN:EF:Y	1551
Db	1488	AE:IP:SP:V:-----PQ:PK:LS:SN:IG:Q:OV:ES:TS:GB:EM:FA:EL:CL:K:IN:EF:Y	1533

QY	1552	GVR.IY.PGODDPHHY.IGWTTQOYHLSDPNOSKYTSKSV.IITDDYDRAVEVNNRQSCVY	1611
Db	1534	GVR.IY.PGODDPHHY.VGWTTQYHLSDPNOSKYTSKSV.IITDDYDRAVEVNNRQSCVY	1599
QY	1612	PADEL.YNVAWEATATKAGSQMG.FIGCSVDJSTGSVSPFCEGKOTS.FPKWEPETGLFPAL	1671
Db	1594	PADEL.YNVAWEATATKAGSQMG.FIGCSVDJSTGSVSPFCEGKOTS.FPKWEPETGLFPAL	1655
QY	1672	FVEATSKBILQIBELGRSATS.LPLSAVAL.PTSDKAVIT.PQFPRLKYQCLAKPHQMARVENQOS	1731
Db	1654	FVEATSKBILQIBELGRSATS.LPLSAVAL.PTSDKAVIT.PQFPRLKYQCLAKPHQMARVENQOS	1713
QY	1732	LOVAL.KLSDIRGSMSCBDAVSNMLAH.IHREBDCIDILB.IEMDKLS.FSHSLT.LYAA	1799
Db	1714	LOVAL.KLSDIRGSMSCBDAVSNMLAH.IHREBDCIDILB.IEMDKLS.FSHSLT.LYAA	1773
QY	1792	LCYQSNRAAHALCTYHDOKL.TALAIOSQVSGCLRGOFYD.LTALHLSHATTMEACKN	1851
Db	1774	LCYQSNRAAHALCTYHDOKL.TALAIOSQVSGCLRGOFYD.LTALHLSHATTMEACKN	1833
QY	1852	EFVILPGLPEL.KALYEEBDMGHSLSR.LQTESVRPQMKWTI-----AESITE	1897
Db	1834	EFVILPGLPEL.KALYEEBDMGHSLSR.LQTESVRPQMKWTI-----AESITE	1892
QY	1898	ISN.IYSYFPL.EVAREEVMOALAEVETNOYHNRDPVGSNSBN.FLPLIKVDRLLLGYM	1955
Db	1894	IDOLYSKFP.LEVVRQOFMEAL.KDAVINQVHNDPI.GWNTBN.FLPLIKLTDRLLLGYM	1953
QY	1958	MRDEVDKLT.IMTPETWDS.FDKEGDEHRKGLLHKMKMA.GALQMCYLLQHLNDIQLR	2017
Db	1954	LTDSDVORL.VMDPEITMDQAFEREGDEHRKGLLTKMKME.GALQMCYLLHLHYDQLR	2013
QY	2018	HRVAA.IIAFAD.FVGD.LQTDQLRRYTEIKOSDPLSAVAAKKTRE.FRCSPREBQMANIISFK	2077
Db	2014	HRVAST.IAFSHDFG.DLQTDQLRRYTEIKOSDPLSAVAAKKTRE.FRCSPREBQMANIISFK	2073
QY	2078	HLEBEDXENPCGSEEL.IARMEFHDITMAVUSLHALDEPDAENQO--PEARQAPGKULYN	2136
Db	2074	NLEBDDDNCTCGELTGR.LGDFPDS.LMOKVSLNALOE.PRGVEGTALBEVYTGPI.TKULYN	2133
QY	2137	IINNVKLEEBEAKA.IEPPKKTPEEKFRKYLQITVYMAESQ.IETPLVEMSSLVRO	2196
Db	2134	PINTVKLEEBGPKEVEBEKKTPEEVKRLIKITVYMAESQ.IENFKLVEMSSLLRO	2193
QY	2197	YDAVGELIRALEKTYVINAKTKLDVAEMVYGLSQIRALL.PVQMSQEBEELMRKLMKULYN	2256
Db	2194	YDTVGELVIRALEKTYVINTRABRDVAEMVYGLSQIRALL.PVQMSQEBEELMRKLMKULYN	2255
QY	2257	NHTFFQHPDLIRVLRVHENTYMAVMANTLGRPAQOSDAPQSSQVAF--DSKEKOTSHEM	2314
Db	2254	NATFFQHPDLIRILRVHENTYMAVMANTLGRPAQOSDAP--PQSEVAAGAPSKEDOTSHEM	2312
QY	2315	VVACCRFLCY.FCPRGRNOKAMFHP.LTLENSIILSRSLRGSTPLDVAYSSLMENTE	2374
Db	2313	VVACCRFLCY.FCGRNOKAMFHP.LTLDNNAIILARPSLRKSTPLDVAYSSLMENTE	2372
QY	2375	LALALRHHYIEKIAVYLSRCGLQSNSESLVEKGYD.LGMDPEVGEERYUDFLRFCVWAVGES	2434
Db	2373	LALALRHHYIEKIAVYLSRCGLQSNSESLVEKGYD.LGMDPEVGEERYUDFLRFCVWAVGES	2432
QY	2435	VEENANVIRILLIRPECGIPALRGEGGLKALVDANKQSERIADRKLREMOEQSDV-	2493
Db	2433	VEENANVIRILLIRPECGIPALRGEGGLFRALVEANRMSERISDRCKMOD--BAEGTIA	2491
QY	2494	--NFSHSLPESDEBEDYITDGAALINRYCTLVDLLGRCADAGYIALGXNLSLRAARILR	2551
Db	2492	GLNFTHPLPGEBEDEDYITDGAALINRYCTLVDLLGRCADAPASVTEBGKNESLRAARILR	2551
QY	2552	SLVPLBLOGLVLSIRFTLNNPAAAGEBRPKSDMPSGLLPGKQSGVGLFLERVYGIETOB.LF	2611
Db	2552	SLVPLBLOGLVLSIKFTLSQTAPEGEERPKSDMPSGGLLPNNKQSVLPLERVYGI.EAODLF	2611
QY	2612	YKLEBEAFPLDRLAATMLDRNDGCESPMALSMNRYSNLSIPLLIKHAIFYNBAENYASTL	2671

QY 1444 RGSSTRASRK-----SKTPDPSPDTEVBERGARRPNQIKY 1482
DB 1347 NFRDSRRKREKAOLROMKANSRSPDAGSLDTSTLPTGQKDVLAASEMPLSGPGRQLTI 1406
QY 1483 SOANORYNGNANPSPRTNLVGSQVGLMATTPODRQKMTSTLAQSAETVNGEIRIDAG 1542
DB 1407 KRGSS-----IKKKKKGAKEALEMEREKKGSIIPMDAQDLVLOEG---DNAA 1452
QY 1543 L-----KLINEFYGVATYPGQDPHTHYIGVNTTOYHLSDKNQSK- VTKSSVILITDDY 1597
DB 1453 LVHKKDKVEYYGIRLPGQDPSQVWGVNTTYQHYVNVNPGSGQVRCRSEADHNG 1512
QY 1598 RYVENNRRQSCYVVRADDELVNEVMAETAKGASQMGPIGCVTSTGVSFTCEGQJTEP 1657
DB 1513 TVVDSVQSONCYVNVNSELATTPDVANTK--VSGTLIGCITDTSIGELSFQVSGYDTGT 1570
QY 1658 KFMGEDETGLPRAIPVEATSKETLOJELGRSATSLSLSAANLPTSDKHVYPOPRPLTKYQ 1717
DB 1571 KFKLBERGAMLFPAATPTPTATEILOPELGRKIKTTPLSAAMFKSCKSLVPCPRPLTYE 1630
QY 1718 CLKPHQMAVNPQSLQVHALKLSDIRGWSMLCEDAVSMALHPIBEDRCIDILEPIEMDK 1777
DB 1631 QIESVYMAVBPVNETLATTLAKSEVKGWSVLQNDPVIRMSVYIPKDGSLDILEMEND 1690
QY 1778 LLSFHSHTLTLYALCYQSNYRAAALCTHVQKOLLVAIQSQYMGPIRGCFYDILLAL 1837
DB 1691 MEFBNQITNLVCKLASHGNHKAHTLCOHIDEDQITVYAIKSHYLSGPMRGPHDILLGL 1750
QY 1838 HLESHTATMEACNKEFVILGPPELKAAL-YEPPMGHSLSLQESVVRPOMKMTDIAEST 1896
DB 1751 HLMSTTAARNSMAKEVYIPLVPOLOIKVNLDPD-----SESXYPQI---TGESVS 1797
QY 1897 EISNLVS-----PYPLEVAREFVQALAEAVETQVHNEPVGSGSNE 1939
DB 1798 MLSQMASBEVKGKVSREDEMKLLPSPVDPEALKKHMSLSQASTHNAVNCNDLIGDVT 1857
QY 1940 NLPLPLIKVDRILLVGMKREDEVEKLLIMNPETWPSFDKXGKDEHKKGLIMKMAAG 1999
DB 1858 NHPEPLFKLPDOLLVGLINDEBELCRLRIHQAFDENVE--TGTQKGJTOLEIAPR 1914
QY 2000 AKLQWQYLLQHLNDIOLRHVREAIIPAFADPVGCDLOTDOLBRYTEIKOSDLSAVALAKT 2059
DB 1915 VKIQVLSIDHLCIDOLKRYRISLSVAFTEGVEGLSDQCKRMETKQDMPRAEAAKKT 1974
QY 2060 REFRCERPQMANALISFKHLEBEDKE-----NCPGSEBILIAMNEFHDTLMAVSL 2110
DB 1975 KEFRCPKPKQMFRLIMCKVKEERDEPILMEDADVQCPMAKBGLQQLARFCELVKGIG- 2033
QY 2111 HALQEPDAE-----NQPEAKPGAFGKLYNITVYKELIEBKAALIEBPCKTPEEKPRK 2165
DB 2034 -NVKGGSDSDQALATIESEBGSWVDSFARI--VVKVPPVLEBGMEMQ---KKGTQNFRE 2086
QY 2166 VLIQITVNNVAESQIETPLVREMPSLVROYDAVAGELIRALKEKYVINAKTKLVAEMW 2225
DB 2087 IIVTMREKAOADPIESKSLINRMFELRKQSGIREIDANSQYTVFERNEKQVTDL 2146
QY 2236 VGLSQIRALLPVQMSQEBELMRKMLVNNHTPEQHPDLIRVVRVHENVNAVMMQTLG 2285
DB 2147 VYLIQIRELTVQPEHTEAAILKRGIMKNNRIPFOHDLWRLLSVHENVMSIMNLI- 2205
QY 2286 RRAQASDAQSPSOPVAEDSKKQTSHEVNVACSRFLCYFCCTGGRONQAMDPHDFLIE 2345
DB 2206 --TAQCGTYEHGDEIKERKAPIKDAS-EMVAVACSFLCYFCCTSSONQKAMFEHLSFLD 2262
QY 2346 NSNIIIRPSLSTGTPDIVAYSGSLMENTELALREHYLEKAYLSRGCOSNEIYWK 2405
DB 2263 NATMLLARSLKGSVPLDAVYSSPMDNNELALALEEBELDKAVAYLSRGCQPSNELTYK 2322
QY 2406 GYPDIGMPDVEGERYLDPLFCVWVGSEVEENANLVITLIRREBCLGAPALRGSEGL 2465
DB 2323 GYPDIGMPDVEGERYIDPLRFCVWINGEVEENANLVITLIRREBCLGAPALRGSEGL 2382

QY 2466 KAIVDANKSERIADRRKILREMOEGDVNPSHP-----LPESD- EDEBYIDT 2511
DB 2383 SAKFEALISBDI-----RLIE-----NDSHPSLSSGLGIBNPRYPKDAEGEDYIDL 2431
QY 2512 GAALINFCYCTVDLGRGAPDAGVIALGKNESIRARAILRSIVLEEDLOGVSLRFTLNN 2571
DB 2432 GAATIDFYSLVDLAKCAPDPMALQAGKDSLRARAILRSILSDLLQQLALRFTTIP 2491
QY 2572 PAA-----GEERPKSDMP 2584
DB 2492 LAAPSIEAVRANAVQASHTRQAVMAHTPAWVASLASEVSNTRRSQTPSGTMLARGLP 2551
QY 2585 ----- 2584
DB 2552 CVBEVDTDSKSDYASVHTSPSSGNELPAPYAEKRYDVLKLNENKYP10RRRSRPN 2611
QY 2585 -----SGLRGKQSVGLFLERYVYGETOELPFYKLEBAFLPDLRAATMLDRNDGE 2636
DB 2612 P1DNTGRLPGLIPNKHGSVLLFLDRVYGLDQDDMLFHYLSQSFLPDLRAATMDSPPALE 2671
QY 2637 SDMALSMRYYIGNSILPULIKHAYFNEAENYASLIDATLHTVYLSKNRMULTGOREAV 2696
DB 2672 SDTALANRYLGNVLPULTTNSHFPADAENHSALLDATLHTVYNNRKLKSITKQNRDV 2731
QY 2697 SDPLVALTSANQPSMLKILKRLTYDVSKLSYTT- VALRLTLHYERCATYGTGACQ 2755
DB 2732 SDPLVALITRELPAMMILKILKKVYITDILTMNMVNLVPLRLTLHYERCATYGTG 2787
QY 2756 GARFASDSEKRLTMMLPSNIPDSLSKMDYBELFGKALPCLIALGCLPPTYLSKNVD 2815
DB 2788 NHYVASSEOKRLSNLFDALFDLTGSRPYDELBGKALPCMTALGSAISPYTLTSGLE 2847
QY 2816 DEFYKEQAAAGDLNDPOYDPOPIINTSSVALNNDLNTIYQKSEBHYDAMASRKIENGWY 2875
DB 2848 DVNRKRREBEQ-----AMIPRVQVSRCEINRDLKMTLPAEHHHDSASAKLEKGVNH 2902
QY 2876 GEGWDSQKTHPRKLPYMLNDYEKRYKEPYRESLKALLAIGSVHSEVDIPSNRRS 2935
DB 2903 GDLVRANFTFHLRPLKPLKDFEKSFYKERCEBCKALMA--WNYSFEMORDANDRAS 2960
QY 2936 MBRQSKSGGRPREIYTDATPE-DYNPHVDMTNLTLSREOMNMBRLADNANDIMAKK 2994
DB 2961 AAR-----TLSGTISNPAKPYDILSSMTLEKQVNAALKEAHSHLIMAKV 3008
QY 2995 KEELVT 3000
DB 3009 MNDLNT 3014

RESULT 3
A37113
ryanodine receptor, cardiac muscle - rabbit
N.Alternate names: ryanodine receptor 2
C.Species: Oryctolagus cuniculus (domestic rabbit)
C.Date: 15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change 09-Jul-2004
C.Accession: A37113, S74212
R.Otsu, K.; Willard, H.F.; Khanna, V.K.; Zorzato, F.; Green, N.M.; MacLennan, D.H.
J. Biol. Chem. 265, 13472-13483, 1990
A.Title: Molecular cloning of cDNA encoding the Ca(2+) release channel (ryanodine recept
A.Reference number: A37113, MUID:90337947, PMID:2380170
A.Accession: A37113
A.Stature: preliminary
A.Molecule type: mRNA
A.Residues: 1-4969 <OTS>
A.Cross-references: UNIPROT:P30957; UNIPARC:UPI000013CACB; GB:M59743; GB:J05564; NID:916
B.Niethide, K.; Otsu, K.; Hori, M.; Kuzuya, T.; Tada, M.
Eur. J. Biochem. 240, 408-415, 1996
A.Title: Cloning and characterization of the 5'-upstream regulatory region of the Ca2+-r
A.Reference number: S74212; MUID:96439071, PMID:8841406
A.Accession: S74212
A.Molecule type: DNA
A.Residues: 1-16 <NIS>
A.Cross-references: UNIPARC:UPI000016C523; EMBL:X99486


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QY 1988 -----RKGLLHMKMAEAGKQMCYLLQHLNDIQLRHVEAIIAPADPVGDLQTDQ 2039
DB 1882 EAKYGRKPKKGLQMKLPBPVKLQMKLLQYLCDCQVRHRIEIVAFSDPFAVKLDONCR 1941
QY 2040 RRYTEIKQS-DLPSAVAAKKTREPRCPBREONNAIISFKLLEBDEKENCSCGSELAPM 2098
DB 1942 FRNENWQALNMAHALTKTKERPSBPQOIMMLNFK---DDSECCPEEINDQL 1997
QY 2099 EFHDTIMAHVSLHALQDPDAENQEPBAKPGAKGLYNIINTVELEEE--AKAIEBP 2156
DB 1998 DFHEDIMTHGIEIDEDGSLDGNLDIR---GRLLSVEKTYLKKQTKRPVSDSR 2053
QY 2157 KTEBEKFRKVLQITIVMAEESQIEFPKLYRBMPSLLVRQYDAVGEIIRALETTYINAK 2216
DB 2054 KS---STLQOLISBTWRMQESYIEDPELRAMFVLLHRQYDIGIVRALPTYTYINGV 2111
QY 2217 TKLDVAMWVGLSQIAPALPYQMSOESEELMRKIMWLNNHTFPQHPDLIRLYAHENY 2276
DB 2112 SVEDTINLASLQIISLSLVNMGKEEKLIRGLDINNKVYQHPNLMRALGMHETV 2171
QY 2277 MAVMNTLGRRAQSDAOPSSQPVAEBSKEDTSHMVAACRPLCYFCRTGRQOKAM 2336
DB 2172 MEVWVAVLG-----GGESEKE-ITPPMVANCGRPLCYFRISRQOKAM 2214
QY 2337 FDHPDULENSNIILSRPSLRGSLPDVAVSSLMMENTELALAREHYLEKIAN-YLSRCG 2395
DB 2215 FDHLSTLENSVGLASPAWRGSLPLDVAAASVMDNNELALAREBDLEKVVARYLAGCG 2274
QY 2396 LOSNSELVEKGYPDLCMDPVEGRYLDPLRFQVWNGESEVENANVYRLIRRPCLGP 2455
DB 2275 LOSQMLVSKGYPDIGNPVEGRYLDPLRFVFCNGESEVENANVYRLIRRPCLGP 2334
QY 2456 ALRGE-GEGLLKAIVDANKSERIADRRKLREMOBQDVNFSPHLPES-----DED 2505
DB 2335 ALRGEQNGILAMEBAIKIAE-----DPRQDPSPTSGSKTLDTREBE 2379
QY 2506 EDYIDPQALINFTYCTLVLDLGRCAPDAGYIAGKRESLRAKILNSVPLEDQVLSI 2565
DB 2380 DDTIHNGNIMFTYALIDILGRCAPBEMLIHAKBKAIRIRISILSLPLGLVYVIST 2439
QY 2566 RFTLNPAPAGEERPKSDMPGSLRGHKOSVGLFLERVYGEIOTELPYKLLEBAFLDPA 2625
DB 2440 ARQMPITAKDGNVPEDMASAGFCPDHKAAMVPLDLYGIEVODPLHLLEVGFLPDLA 2499
QY 2626 ATMLDNDNCESDMALSMNRYYIGNSILPLIKHAYFNEAENYASLLDATTLYVRLSKN 2685
DB 2500 AASLDPAALSATDMALANRYLCTAVLPILTRCAPLPAETEHNASLIDSLHTVYRLSKG 2559
QY 2686 RMLTKQREAVSDPLVALTSANOPSMILKILKLTVDVSKLSYTTVALRLTLHYERCA 2745
DB 2560 CSLTKAQORDSIEVCLLSICGLRPSMOMHLRLVDPVPLNHAHAKPLKLTNNHYERCM 2619
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DB 2620 KYICLPB-GWGNFGAASBEELHLSKLPNGIFPALQOKYEOELFKALPCLSAVAGALP 2678
QY 2806 PYSLSKANYDDEFYGEQAAGLDLNPQYDQPIINTSSVALNNDLNTIVOKFSEHYHDAWA 2865
DB 2679 PLY-MESNTVNMW-EKQSSMDESG-NFNPQPYDVTNIIIPKLEAFIKVYAEHSHDKMS 2734
QY 2866 SKRIENGWYVGEWSOSQKTHPLKPYMNLNDYERKRYKPVRESLKALLAIGWSVEHSE 2925
DB 2735 MOKLAWGMYIGEYISDSXKIQPLMKPYKLSBEKEKIYRWPPIKESLKTMLAWMRTERR 2794
QY 2926 VQIPSNRSMRQOSGGRPREIYVDSATPPDYNNHPVDMTMLISREMONABEILADN 2985
DB 2795 ----EGDSNALYKTRIRISOTSOVSDAA-HGYSFRAIDMSNVTLSRDILHAAEMEAEN 2848
QY 2986 AADIWAKKKKEEL 2998
DB 2849 YHNIMAKKKKLEL 2861
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RESULT 4
S72269
ryanodine receptor isoform 2, cardiac muscle - human
N/Alternate names: calcium release channel protein isoform 2
C/Species: Homo sapiens (man)
C/Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #ext_change 09-Jul-2004
C/Accession: S72269
R/Turnell, R.E.A.; Wickenden, C.; Bertrand, B.M.A.; Shevchenko, V.I.; Walsh, M.B.; Allen
Biochem. J. 318, 477-487, 1996
A/Title: The human cardiac muscle ryanodine receptor-calcium release channel: identifi-
A/Reference number: S72269; NID:96404895; PMID:8809036
A/Accession: S72269
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residue: 1-4967 <TM>
A/Cross-references: UNIPROT:Q92736; UNIPARC:UPI0000013594; EMBL:X98330; NID:91526977; P
A/Experimental source: cardiac muscle; sarcoplasmic reticulum
C/genetics:
A/Gene: RYR-2
C/Complex: homotetramer
C/Function:
A/Description: mediates rapid release of Ca2+ ions from intracellular stores during car-
C/Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homolo-
C/Keyword: alternative splicing; calcium channel; cardiac muscle; glycoprotein; heart;
F/10-715/Region: adenine nucleotide binding #status predicted
F/1148-1153/Region: adenine nucleotide binding #status predicted
F/2338-2342/Region: adenine nucleotide binding #status predicted
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F/4844-4867/Domain: transmembrane #status predicted <TM06>
F/440_301/Binding site: phosphate (thr) (covalent) (by CAMP- and calmodulin-dependent kin
F/2808/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status
F/4794/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 43.0%; Score 6769; DB 2; Length 4967;
Best local similarity 45.6%; Pred. No. 0;
Matches 1399; Conservative 536; Mismatches 854; Indels 276; Gaps 58;

QY 4 AEGASBDDVSPFLRTDMVCLSTAT---GERVCLAAGFGNRCFLNIAD-NNIP 58
DB 2 ADGEGE-DEIOFLRTDENVLQCTATIHKEQKCLAEAGFGNRLCFLESTNSKNVPP 60
QY 59 DISOCYFVIEQLSVRALQELVTAAGSENGK-----TSGHRTLYGNMI 104
DB 61 DLSICTFVLEQSLSVRALQELML-ANTVEKSEQVDVEKKYKFMKTAQGGGHTLLYGHAI 119
QY 105 LRLHNSDMYLACLSTS--SSODKLAFDVGLQOHSQGEACMTLHPASKORSEGEKRVGD 163
DB 120 LRLHVSQMYLCCLSRSTSDKLAFDVGLQDITGEACMTLHPASKORSEGEKRVGD 179
QY 164 DLIVSVATERLYLTKNEVSIINASPHVTMSVQPYGTGISRMKYGVYFGGDVLRPF 223
DB 180 DLIVSVSEERYLHLSYNGKSLHVDAAFAQQLTMSVAPISGSEAAQ--GYLIGDVLRL 237
QY 224 HGG-DECLTIPETWKDGGQNIYVYEGGSVMSQAASLWPLLELARTMAGGFLNWHYPMI 282
DB 238 HAHMBECLTVPSGEHGEEDRRVNHVEGAVSVHASSLWPLLELTVAVMSGSHLRWQPFRL 297
QY 283 RHITGRYLVGVDQNELVYSREETAASCAFLQOEKODQOVLEDKOLEYVAPILKY 342
DB 298 RHVTTGKILSLMEDKLLMDKEKADVSTATPSSK-EKLDVGRKREVDGKGTSEIKY 356
QY 343 GDSVIVQHSFTGLWSTYSKYETKKKGKGVKEKQALIHBEGRMDGLDPSRQSEEST 402
DB 357 GDSVCYIQLVDTGLWLTQSVVVKSVRSGISGR-ALMHHEGHMDGILSLRSQHEEST 415
QY 403 ANVIRKCSLPTKFNGLTLOENRRHSMFPAASVNLGEMVMDLEDLINFAQPDMEHE 462
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Db 416 ARVISTVLEFNRRFRGLDALSKKAKAST--VDLPISVSLQDLIGYFHPDEHLEHE 473
 Qy 463 EKONKPRALRNODIPEQEEGILNLIJEADIKINVTSGOFLAGFLAGDSGOGMEMISGX 522
 Db 474 DQONLRALRNKONLEQEEGINTLVLECDRLHVTSSAAHFPAD-VAGREAGESKXILNS 532
 Qy 523 LYOLLAALIKGNHTNCAQFANSNRLNMLPRLSOSQASGEGTGLDYLHCVLIDSPBALM 582
 Db 533 LYELLAALIRGNRKONCAQFSGS--LDWLI5RL--BRLBASGILBVLHCVLVESPALNI 588
 Qy 583 MDEBNIKVILSLBKRGDPKTLVDICSLCVGNVAVRSGONNICVLLPGRKMLLOTLY 642
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 Qy 643 VHVSVRPNIPIVGVSGSAVVRKYBYVTMDIEK-TTHMHPHLIGMANTGYVPG 701
 Db 649 VHVSVSRNPIFGVSEGSQYKMYELMVDHTEPVTAEATHLVGNASTEGSPYIG 708
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 Db 1066 AP--DQDHABABAVCSGTGERPRIIPRAEKTYAVKABWTFEFETVIAAGMRVGMSPGQ 1123
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 Qy 1178 MDALGETTFADVO-GDNVVPACTLGVQKARLTGYQDVNTLKYPTTCGLQBGVEPFCN 1236
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 Db 1243 THRDITMMLSKLPOLOVPNSNR-HIETRIDGTIDSSPCLKVTOKSRGS-QNSMTDLM 1300
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 Db 1333 DLEDYDADSDFEVL---MKTA-----HGHVDPDRVD----- 1360
 Qy 1413 MAKYDLGAQGLTDDKDKRGRGAPPKFPRSKRGESSDRAKSRKXTPDPSPDTEVSPERG 1472
 Db 1361 -----KDKEA-----TKPERN 1371
 Qy 1473 ARRPNOIRVSOANQRYNGKNNAPSRNTLVGSQVGLNMATPTDORQMTSTLAQATET 1532
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Qy 1533 VGNBIFDAECLKLINEFYGVARIYPODPTHVYIGVNTQYHLSKDFENQSKVTXSVII 1592
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 Db 1705 LLIIDHLSYATARLMMNNEYI VPMTEBKSITLPEDEKKGGLPGIGLSTLRPMQOS 1764
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 Qy 1947 KLVDRLLVGMREDDEVEKLIM-----TNPETMDSPDK-----GKOB 1986
 Db 1823 KLFYTLIINGIFHNEIDLKHILOLIBSVFEKATPEEESDTEKLESVDAKIQAAGEEB 1882
 Qy 1987 -----HRKGLHMKABEAKIOMCYLLOHNDIOURHVSVAIIFAHFVGLDLOTDLR 2040
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 Qy 2041 RYTEIKOS--DLPSAVAKKTREFRCPPREONNAIISFKHLEEDKENCPCGBELIARMB 2099
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 Db 1999 FHEDITMHGIEIDBEDGSDGNSDLTIR-----GRLLSTBEKYVYLKKQAEKVESDSXK 2054
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 Db 2055 S--STLQOLISETMVWMAQESVIBDELVRAMFVLLHROYDGLGLVRLPKTYTINQVS 2112
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 Db 2113 VEDTINTULASLOQIRLLSVRQKBEKLMIGLQGIYNNKVPYQHPNMRALGMHEITW 2172
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 Db 2173 EYVNVNVLG-----GGSKE--ITFPMTVANCRFLCYFCRISRONQKMF 2215
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 Qy 2398 SNSLEVEKYPDGLGMPVVEGERLIDPLRFCVWVNGSVSEENANLVIRLIRREPCGAPL 2457
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 Db 2387 AINTFYSAIIDLGRCAPKMHIIHAGKEAIRISITRSLIPGLDVGVSIAFQMPPTIA 2446

Qy 1363 QEBLSSKMKRLPSRPPKSGMTRGVITIQNYNNLQPGVNGMHRSTSEAEAKYDLAGAG 1422
 Db 1349 EKDL-----AKETPKBPK----- 1362
 Qy 1423 LTPDDKDKGKRSFPKFRKSGSSDPAKSR-----KSTPDPSDTEVSEBGRARRNP 1478
 Db 1363 --PENEXO-----TTTEKTKRGGLFKFKKPAFISTPVPV- 1396
 Qy 1479 QIKVSQANORVNGMARRSRRTNLVGSQVGLMAMPYQORQMWTSTLAQSAETGVNEIF 1538
 Db 1397 -----TMRKKEVVPDDRD 1411
 Qy 1539 DAECIKLINEYGVRIYVPGODPTHVYIGMVTTOYHLHSKDPNOSKYTKSSVIIITDDYDR 1598
 Db 1412 DPEIIRMTTYYGSRVAPAGBPTGWIWTLPRYHLIDMFMFLDKVKNANATITMGDDKGN 1471
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 Qy 1839 LESHATMEACKNFVPLIGBELKA--LYEBPMGHSLRSL-QRVSBPQMKMTDIASI 1895
 Db 1709 LESAKRGMTNSETIVMTQTSITLFPENKKGHGPVGWMSCTCLPELBSFTSC-FV 1767
 Qy 1896 TEISNLY--SPYPLEVAREBFVOMALBAVETNQVHNDPVGSGNENLFLPLIKLVDRLL 1953
 Db 1768 STIELVQHSFYIPLDILKTAIMLTESVODGCHTDPVGVSGVFPVVLKLISTLL 1827
 Qy 1954 LVGMARDBVEKLLIMTNPETW---DPSFD----- 1980
 Db 1828 IMGVFQDDVYHILMIBPNVFSBEPAREEGEBEGEKATEKGESEGEVEGEQEKTED 1887
 Qy 1981 -----KEGDHKKGLLMMKMAAGATQWCTYLOHNDIOLBRHVATIAFA 2027
 Db 1888 GBEKTEVEDGAABEERALEBGLQMTLPSVYLQMCNLLQYFCDRLOHREVAIIAFA 1947
 Qy 2028 HDVFGDLOTDQRLRYTEIKOS-DLPSAVAAKKTRBFCPPREOMNALISFKHLEBEDEN 2086
 Db 1948 ERHMDSLQTNQRHRYKELMOPATMSAETAKRTBFRFPBOQIMLVNFKNITBEE-- 2004
 Qy 2087 CPCEBELIARMEFHDLMALHVSIALQEPDAENQEBEAKFGAGLKNYINTVKELEB 2146
 Db 2005 YPVEBEIRDEHIDFHADLHAQGYM-----EGEBEEOBDSLSARRLSLVBKXKOLRG 2059
 Qy 2147 EAKAIEBPCKTPBPK--FRKVLQITVYNAESQITPVLVEMESLRYQYDAVEL 2203
 Db 2060 KKQPEPEBPEQEBKPTLQBELISHTVYNAOESFIONPELVWRFSLRHOYDGLBL 2119
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 Db 2120 IRANPKAYTINAVSEDTMMLLSIGRTSLIYOMGBEERLMAQSIGNIMKNKVFYQH 2179
 Qy 2264 PDLIRVLVHEBNVAVVMMNTLGRRAQASDAQPSQPAVEDSKEDTSHENVAVACRFLC 2323
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 Qy 2324 YFCGTGRNQKAMPHPDPLLENSNILLSRPSLRSTPLDVAYGSLMENTALALAREHY 2383
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 Qy 2384 LKXIAVYLSRCGLQSNBELVKEGYDGLGMDPVGGERYLDPLRFVWVNGSEVENANLYI 2443

Db 2280 LKRVSYLAGCQLOSCPMTLAKGYPDIGWMPVGBERLIDPLRAVFNVGSEVENANVYV 2339
 Qy 2444 RLILRRPCCGPAIRGB-GEGLIKAIYDANKMSRIA-----DRKILREMOEGDVN 2494
 Db 2340 RLILRRPCCGPAIRGBGNGGLGALIDALIKSIDPARDEPTKYKDRR---ELYGG-- 2393
 Qy 2495 FSHPLPSBDEDEDYIDTGAALINFCYLLVDLGRCAPDAGVIALGKNESLRARAILRSIV 2554
 Db 2394 -----BEPHEKNVHIGNAIMSFYALIDLGRCAPBEMHIOGKGBALIRAILRSIV 2447
 Qy 2555 PLBLOQVLSLRFTLNNPAAGER---RPSMDPSGLIPGHOSVGFLELVYGIETQEL 2610
 Db 2448 PIEDLVAGYIS-PLQIPAFGKDGNITBPK--MSASFVPDHKAMVYFLDRVYGIIDQDF 2503
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 Db 2504 LLOVLEGVFLPDMRAAASLDTPAASPTTEMALNNRVLCSAVLPLITKCAPLPSGTERAI 2563
 Qy 2671 LLDATLHTVYRLSKRMILTKGQREAVSDFLVALTSAMQPSMLKILRLTVDSKLSERT 2730
 Db 2564 MVDSMHTHTYLSGRSLITKQGRVIRECLMGLGRFLRPSYLQHLRLRVDFVILNFS 2623
 Qy 2731 TVALRLTLHYERCAKYYGSTGACQGAFGASDSBEKRLTMMLPSNIPDSLSKMDYBPLF 2790
 Db 2624 KMPKLKLTNHYERCMKY-CLPTGMANYGVSEBELILTRKLFNGIFESILAHKRFDAELY 2682
 Qy 2791 GKALPCLIALGCAIPRYSLSKNYDDEFYGEQAAGOLD-NPOYDPOPIINSVALNNDL 2849
 Db 2683 KITMPCCLALAGALPPDY-----VDASTYSTDKKASVADAGNDPKEVETLNVITPEKL 2737
 Qy 2850 NTIVQKSEHYHDAWASRKIENGWYVGEWSDSQKTHPLKPYMLNDYERKRYKPYRE 2909
 Db 2738 DGFINKYAEHHDKMAEBKIQNNMSYGETIDEAKTHPMLRPHYTPSSKDEIRWPIKE 2797
 Qy 2910 SLKALLAIGSVR--HSEVDIPSNNSMRQSGGR--PBEIVTDSATPDPYNPV 2964
 Db 2798 SLKMIAMEMVLEKAREGEED-RTEKTKTKRKISQTAQOTYDPMVQT-----FSPPI 2849
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 Db 2850 DLGTGLTSRLQSMALQALBNYHNTWGRKKVELET 2885

RESULT 6

146646 ryanodine receptor, skeletal muscle - pig
 N/Alternate names: calcium release channel protein
 C/Species: Sus scrofa domestica (domestic pig)
 C/date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
 C/accession: 146646, 146645, S31395, 147133, S26624, A37105, 147212, S18135
 R/Full, U: Otsu, K.; Zorzato, F.; De Leon, S.; Khanna, V.K.; Weiler, J.E.; O'Brien, E.
 Science 253, 448-451, 1991
 A/Title: Identification of a mutation in porcine ryanodine receptor associated with mal
 A/reference number: 146645, MUID:91320118, PMID:1862346
 A/accession: 146646
 A/status: preliminary; translated from GB/EMBL/DBJ
 A/molecule type: DNA
 A/Residues: 1-5035 <FUJ>
 A/Cross-references: UNIPROT:Q29105, UNIPARC:UPI00001101C2, GB:M91452, NID:9164647, PIDN
 A/accession: 146645
 A/status: preliminary; translated from GB/EMBL/DBJ
 A/molecule type: DNA
 A/Residues: 1-614, 'C', 616-5035 <FUJ>
 A/Cross-references: UNIPARC:UPI00001101C1, GB:M91451, NID:9164645, PIDN:AAA31118.1; PID
 A/Submitted to the EMBL Data Library, November 1992
 A/description: Genomic organization of porcine skeletal muscle ryanodine receptor gene
 A/reference number: S31395
 A/accession: S31395
 A/molecule type: DNA
 A/Residues: 1542-2643 <LRB>
 A/Cross-references: UNIPARC:UPI00001741C8, EMBL:X69465

R,leeb, T.; Schmoelzi, S.; Brem, G.; Brenig, B.
Genomics 18, 349-354, 1993
A>Title: Genomic organization of the porcine skeletal muscle ryanodine receptor (RYR1) g
A/Reference number: A48915; MUID:94117003; PMID:8288238
A/Contents: annotation
R,Harblitz, I.; Kristensen, T.; Boesne, M.; Kran, S.; Davies, W.
Antl. Genet. 23, 395-402, 1992
A>Title: DNA sequence of the skeletal muscle calcium release channel cDNA and verificati
.
A/Reference number: 147133; MUID:93036581; PMID:1329581
A/Accession: 147133
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 2-2091, 'A', 2093-3494, 'U', 3496-4163, 'S', 4165-4182, 'R', 4184-4411, 'W', 4413-4974
A/Cross-references: UNIPARC:UPI00001687C5; EMBL:X62880; NID:91936; PIDN:CAA44674.1; PID:
R,Harblitz, I.; Kristensen, T.; Kran, T.; Davies, W.
Submitted to the EMBL Data Library, August 1992
A/Reference number: S26624
A/Accession: S26624
A/Molecule type: DNA
A/Residues: 482-706 <HAM>
A/Cross-references: UNIPARC:UPI00001741C9; EMBL:X68247
R,Harblitz, I.; Chowdhary, B.; Thomsen, P.D.; Davies, W.; Kaufmann, U.; Kran, S.; Gustave
Genomics 9, 243-248, 1990
A>Title: Abslgment of the porcine calcium release channel gene, a candidate for the mal
A/Reference number: A37105; MUID:91065640; PMID:2174405
A/Accession: A37105
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 4785-4971, 'R', 4973-5035 <HA2>
A/Cross-references: UNIPARC:UPI00001666A7; GB:M32501; NID:g164428; PIDN:AAA31022.1; PID:
R,Leibetzer, M.W.; Peitner, J.K.; Louis, C.F.; Mickelson, J.R.
J. Biol. Chem. 269, 31544-31551, 1994
A>Title: Tissue distribution of ryanodine receptor isoforms and alleles determined by re
A/Reference number: A55660; MUID:95081095; PMID:7989322
A/Accession: 147212
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 516-676 <LED>
A/Cross-references: UNIPARC:UPI0000000551; EMBL:U15965; NID:g562095; PIDN:AAA60467.1; PI
C/Genetic:
A/Gene: RYR1
A/Introns: 521/1; 558/1; 598/3; 643/2; 1570/3; 1646/2; 1850/3; 1939/3; 2006/3; 2044/1; 2
A/Note: the list of introns may be incomplete
C/Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homoid
C/Keywords: calcium channel
Query Match 41.0%; Score 6453.5; DB 1; Length 5035;
Best Local Similarity 44.2%; Pred. No. 0;
Matches 1367; Conservative 531; Mismatches 894; Indels 303; Gaps 63;
QY 5 EGGASBDDVVSPLRTEDMVCISCTAT----GERVCLAAEGFGRNRCLENIAD-KNIPD 59
DB 3 DGEGR-DEVOFLRTDEVVLQCNATYKQLKCLAAEGFGRNRCLETSNAQNVPP 61
QY 60 LSGCVFVIEQALSVRALQELV---TAAGSETGKGTSGHRTLLYGNAIILLRHNSDYLA 116
DB 62 LAICCFLEBQSLSVRALQELAVTVEAGVSSQ--GGGHRTLLYGAHILLRHNSGYLIS 119
QY 117 CLTSSSQ-DKAPDVGLQOHSGEACWTLHPASKRSGEKVRVDDILLVSATERY 175
DB 120 CLTTSRMTDKLAPDVGLQDADGEACWTLHPASKRSGEKVRVDDILLVSASERY 179
QY 176 LHTTKENEVSIIVNASSFVTHMSVOPVGTGSRMKYVGVFGDVLRFPHGG-DECLTIPS 234
DB 180 LHTSTASGEIVDASFPQTTIMNMFISGCEB---GYVGGHYLRFHGHMDECLTI-S 234
QY 235 TWTKGQNTVYVEGGSVMSQASLWMLRLARTKMACGFINWYHMKIRHITTYGRYLVN 294
DB 235 PADSDQRLVLYVEGGSVCTHARSLWMLRLPRLISWGSLSHLMWGQPLRIRHVTYGRYLA 294
QY 295 DNEELVYSREKATYASCACLAQEKDDQVLEDDLEVTGAPITIKGISTYIVQHSRT 354

DB 295 EDQGLVVVDASKAHTKATSCFRRISK-EKLDTPAKRDVEMGPPEIKYGSGLCFVQIVAS 353
QY 355 GLMSTYSYETKTKKGVKEKQAILHEBGMDDGLDFSRQSESRATVIRKCSLET 414
DB 354 GLMTYAAPPKYLRIG-VAKKAILHQBEMDALSITCQDESSQAAKVIYTAGLYN 412
QY 415 KPIINGETLOENRHSNFEA--SVNIGEMVCLDELINYPAQPDDEMEHEKONKFRALR 472
DB 413 HFTKGLDSFSGKPRGSGAPAGTALPLEGVTLSLDLIGFEPPEELQHEKQSKLSLR 472
QY 473 NRQDLQEBGILNLILIEIDKINVTISQGLAPLADGEGGQSEMISGVLYOLAAIRK 532
DB 473 NRQSLFQEBGMLSLVNLICDLRLNVYTTAAHFAE-AGEBAESWKEIVNLLEYELASLR 531
QY 533 GNHTNCAQFANSRLNLMLFSLRGS-QASGEGTGLDVLHCVLIDSPEALMMRDEHFKVI 591
DB 532 GNAANCLF--SNNDMLVSKDLRLERS--SGILEVLYCVLIESPEVANIQGNHIXSI 586
QY 592 ISLIERGRDPKVLVDVLSLCVGNVAVRSQNNICDYLPGKNLLQTLVDHVSVRP 651
DB 587 ISLIDKGRHKLVDVLSLCVGNVAVRSQNNICDYLPGKNLLQTLVDHVSVRP 646
QY 652 NITVGRVAGSAYRKYFEFTMDHIEK-TTHMPLHRLIGANTTYVYRGGEGKMGNG 710
DB 647 NITVGRVAGTQYSKYFEFTMDHIEK-TTHMPLHRLIGANTTYVYRGGEGKMGNG 706
QY 711 VGDDIYSYGPDAVYLSGGRKTPVNRTHAEPYRKGDVGCALDITVPIINFMGNRV 770
DB 707 VGDDIYSYGPDAVYLSGGRKTPVNRTHAEPYRKGDVGCALDITVPIINFMGNRV 764
QY 771 TSGFTFNIEGMFPVYISGSKLSRPLGEGHRLRYAAEGSYPLVESLLPQOLISLE 830
DB 765 QGFEAFNLINGLFFPVVFSAGVYRFLGGRGKFEFLPPGPAPCHBAVLPRELRLE 824
QY 831 PCYFPGNLSRA--LAGPRLVQDDTAVPVRVDTLQITLPTVYQIRDKLAENIHEMAM 888
DB 825 PIKEYREGRGPHLVGPRCSHTDFPVPVTVQIVLPRHLERIREKAENIHEMAM 884
QY 889 NKIEAGMYGDDQREDLKIHPLCLVPEPRLPRAEKRDIOALAVOTLKLALGYIYL-D 946
DB 885 TRIEQWYTPGVYDNDKRLHPLCLVDFHSLPEPRRYNINLQMSGETLKLALGCHVGAD 944
QY 947 KPPARIRNVLNPEPMQSNVGYRPLDLSAVTLTPKMDLVOLAEINTNLAREEIQ 1006
DB 945 KADNIRKTLCP-KTYMMSGYRPAPLDLSHVALTPAQTLVYRLAENGHWARDRVAQ 1003
QY 1007 GWTYGLNEDSDMHRSHLVYPRKVDALIKKANDTASVYRITLLVGYMLDPPREGHEA 1066
DB 1004 GWSYSAVQDIPARRNPLVPRYRLDERTKRSNDSLCQAVRTLLGYGNIERPQDEPSQV 1063
QY 1067 LLLASKOKQADPRTYRAEKYAVSSGKYFEFEILTLAGPMRVGMADMAPGMMLGQDE 1126
DB 1064 ----ESQSRMDRRIIRAESYAVQSGRYFEEBAVTTGEMRGMARPELRPVELGAD 1119
QY 1127 NSMAPDYNEEKYYSNTGESFGQMAVGVGVFLDLIDKTSFSLNGELMLDAGEYT 1186
DB 1120 LAYFVGHGQRWHLG-SELFGPRMQSGDVVGCIMDLTENTITLFTLNGEVLMDSGSETA 1178
QY 1187 FADVQ-GDMPVPRCTGVQVQKALTYGQDVNTLKYTTTGLQSGYRPPCMMRDVTHNY 1245
DB 1179 FRIEVDGFLPVCISLGPQVGHNLNAGOVSSLRFAIIGLQGFEPFALNMPRPVTTWP 1238
QY 1246 TKDQPIFENTDEMIDRIVTRIPASDTPPCIKISHTFETMEK-ANNEFLRLSLPVIC 1304
DB 1239 SGLSPFEAV-PLFNHYEVSRYDGVYDVPICRLRHLRHTMGSNLSVEMFLRLSLPVIC 1297
QY 1305 HNEFIDEAKARWWEIKDROQILMKEAVEAQMPRAHIDIMSGFTMNDIKGLHYEDNOR 1364
DB 1298 HQHFRCTA-----GAT----- 1308
QY 1365 ELPSSMKRLPBRPPKSGMTGVTIQNNINLQPGVNGMHRSTSAEMAKYDLGAGLT 1424
DB 1309 -----PLAPP-----GLQF-----PADE-----ARAAE 1327

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1425 PDDKCDKRGSPFKFRRSKGESSDRAKRSKSTPPDPSDTEVSPERGARRPNQIKVSO 1484
1328 PDPEYBILRSAGWGEABEGKEGTAKGAPGCTAQ--AGVEADPPRA--ENKEDATTE 1382
1485 ANORYNGMNAAPSRHTN.YGSGVGLMMATPTDOKQMTSTSLAQASATTV--GNBI.FDAECL 1543
1383 KNKK-----RGFLFKAKGAMMTQRP-----ATPFLPRLPHVEVPADDDDDPDI 1427
1544 KLINBYGYGRIYTGODPTHYITGVYTTQYHLBKDPKQSKVTSVYITDDYRVAVNV 1603
1428 LMTTYYYSRVAVFAGQBS.CWVGWVTPDYHQHDMNDLTVCRAVYTMGEQGNHISL 1487
1604 NROSCYVRADELNEVMAEATAGASGMPFSGSVPTSGSVFTCEGDKTSFKPKMER 1663
1488 KCSNCIHWGDF---VSPQGGRI.SHTDVLITGCLVDLATLMTFTANGKSNSTFFQVER 1544
1664 ETKLPRAIPVEATSKELIQELGRSATSLPLSAAVLP.TSDKHVLPQPPRLKVOCLKPHQ 1723
1545 NTKLPAVAVFVLP.THQVNIQFELGKQKIMPLSAAAMP.LSBRKNPAPQCPRLMGMMPVS 1604
1724 WAPVNSLOVHALKSDIRGSM.LCEDAVSM.LAHIPBEDICDILPEIMDKLSFHS 1783
1605 MSRPNHFLRVETRAGBRLGMAVOCBP.LTMALH.IPEENRCMDI.LELSERLDLOQFHS 1664
1784 HTLFLVLAALCYOSVYRAAHALCTHVQKQLIYAIOSQVMSGRLRGFPYDLILALHLSHA 1843
1665 HTLFLVAVCALGNRRVAHALCSHVDAQQLHALHEDAILPEPLRAGYIDLILSHLSAC 1784
1844 TYMEACKNBFVLP.LGPBLKAL-----YEPDMGHSLSL--QTESVRP----- 1884
1725 RSRSMSLSBYVLP.LTPETRAITLTPPGKRTENGPRRHGLPGVYTTGRLRPHHSAPCV 1784
1885 -QKMTDIASITEITSM.LYSYPPLEVARFEFMQALAEVTTQVNRNDPVGSGNEMFL 1943
1785 AALPAVGAABAPAL-----SPSIPLEALRD.KALHMLGEAVDGGQAHADPGSGVVERQV 1840
1944 PLILVLRILLVGMNRDEDEVEKLI.MTNPETW-----DPSFKGKDEHRK----- 1989
1841 PVLKLVSTLVMGIFGEBDVAKQILMTEPEVFTEEBEESBEEBEEBEEBEEBEEBEE 1900
1990 -----GLLHMMAEGAKLQMCYLLQHLNDLQLRHVEAII 2024
1901 AREKEDBKBKEEFTABGBKERYLEBGLQMKL.PPSVQLQKMLLEYFDQDELQHRVSLA 1960
2025 AFAHDFVGDLDQDLRRY--TEIKOSDLP.SAVAAKTBFCRPPREQKNAIISFHLBEB 2083
1961 AFAERYVDKIQANORDRYGILMKAF.TWTAAETARTRETFESPPQEOINMLLHFK--DGED 2018
2084 KENPCGBELIARMBEFDTLMAHVSL.HALQEPRAENQBEAKGAFGKLYNIINTYKE 2143
2019 BEDEPLRDEIRQDLLEFHQDLTHCGIQOL-----EGEBEESBEEATYIGSRMLSLKRL 2073
2144 L-BEBAKAIEBP--KCTPEEKFRKVL.IQTIVNMAEESQIETPKLVREMFSLVROYAVG 2201
2074 VKCKEESBEEPRABEKGQSLQELVSTTVRMAQ.BDVQSBELVRAMFSLRHQYDGLG 2133
2202 ELIABEKTYVINA.KTLDVAEMVVGSLQIRALI.PVQMSQEEBELMRQLKLVNHTFF 2261
2134 ELIALPRAVYITSSVEDTWSLLECLGQIRSL.IVQMGPOEBENIMQISIGINMNKIFY 2193
2262 QHPRLLIVLRVHEVMVVMVMTLGRBAQSDADAPSSPVVADSEKEDTSHEMVACRF 2321
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2322 LCYFCRTGRQKQKAMPFDFELKNSNITLSRPSL.RGSTPLDVAVYSIMBETELALARE 2381
2237 LCYFCRISRQKQRMFHLSTLNSGLG---GMQGSTP.LDVAAASYIDNNELALALQGE 2293
2382 HYLEKIAVLSRGLQNSSELVEKGYPLGMDPVYBGERIYDPLR.PCWVNGESVYEBNALT 2441
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Qy 2442 VIRLLIRREPCLAGP.LNGE--GEGLLKALVANDAKMSERIA-----DRKKLRMEQGD 2492
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Qy 2493 VNFSHPLPESDEDEBDYIDTGAALINPYCTVLVDLGRCAPDAGVYALGKMSLRARALRS 2552
Db 2409 -----EESPENRVLHGAIAIMS.FYAAIIDLGRCAPEHWHLOAKGEGALRIARALRS 2460
Qy 2553 LVPLEDLQVLSLRF.LTANPAGEE-----RPKSDMPGLIPGHKQSVGLFLERYYGLETQ 2608
Db 2461 LVPLDLDLVGILSL--PLQIPTLGGDGLVQPK--MSASFVPDHAASVLP.LDHYGILENQ 2516
Qy 2609 ELFYKLEBAFLPDLRAATMLDRNDGCSMDALSMNRVIGNSILPLLIKAYFYNEAENT 2668
Db 2517 DFLHVLVDVGLPDMRABASLDATPSTETMALANRYLGLAVLP.LITKCAP.PAGTEHR 2576
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Db 2577 AIWDSMLHTVYR.LSRGRSLTKQRDVIRECLMALCRYIRPSMLQHLRLRLVDPVPLTB 2636
Qy 2729 YTTVALRLTLHYERCAKYYGSGTGAQAGASDSEKRLTMM.LFSNIFDLSLMDYEP 2788
Db 2637 FAKKPLKLTNNHERCKKTY--CLEPTGANFVTSBESLHLTRKLFMGLIFSLAHKTYDPE 2695
Qy 2789 LFGKALPCLIAIGCALPPDYSLSKYDDEFYGEQAAGDLD--NPQYDQPIINTSVALLN 2847
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Qy 2848 DLIATVQKFEHYHDAVASKIENGWYVYGGMSDSQKTHPRLKYPMYNDLBEKERYKPV 2907
Db 2751 KLSDFINKPABYTHEKAPDKIQNMWSYGENIDBELTTHMLP.PYKTFSEDKIYWPPI 2810
Qy 2908 RESIKALLAGMSVHSEVDYIPSNRSMRQSGRSGRPPIYVDSATPPD---VYHPH 2963
Db 2811 KESIKAMIAEWETI-----KAREEKEETKCKTKRKISQSAQTYDAREGINPQ 2860
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RESULT 7
A35041
Ryandoline receptor type 1, skeletal muscle - human
N:Alternate names: calcium release channel protein
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text, change 09-Jul-2004
C:Accession: A35041; 184622; 566630
R:Corraco, F.; Fujii, J.; Otsu, K.; Phillips, M.; Green, N.M.; Lai, F.A.; Meisner, G.;
J. Biol. Chem. 265, 2244-2256, 1990
A:Title: Molecular cloning of cDNA encoding human and rabbit forms of the Ca(2+) release
A:Reference number: A35041; MUID:50130482; PMID:228749
A:Accession: A35041
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-5032 <ROR>
A:Cross-references: UNIPROT:P21817; UNIPARC:UP1000055A9F; GB:J05200; NID:g337721; PIDN
R:Otsu, K.; Phillips, M.S.; Kanna, V.K.; de Leon, S.; MacLennan, D.H.
Genomics 12, 835-837, 1992
A:Title: Refinement of diagnostic assays for a probable causal mutation for porcine and
A:Reference number: 146644; MUID:92347887; PMID:1639409
A:Accession: 184622
A:Status: translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 598-722 <RES>
A:Cross-references: UNIPARC:UP1000016AFDE; GB:M91455; NID:g337723; PIDN:AAA60295.1; PID
R:Lynn, S.; Morgan, J.M.; Lamb, H.K.; Meisner, G.; Gillepie, J.I.
FEBS Lett. 372, 6-12, 1995
A:Title: Isolation and partial cloning of ryanodine-sensitive Ca(2+) release channel pr
A:Reference number: 566630; MUID:96032536; PMID:7556644
A:Molecule type: mRNA
A:Residues: 4690-4968 <LYN>

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A:Cross-reference: UNIPARC:UP100001741C7
A:Experimental source: myometrial smooth muscle
C:GeneID: 81
A:Gene: GDB:RYR1
A:Cross-reference: GDB:120359; OMIM:180901
A:Map position: 19q13.1-19q13.1
A:Initrons: 642/2
C:Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homolog
C:Keywords: calcium channel; homotrimer; phosphoprotein; skeletal muscle; transmembran
F:1788-1984/Domain: transcription initiation factor sigma region 1 homolog <SR1>

Query Match 40.9%; Score 6442.5; DB 1; Length 5032;
Best Local Similarity 44.3%; Pred. No. 0;
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QY 56 IPPDLSCVFIQALSVRALQELV---TAAGSTGKTGSGHRTLLYGNAILLRLNSD 112
D 57 VPPDLATCCFVLESGSLSVRALQELMANTVAGVSSQ---GGGHRITLLYGNAILLRHAHSR 114
QY 113 MYLACISTSSQ-DIKLAFDVLQGHSGCAQMTLHPASKORSRGEKVRGDDLLIYSA 171
D 115 MYSLCLTTSRSMTDKLPDVLQEDATGEACQMTMHPASKORSRGEKVRGDDLLIYSA 174
QY 172 TERYLHTTKENEVSIVNASFHVTHMSVOPYGTGISRMKYYGVYFGDVLRFPHGG-DECL 230
D 175 SERLHLSTASGELQVDASFMQTLMMNPI---CSRCE-BGFVYGGHVLALFHGHMDECL 230
QY 231 TISTWTGQGNIVVTEGGSVMSQASRLBELARTKMAAGFLNMYHPRIRHITTGARY 230
D 231 TI--SPADSDQORRLVYVEGAVCTHARSILWLEPLRLISWGSGLRMQCPRLRVHVTGGY 289
QY 291 LGVNDQNELVYSEBEATTASCAFCLEQEKDQOVLEDKLVIGAPIIKYGDSTVIYQ 350
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D 702 GGNVGGDDLSYGFDAAYLWSGRKTPVNRTHAEEPIRKGVYGCALDITVPLINMFN 759
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D 760 GCPVQGFESFNLIDGLFFPVVPSAGVKAFFLLGGRHGEKFLPPPGVACHEAVLPRR 819
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DB 999 RVQGWSTYSAVDIIPARNRPLVPLRLDRTKSNDSICQAVRTLLGVTNIBPDQ 1058
QY 1063 QHEALLLEASKOKAD-FRTYRAEKYVAVSSGKYEFEFLITGPMRVGMAHDMAPGM 1121
DB 1059 PS-----QVENQSCRVRIFRAEKSYTQSGMYTEFEAVTTGEMRVGARBELARDE 1113
QY 1122 LGQDENSMAFDGYNEEKVYSGNTSEFGKQMAVGVFLDLIDKTISEGLBELMDAL 1181
DB 1114 LGADELAVYFNHGRGQRMHLG-SEPPGRPMQPDGVGCMIDLIENTIIFTLNGBVLMSDS 1172
QY 1182 GGETPADVQ-GDNFVPACTIGVGAKRLTYGQDVNTLAKFTTCGLQEGYBPCVMKRD 1240
DB 1173 GSETARRELEIGDFLPVCSLPGQVGHNLGQDVSSLRFAICGLQEGYBPCVAINQRP 1232
QY 1241 VTHMYTKDQPIPENTDMLDTRIDVTRIPAGSDTPCLKISHNTPEMTEK-ANMEPLRLS 1299
DB 1233 VTTWTFKGLPQEPFV-PLSHPHYEVSIRDGVDTTPCLRLTHRTWSQNSLVMLFLRLS 1291
QY 1300 LPVTCNEPIDEAEKRRVWEIKDROOILMKEAVEAMPAHIDQIMRSGTMMNDIGLAY 1359
DB 1292 LPVQFQHFQCTA-----GATPLAPPL-- 1314
QY 1360 EDQBELSPKMYRLSPRPKSGMTGVTIONYNLQEPQVNGMHRST--SEAEAKY 1416
DB 1315 -----QPAEDBAABEDPYENK-----RSAGMSBAENKGE 1349
QY 1417 DL---GAOGLTPDDKKDGRSPFKFPRSKRGSSDRASRSKTPDPFSDEVSPERG 1473
DB 1350 GTAKEGAPGPT-----QAGRGAP-RAENKQAT-----TEKNKRGF 1387
QY 1474 RRPNPQIKYSQANQRYGNAPRSRTNLVGSQVGLMAATPTDORCKMTSTLAQATETV 1533
DB 1388 LPRKXKV-----AMTQPR-----ATPLPR-----LPHDVVAD 1417
QY 1534 GNEIPFAECLKLINEFYGRITPGODPTHVYIGVWTVGYHLSKDFQNSKVTKSSVIT 1593
DB 1418 NRD--DPEIILNTTYTYSVRVAGQBPSCVMAQVTPDTHQMSFDSKVAVTVTWG 1475
QY 1594 DDYDRVENVNRQSCYVNRADBELVNEVMAEATKASQGMFIGSVDTSTGSVFTCEGK 1653
DB 1476 DEGNVHSSLSKNSCNQMWGSDP---VSPQQRISHTDLVIGCLVDLATGMLTFRANGK 1532
QY 1654 DTSFKKMBEYTKLPALITVATSKELQIEGRATSLPLSAVLTPTSDKAVIPQPPR 1713
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DB 1593 LEMQMLPVSWSMPEHFLQVETTRRGERLGMVAVQOQEPVLTMLALHPEENRMDLLES 1652
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DB 1653 ERDLQRFHSHTRLRYALCALGNRRVNAALCSHDQADLHLEBAHLRGPRLAGTYDL 1712
QY 1834 LIALHLESATTEACKNEFVILPGLBELKALYEBP-----DMGSLRSIQ---TESVRP 1884
DB 1713 LISIHLESACRSRSMLSSEIVLTFETRAITLTFPGRSTENGPHRHGPGVGVTTSLAP 1772
QY 1885 QMKMTD-----LSEITFEISNLVSPVPLVAREFVQALAEAVETQVNHNRDVGGS 1937
DB 1773 PHHFSPPCVALLPAAGAABAPRUSPALPLEALRDKALRMGEAAVRDGGQHRADVGAS 1832

1936 NEULPPLKLYRLLLVGMARDDEVEKLLIMTNPETW-----DPSFKGKDEBRK- 1989
 1833 VERQFPVVKLVSTLVMGIFGDEBDVQIILKMTIEPIFTEBEEDEDEBEEBDEBEEKE 1892
 1990 -----GLIIMMAAGAKLQWQCYLLQHLNDIQLRH 2018
 1893 EDEBEETAQBKDEBKEBBAABEGKEBGLQWMLPSSVKLQWCHLLEYPCDQELQH 1952
 2019 RVEAIIAPANDPFGDQDQRLRY-TIKOSDLSANAACKTTERFRPREBOMALISRK 2077
 1953 RVESLAAFAERYVDKIQANQSRGILLIKAFSMTAARTTRFRSPPOBQIMMLQFK 2012
 2078 HLEBEDKENCPCBELLARMBNPFIDTMAVSHALQEPDALEQBEBAFGAKLYNI 2137
 2013 --DGTBEDCPLEBEIKQDLDHFDHLLAHGCLQ-----DGESEBEEETTLGSRMLS 2065
 2138 INTVK-----BLEBEAKAIEBPCKTPEKPRKVLQITVWMBESQIETPLVREMP 2190
 2066 LEKRVLVKKKBKREBERSABESPRSLQ-----LVSHMVVRAQEDPVOSEPLVRAVF 2120
 2191 SLVROYDAVGEILRALEKTYVINAKTKLVAKEMVGLSQIRALLPVQMSQEBELMKR 2250
 2121 SLIHRQYDGLGELIRALPRAVTTISPSSEVDTMSILECTQIRSLIYQMGPOBENLMIQS 2180
 2251 LMKLVNNHTFPOHDLIRVLRYHENVVWAMVNTLIGRAAQSDAQSPSQVABDSKXKOT 2310
 2181 IGIMNNKVFYQHNLMLRALGMHTVMEVWNVLG-----GGESEK-IR 2223
 2311 SHEMVVACSRPLCYFCRTGRQONKAMPDHPDLLNSNILLSRPSLNGSTPLDVAVSLM 2370
 2224 FPMGVVSCRFPCFICISQNRQSMVDHLSYLENSGIGL---GMGSGIFLDVDAASVI 2280
 2371 ENTETLALAEHNYLEKTAVLSRCSGLQSNSELYEKYPDJGMDPVESEKRLDFRCPVWV 2430
 2281 DNNEELALALQEOBLEKVASVLAGCQSCPMPLVAKGPDJGMRKCGSERVLDLFRVAVFV 2340
 2431 NGRSVENANLVRLIRREPCICGPRALRG-GEGLIAYIDANQMSERIA-----DR 2481
 2341 NGRSVENANVVRLLIRKEPCFPRALRGEGSGLLAIEBARIRISDPADRGCGIRDR 2400
 2482 RKLRREMOEGDVNFSHPLEPSDEDEYIDTGAAIINFYCTLVLDLGRCAPDAGVIALGKN 2541
 2401 RR-----BHFQ-----BEPRENNVHGHAINSTYVALIDLGCABEMHLLQAGKG 2447
 2542 ESIRAPARILSLVPLEDQVLSIRFTLNNPAAEE---RPSKDPMSGLPGHKOSVGL 2557
 2448 EALRIRAILRSLVPLEDVGIIISL--PLQIPTLGKDGALVQPK--MGASFPVPHKASML 2503
 2598 FLERVVCIETQELFYKLEEARFLPDLBAATMTLNDGCSBDMLSMNRVYIGNSTLPLIK 2657
 2504 FLRVVGIENODFLHLVLDVGFPLRMDPAASLDATSTTEMLAVNRYICLAVLPLITTK 2563
 2658 HAFVYNEAENVASLLDALTHTVYRLSKRMULTKQORAVSDPFLVALTSAMOPSWLLKLR 2717
 2564 CAPLPACTEIRALVWDSMLHTVYRLSRGRSLTKQROVIDCLMSLCRYIRFSPSLQHLIR 2633
 2718 KLTVDVSKLSBYTTVALRLTLHYERCAKYYGSGAOGAFGASDEBKLTMMLPSNIF 2777
 2624 RLVDVPIILNFAKMPKLTLNHYERCMKYV-CLPTGMANFVTSBEELHLTRCLFGMIF 2682
 2778 DLSKMDYBEPLEFKALPCLIAIGCALPPDYSLSKATYDDEYEGEOAAGLD-NPQVDPQ 2836
 2683 DSLAHKKYDPELVWMPCLCALAGALPPDV---VDASYSVAEKKATVDAAGNDPFR 2737
 2837 PINTSVALNNDLNTIYQFSESHYDAWASHKRIENGWYGEGBWDSQKTHPRLKPYMLN 2896
 2738 PVELTANVTIPEKDSFINKRAEYTHKMAKPKIKNNMSYGNIDBELKTHMLRPYTPFS 2797
 2897 DYKERYKEPVRESLKALLAIGSVESHEVDI PSNNRSMKROGSKGGRPEIYDTSATP 2956
 2798 EKDKIYRWPIKSLKAMIAEWETIE-----YARBESEKTEKKTAKISQASQOT 2847

QY 2957 FD-----YNPVPDNTLITLSREKQNAERLADNAHDIMAKKKEEL 2998
 Db 2848 YDPREGYNPQPPDLASVTLISRELQAMAEALENYHNTWGRKKQOEL 2893
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 B35041
 Ryanodine receptor, skeletal muscle - rabbit
 N/Alternate names: calcium-release channel protein; junctional channel complex
 C/Species: *Oryctolagus cuniculus* (domestic rabbit)
 C/Date: 27-Jul-1990 #sequence, revision 10-Mar-1994 #text, change 09-Jul-2004
 C/Accession: S04654; B35041; A36181; S53794; S32504
 R/Accession: S04654; B35041; A36181; S53794; S32504
 A/Title: Primary structure and expression from complementary DNA of skeletal muscle rya
 A/Reference number: S04654; MUID:89262082; PMID:2725677
 A/Accession: S04654
 A/Molecule type: mRNA
 A/Residues: 1-5037 <TAK>
 A/Cross-references: UNIPROT:P11716; UNIPARC:UPI000013C4CA; EMBL:X15750; NID:g1709; PIDN
 A/Note: part of this sequence was confirmed by protein sequencing
 R/Zerzato, F.; Fujii, U.; Otsu, K.; Phillips, M.; Green, N.M.; Lai, F.A.; Meisner, G.;
 J. Biol. Chem. 265, 2244-2256, 1990
 A/Title: Molecular cloning of cDNA encoding human and rabbit forms of the Ca(2+) releas
 A/Reference number: A35041; MUID:90130482; PMID:2298749
 A/Accession: B35041
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-66, 'Y', 68-2014, 'D', 2016-3246, 'E', 3248-3480, 3486-4497, 'LR', 4498-4521, 'Q', 4
 4748-4758, 'N', 4760-5037 <2OR>
 A/Cross-references: UNIPARC:UPI000017CF33
 R/Marks, A.R.; Tempst, P.; Hwang, K.S.; Taubman, M.B.; Inui, M.; Chadwick, C.; Fleische
 Proc. Natl. Acad. Sci. U.S.A. 86, 8683-8687, 1989
 A/Title: Molecular cloning and characterization of the ryanodine receptor/junctional ch
 A/Reference number: A36181; MUID:90046851; PMID:2813419
 A/Accession: A36181
 A/Status: nucleic acid sequence not shown; not compared with conceptual translation
 A/Molecule type: mRNA; protein
 A/Residues: 'X', 1223-1235, 'XX', 1238-1251, 1334-1348, 1566-1569, 'X', 1571, 'X', 1573, 1597-160
 -4679, 'X', 4681-4689, 'X', 4691-4693, 'X', 4695, 'X', 4697-4700 <MR>
 A/Cross-references: UNIPARC:UPI0000177940; UNIPARC:UPI0000177941; UNIPARC:UPI0000177942
 947
 A/Note: the proteolytic fragments sequenced here from the junctional channel complex as
 R/Varasny, M.; Meyer, H.B.
 Biol. Chem. Hoppe-Seyler 376, 45-49, 1995
 A/Title: Sarcoplasmic reticular Ca(2+) release channel is phosphorylated at serine 2843
 A/Reference number: S53794; MUID:95336639; PMID:7612188
 A/Accession: S53794
 A/Molecule type: protein
 A/Residues: 2841-2852 <VAR>
 A/Cross-references: UNIPARC:UPI0000177948
 R/Ikebe, H.; Nishimura, S.; Nishitani, M.; Ikeda, M.; Sugimoto, T.
 FEBS Lett. 322, 105-110, 1993
 A/Title: A brain-specific transcript from the 3'-terminal region of the skeletal muscle
 A/Reference number: S32504; MUID:93245969; PMID:8097730
 A/Accession: S32504
 A/Molecule type: mRNA
 A/Residues: 4163-5037 <TAM>
 A/Cross-references: UNIPARC:UPI0000177949
 C/Superfamily: ryanodine receptor; transerption initiation factor sigma region 1 homol
 C/Keywords: calcium channel; glycoprotein; phosphoprotein; skeletal muscle; transmembra
 F/699-704/Region: adenine nucleotide binding
 F/841-954, 955-1068/Region: 114-residue repeats
 F/1344-1359, 1371-1386/Region: 16-residue repeats
 F/1789-1985/Region: transerption initiation factor sigma region 1 homology <SRI>
 F/2370-2375/Region: adenine nucleotide binding
 F/2725-2844, 2845-2958/Region: 120-residue repeats
 F/4564-4580/Domain: transmembrane #status predicted <TM1>
 F/4541-4666/Domain: transmembrane #status predicted <TM2>
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 F/4918-4937/Domain: transmembrane #status predicted <TM4>
 F/128, 286/Binding site: phosphate (Thr) (covalent) (by cAMP- and calmodulin-dependent k
 F/2843/Binding site: phosphate (Ser) (covalent) #status experimental

2029 DPAVDLQTDQLRRYTEIKQS-DLPSAVAAKTRFRCPPREONNALISFKLBEEDKENC 2087
2088 PCGGEELIARNEPFDITLMAHVSLLALQSPDAAEQOEPAKFGAKKIYNIINTYKELEEE 2147
2022 PLPEDIDQDODFDQDILAHGCIOL-----EGEHEEBEBEETSLSRSRLLETALVYKCK 2076
2148 AKAIIEE--PPKKEEBEERKAVLIQTIYVMAEESQIEPCKVREMFSLILVROYAVGELIR 2205
2077 EKEKEEELPAEBKKPQSLQELVSHMVRMAQEDYVQSEBELVRANFSLHROYDGLGELIR 2136
2206 ALEKTYVINAKTKDLVAMWVGLSQRALLPVQMSOESEBELMRRLKLVNNTFPQHPD 2265
2137 ALPAAVITSPSSVEDTMSLIECQISLILVQGPQEBNLMIGISGINNNKVFYQHPN 2196
2266 LIRVLVHENVMAVMNTLGRRAQSQDAPQSSQPAVADSKEKOTSHBMYVACCRFLCYF 2325
2197 LMRALGMHETVMEVWVNLG-----GGETKE-IRFPMVTSCCRFLCYF 2239
2326 CRTROROKAMPDHPDLBENSNILSRPSLRGSTPLDVAVSSIMMENTELALREHYLE 2385
2240 CRSRQORSMFHLSTYLBNSIGL---GMQGSTPLDVAAASYIDNNELALQEBDLB 2296
2386 KIAVYLSRCGLQSNSEIVEKGYPDLGNDPVGERYLDPLRFCVWVNGSBVENANLYRL 2445
2297 KVVSYLAGCGIGQSEPMILAKGYPIGNNPCGGERYLDPLRAVAVNGESVENANVYRL 2356
2446 LIRREPLCGPALGE-GEGLIKAIVDANKSERIA-----DRKLRKEQEGDVNFS 2496
2357 LIRKPECFGRPALRGESGGLAAIEBAIRISEDPARQPGVRRRRR---EHFG----- 2407
2497 HPLPESQEDREYIDTGAALINFCYTLVDLGRCAPDAGVIALGNESIRARALIRSLVPL 2556
2408 ----EPPREBRRVHLGHAINSFYALIDLGRCAPEMMLIOAGGEALRIALIRSLVPL 2463
2557 EDLOGVSLRFTLNNPAAGBE---RPKSDMPGSLIPGHKQSVGLFLERVYGIETOEFLY 2612
2464 DDLVGIISL--PLQIPITLKGXGALVQPR--MSASFVDPHKASVMLFLDRVYGINQDPL 2519
2613 KLBEBARPLDILRAATMLDRNDGCSDMALSMRYIGNSILPLIKHAFVFNBAENVASL 2672
2520 HVLQVGFLEPWRRAAASLDIATFTSTTEMALINRYICLAIVPLITKCAPLFGATEBRAIMV 2579
2673 DATLHTYRLSKNMTLTKGQREAVSDPLVALTSAMQSBMLKLARKLTVDSKLSKTTV 2732
2580 DSMHTYRLSRGRSLTGAQDVIDECLMALCRYIRBSMLQHLIRLFLFDPVILNBFKAM 2639
2733 ALRLTLHYERCAKYGSTGAGQAFGASDBEKRLTMMLPFNSIPDSLSKMDYEPFLFGK 2792
2440 PLKLTHTHYERCKYTY-CLPTGMANFGVTSBEBELHTRKLFMGIFPDSLAHKVQOELRYM 2698
2793 ALPCLLIGCALPPDYSLSKNYDDEFGKEQAAGLDL-NFOYDPOPIINTSSVALNNDLNT 2851
2699 AMPCLCAIAGALPPDY-----VDASYSKAKKATVDAEGNFDPRPVETLLAVIIPKLD 2753
2852 IVQKPSREHYHMAASRKTIENGVYGEQMSDQKTHPRLKPYNMLNDYKEKYPVBSL 2911
2754 PINKPABTYHEKMAFDKIQQNWSYGENVDEBLKTHPMLRPKYTSEKDKELIYRWPIKESL 2813
2912 KALLAIGSVSEHSKVDIPSNRRSMWRQSKSGRPPELVTSATPFD---YNHPVDMT 2967
2814 KAMLAEMTIIKABEG--EERTKCKTKRK-----ISQTAQYDPRBEGTNQPPDLS 2863
2968 NLTLSREMONNAERLADNADIWAKKKEEL 2998
2864 GVTLSRELOAMARQOLABRYNHTWGRKKQEL 2894

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874173
ryanodine receptor 3 - Mustela sp.
C/Spectres: Mustela sp.

C/Date: 23-Apr-1998 #sequence_revision 01-May-1998 #text_change 09-Jul-2004
C/Accession: 574173
C/Merzajali, G.; Rossi, D.; Giannini, G.; Charlesworth, A.; Sorrentino, V.
FEBS Lett. 394, 76-82, 1996
A/Title: cDNA cloning reveals a tissue specific expression of alternatively spliced tra
A/Reference number: 574173; MUID:97074208; PMID:8925932
A/Accession: 574173
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-4859 <MAR>
A/Cross-references: UNIPROT:Q7M2T9; UNIPARC:UPI000017CE14
A/Experimental source: mink lung epithelial cell line CCL64
C/Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homolog
C/Keywords: alternative splicing; calcium channel; glycoprotein; phosphoprotein; trans
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F/2714-2792/Domain: repeat #status predicted
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F/3862-3880/Domain: transmembrane #status predicted <TM2>
F/3914-3932/Domain: calcium binding #status predicted <CAL>
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F/4184-4204/Domain: transmembrane #status predicted <TM4>
F/4399-4420/Domain: transmembrane #status predicted <TM5>
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F/4659-4678/Domain: transmembrane #status predicted <TM8>
F/4701-4720/Domain: transmembrane #status predicted <TM9>
F/4736-4759/Domain: transmembrane #status predicted <TM10>
F/130-290,1243/Binding site: phosphate (Ser) (covalent) (by cAMP- and calmodulin-depend
F/2706/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status
F/4686/Binding site: carbohydrate (Aam) (covalent) #status predicted

Query Match 40.9%; Score 6438.5; DB 2; Length 4859;
Best Local Similarity 43.7%; Pred. No. 0;
Matches 1336; Conservative 513; Mismatches 843; Indels 363; Gaps 50;

4 AEGGASQDDVSPFLRTEDMYCLCTAT---GERRVCLAAEGFGRNCPLENIAD-KNIPP 58
2 AEGGEGEDBIQFLRTEDVVLQCIANIHKQRFKCLAAAGLGNRLFLPRTSAKYVP 61
Db
59 DLSCGVVITQALSVRLQELVLTAAAGSEKGT--SGGHTLYGNAILRLHNSDMYLA 116
62 DLGVNVLQSLSVRLQELANTNGNGGGAQGGHRTLXGHAILLRHSFGMYLT 121
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122 CLTTSRQDTKLAADVLRNATGEACMWTIHRPSKRSBGEKRIQDDLLIVSSERY 181
Db
176 LHTTKENSVIVNASFVHTMSVQPYGTGIRMKVGVYFGQDVLRFPHGDECLTTPST 235
182 LHLSSNGNVQVDSFVQTLMNVPPTCGSSIEE--LYLLGSHVVRFLFHGDECLTTPST 239
Oy 236 WTDGCGQIVYVYEGGSVMSQARSIMRLBLARTKAGGFIMYHNMRLRHITTGYYLVND 295
240 DONDAQRRIRFYEAGAGTRRSIMRVDPRLISVSSGNIRMGQAFRLRHITTGYYLVTE 299
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296 ONELVYLSREATTAACAFCLROEKDOQOV--LEBDQLEVTGAPITIKYGDSTVIYVHSE 353
300 DQGLLDPRKASDPTKSTAFPSRASKIKKGLDSHRKDIQMGVPEIKYDGVCFQVGHIA 359
Db
354 TGLWLSYKSYETKKGVGVKVEKQALLHEBGKMDGLDFRSQGEERTAVIRKCSLF 413
360 SGLWVYTKAQDAKTSRLGLPKRK-VILHGGHMDGLTLQRCORSEQAARIIHNTYALF 418
Oy 414 TKPINSLETQZRNRHSMFPASVVLGEMWCLBDLINVPAQPDMDMEHEKONKFRALRN 473
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 866572
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 C/date: 14-Feb-1997 #sequence_reviseion 13-Mar-1997 #text_change 09-Jul-2004
 C/accesion: 866572
 Biochem. J. 315, 207-216, 1996
 R/oclatn, L.J. Matzali, G.; Concl, A.; Charlesworth, A.; Sorrentino, V.
 A/ritle: Alpha and beta isoforms of ryanodine receptor from chicken skeletal muscle are
 A/reference number: 866572; MUID:9620583; PMID:8670108
 A/accesion: 866572
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 A/molecule type: mRNA
 A/residue: 1-4869 <OTT>
 A/cross-references: UNIPROT:Q09085; UNIPARC:UP1000017CF35; EMBL:X95267; NID:91212911; P/ C/superfamily: ryanodine receptor; transeriction initiation factor sigma region 1 homolo

Query Match 40.8%; Score 6423; DB 2; Length 4869;
 Best Local Similarity 43.7%; Pred. No. 0;
 Matches 1339; Conservative 498; Mismatches 849; Indels 380; Gaps 50;

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 Db 2 AEGGEGGEDEIQFLRTDDEVVLQCVSSIHKEQKFCCLAAGLGNRLCFLEPTSEAKYVP 61
 Qy 59 DLSCQVFLIEQALSVRALQELVTAAGSETEKGTG-SGHRTLLYGNAILLHNLNSDMYIAC 117
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 Qy 118 LSTRSSGQ-DKLAADVGLQOHSQGAQCAWTLHPASKQSSGSKRVGDDLLVSYATERYL 176
 Db 122 LTSRSRGTDLKAPVGLRERNAAGCAWMTIHPASKQSSGSKRVYIGDILLVSVSEHYL 181
 Qy 177 HTTKENSVSLVNASFNHTHSVOPVGTGIGSRMKVGVGVPGDVLRFPHGDECTIPSTW 236
 Db 182 HLHNSNGSIQVDSFMQTLNVAHFTCGSNITR--GTLGSHVRLPHGHDEYITLITSD 239
 Qy 237 TKDGGQNIIVYEGGSVNSQASLRLRLAATKNAAGFINMYHPKRIHITTRGLYVNDQ 296
 Db 240 QNSOQKQVLYETGAGVARSLSLRVPLRISWGSNIRWQGPRLHITTYGVALAND 299
 Qy 297 NEYLVRBEATKASCAFCRQEKD--DQKQVLEDKLBYAGATIKYGSSTVYVQSET 354
 Db 300 EGVMLDRKSDITSSAFCFPASKELEBKODSTLKDIDGQVBEIKYGDVCPICQHAS 359
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Db 360 ALWLTYPADPAKASARGLKRR-VIIHQSHDDGLTLRCQHEEQQAIIINTYSLFS 418
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 Db 419 QPISG-----NNTLTPALPVE-EMQTLQDLITYFOPGEDLEHEDQNKLRSLKRR 471
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 Qy 535 HTNCAQFANSNRNLMLPSRLGSAQSEGTGMLDVLCVLIDSEBALNMRDEHIKYIISL 594
 Db 531 RNNCTQF--SSNIDMIISKLDRLES--SSGILEVLHCILIESPEALNIIAEEHIKISISL 586
 Qy 595 LEKHGDRPKLDVLCGLCYGNGVAVRSSQNNICDYLPGKNLLQTLALVDHVSVPNIF 654
 Db 587 LDRGRNRYKVLVLCGLCYGNGVAVRANQMLICDNLPRDLQLQTLINDVTSIRPNIF 646
 Qy 655 VGRVESAAYRKYPFVYMDHIKTTNMP-HLRIGMANTTYGVYPGGEKYGNGVD 713
 Db 647 LGVAEGSAQYKRYFELIIDQVDFPLAEPYHLRVGMASISGYAPFPGGEGMGNGVD 706
 Qy 714 DLYSYGPDGAYLWSSGKRTPVNETHABEYIRKQVIGCALDTPVINFENGVYTG 773
 Db 707 DLYSPGFDGLHWSG--RVPRVAVSVNQHLLSDDVVSCCLDVGVPISPRINGQPVQGM 764
 Qy 774 PTNPNLEGMFPFYTSSSKLSGFLGSHGRRLRYAPBEGYSLVLSILPQQLISLPCF 833
 Db 765 FENFCTEGFFFPVSLSAGYKARFLGRRGEEKRFPPTGYACYEALPEKEMKLEPVK 824
 Qy 834 YFNLK--RALLAPPLVODDTAFVPPVDTLQITLPTYEQIARDKLAENIHMMAMNKI 891
 Db 825 EYKQSDGVRLDGLTQFSLQASFCPIPTDSIALPRLHEKIRDLKLAENIHLMGMNKI 884
 Qy 892 EAGMNTGDQREDLAKHPCLVPERLPRAEKRYDQLAVQTLKTIILAGYIISLDKPPAR 951
 Db 885 ELGMYTGKIRNDKRRHPCLVSEPSKLPETKYNLQNSTETLKTLLAGIYHAPPAE 944
 Qy 952 --IRNRLPRPMPQSNNGYRPAFLDSAYTLTKRMDELVDQLAENTNIMARERIQGWT 1009
 Db 945 EDKKYVLPKN-YIMNSGYRPAFLDSEVLLPSQELVKNLENNANVAKRIKQGT 1003
 Qy 1010 YGLNDSMDHRSPLVLPYKVDALIKKANRDTASEYRVLTVYGYMLDPPTGEOHEALL 1069
 Db 1004 YGIGQDLKAKNRLPYDLIDERTKSNRDSLEAVKTRAGVGNVPRPDQILADQVE 1063
 Qy 1070 EASKQADPRTYRAEKNTAVSSGKMYFEFELITAGPMRVGMADMAPGMALGQDENW 1129
 Db 1064 KVSIDK--IRFVRVSGSYAVKSGMYFEFEAVTGGDMRVGMARPGCRPDIELGADDAF 1120
 Qy 1130 AEPGYNBEKRYSGNTSFGQMAVGVYVFLDLIDKTFISFSLNGELMALGGETTFAD 1189
 Db 1121 VFEGSQQRWQHOG-SGFGRSQPQGVGVGMINDKDSIIFTLNGELLITSSKSELAFAF 1179
 Qy 1190 VQGDN-FVPACTLVGQKALTYGQVNTLKYFTTGLQSGYEPFCVNMKRDVTHMYTKD 1248
 Db 1180 FGISGVPVPCSLGSLGSHNLMAMDASTIKYITMGLQGFEPFAVNMARDVAMFSKR 1239
 Qy 1249 QPIFNTYDEMIDIRIDTRIPAGSDTPPCLKISHNTPEYI-ERANMEFLLSLPLVICHN 1307
 Db 1240 LPTFVAVPKR-NHPIEIMRIDGTIBSPRLKVTNHKTLGTQNSNDMLYGLSLMPI-----E 1294
 Qy 1308 FIDBAEKARWVEIKDRQQLMKBAVAQMPAHIDQIMRGFPYANDIKGLHYEDNOBELP 1367
 Db 1295 F-----RSSFNF----- 1301
 Qy 1368 SSIMKRLPSRPPKSGWTRGVTIQNYNNLQPGVNGMHRSTSEAMAKYDLAAGLTPDD 1427
 Db 1302 -----GVGVN----- 1307
 Qy 1428 KDKRGRSPKFPFRSKGSSDRAKRSKTPDPFSDTEVSPRGARRPNQIKVSGANQ 1487

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Db 1308 -----ASDALKQKKSQEPASST----- 1327
Qy 1488 RYNGMNPARTNLYGSOVLNMAPPTQDRKOMTTSLAOSATEVGNIEJDAECLKLN 1547
Db 1328 -----TC----- 1329
Qy 1548 EYFVQVRIYRGPDPHTHYIGMTTQYHLKSDPNQSKVTSVITTDYRVANNVRS 1607
Db 1330 --FYSLSIFAGQDPSSVWGVWVTPDYHYPSENFINDKNCVTYVTLGDERGRVHSVRSN 1387
Qy 1608 CYNVRADENYVWAEATAKGASQ-GMFICGSVDTSTGVSFTCEGKTSFPKFMEDETK 1666
Db 1388 CYNWVG----GDIAANSQRBGRSNVDEIGCFUDLAKGMSFTANGELTGCQVEENYTK 1443
Qy 1667 LFPALFYEATSKELLQIELGRSATSPLSAVLPSTQKHVLPQRPRLKYQCKPHQW 1726
Db 1444 LFPAAFOPTSTNLIQFELGKLKNTMPLSAIFKSEBRNPVQCPRPRLDQTTTPVLSR 1503
Qy 1727 VPRQSLQVHALKSDIRGMSMLCEDAVSMALNHPEEDRCIDILIEPTEMDKLSFHSHTL 1786
Db 1504 MPNSFLKETERESERHGWVQCLEPLQMMALHPEENRCVDILIELCEODELMKFHHTL 1563
Qy 1787 TLVAALCYGNSYRAAHLCTHVDOKOLLYAIOGYMGGPLRGPFYDILLHLHESHTM 1846
Db 1564 KLYSSVALGNTVAYALCCHVDI SOLFTINDQYLGILRSQFYDILLIHLHAKQAK 1623
Qy 1847 EACKNEFVPLGELKA--LYEERPMGHSLSLQTES-VAPQMKMTDIASIT-EISNLY 1902
Db 1624 LMANNFEIIPVTEBTRITKLYPDETKGGLPGVGLSTCLKPSFNFSPCRTVISEHQTS 1683
Qy 1903 SPFPPLVNAEFWMQALAEVETNOVHNRPVGSNENLFLPLIKVDRLLLYGMKDED 1962
Db 1684 SPPIPLDTLTKSKAISMLTEAVQCSGSHIRDPVGSHIAPFQVPLKLIATLLVWGVDDDD 1743
Qy 1963 VERLLIMTNETW-DESFDEKGEKDEHR-----KGLHMKKA 1997
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Qy 1998 EGAKLQMCYLLQHLNDIQLHRVBAITAFANDVGLQTDQLRRYTEIKOS-DLPSAVAA 2056
Db 1804 ESYKLOMCHILANFCCELOHREVAIYSFADHYVSKQVYKRYNEMQALMSALTA 1863
Qy 2057 KTRERERCPRRQMANALISFKHLEEDKENCPCGSEETIARMEFHTLMAHVSIAHQEP 2116
Db 1864 KKKKERSPQOEDINMLNF-----QIGEDCCPBEIRBELYDFHDLHICGI----- 1912
Qy 2117 DAENQEPKAPGAFGLYNIINTVKELEBAKAIEBPPKPEEK-----FRKVLQ 2169
Db 1913 PLEEEEBEEDSSLTGKLSLIYK-----KGPPEKIEPREBEDKSPTTLKELISO 1965
Qy 2170 TIVNMAESQIETPKLVREMFSLVQYAVGELIRALEKTYVINAKTKLDVAMWVGLS 2229
Db 1966 TIVRWQEQDQIOPELVRIMYTLRLRQYDSIGELLQALRKAYITSAASVDTINLALG 2025
Qy 2230 QIRALLPYQMSQSEELMKRLMKLVNHTFFQHPULIRYLKRVHEVNAVMANTLCRRQ 2289
Db 2026 QIRSLISVMGKEEELMTNGLDIMNKKFYQHPIMRLVGHREFTVMVNVGLG----- 2081
Qy 2290 AGSDAPSSQPVAEDEKSDTSHENVAACRPLCYCQRTGRONQKAMPDPDLLENSNI 2349
Db 2082 -----GKSQIAPFKMYASCCRFLCYCRISRONQKMFHSLTLENSNV 2127
Qy 2350 LLSRPLSGSTPLDVAVYSSIMMENTELALRBEHYLEKIAVYLSRCGLQSNSELEVEGYD 2409
Db 2128 GLAPFMRGSTPLDVAASVMONNELALMBEPDILKVTYTLACGLQCPVLLAGCYD 2187
Qy 2410 LGMDPVEGERYLDLFLPCYMWVNGSEYENANLYIRLIRPCLGALRGE-GEGLIKAI 2468
Db 2188 IGMNPTEGGRYLSLFAFVFNSEYEVNAYVVKLLIRPBCFGELGEGGNGILLAM 2247
Qy 2469 VQANKSERIADRRKLRKREMEQDVNFHPLPESDEDEYIDTGAAILNFCTIVDILGR 2528
Db 2248 QEAIRISEPTDLPQGYKRRBGD-----EEEBEEBETVHNGAIVSALIDLGR 2300

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Qy 2529 CAPDAGVIALGKNESLRARALIRSLVPLEDLQCVLSLFTLANNPAAGERPKSDMPGLI 2588
Db 2301 CAPEMHLOGKGEALIRINSILASLVPTEDLVGIIISPLKSLVYNDGTNEEDMSANFC 2360
Qy 2589 PGHKQSVGLFLENVYGIETQELFYKLEBAFLPDLRAATMLDRNDCESMALSMNRYIG 2648
Db 2361 PDHKAEPVFLDRVYGIKQOSPLMLHLEVGFLPDLRASASLDPVLSLSTTAAALANRYIC 2420
Qy 2649 NSILPFLIKAYPYNEAENVASLDDATLTIVRLSKNRMILTGORBAVSPFLVALTSAMQ 2708
Db 2421 SAVFPLIKCAPLPSTGTEHNASLVDSMLHTIYLSGRSLTKAQDITECLATLCHHR 2480
Qy 2709 PSMILKILKRLTYDVSKLESEYTVARLLTLHYERCAKYYSIGAOGAFAASDEBKRL 2768
Db 2481 PSMLOQLLRVLDPVPLNBVCMPPLKLTINHYEQCMKY-CLPSGMGSGYIAABEILH 2539
Qy 2769 TMLPESNIPDSKMDYBEPRLGKALPCLALIGCALPPDY-----SLSKATDDEFGK 2821
Db 2540 TEKLFMGIFDSLSHKKYDEPLFMALPCLSAIAGALPPDYLDTRIRSTLEK----- 2590
Qy 2822 EQAAGDLNPQVDFOPINTSVYANNNDLNTIYQKFEHNDAAVASHKTEGMYGSGMSD 2881
Db 2591 -QTSVDEG-NEDPKVNTANLVLPKLEYISKTAHSHDKAPFKTNNGMYGVSLE 2648
Qy 2882 SOKTRPLKPYMMLNDYEKERYKEPYRESIKALLAIGWSEHSEVDIPSNRSSMRQSK 2941
Db 2649 NTKTHPLIRPFLVTEKEIEYRWMPRESLKTMLANGSLE-----RTK 2692
Qy 2942 SGG-----RPPR---TVTDSATPPDYNPVPDMTMTLSREKQMAERLADNADIMAK 2992
Db 2693 EGBEGMLQRENEKLSISQSSQNGSGSPAPDLTVVLSRBLQGVWEVAENYHIMAK 2752
Qy 2993 KKKKEEL 2998
Db 2753 KKKMEL 2758

RESULT 11
B54161
ryanodine-binding protein beta form - bullfrog
C/SPECIES: Rana catesbeiana (bullfrog)
C/DATE: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C/ACCESSION: B54161
R./YOMADA, H.; Mureyama, T.; Takegi, T.; Iino, M.; Iwabe, N.; Miyata, T.; Ogawa, Y.; Eto
J. Biol. Chem. 269, 17206-17214, 1994
A./TITLE: Primary structure and distribution of ryanodine-binding protein isoforms of the
A./REFERENCE NUMBER: A54161; M01D:94274714; PMID:8006029
A./ACCESSION: B54161
A./STATUS: preliminary; not compared with conceptual translation
A./MOLECULE TYPE: mRNA
A./RESIDUES: 1-4868 <OVA>
A./CROSS-REFERENCES: UNIPROT:Q91319, UNIPARC:UPI0000110256, GB:D21071, NID:g1856973, PDB
C./SUPERFAMILY: ryanodine receptor; transcritpion initiation factor sigma region 1 homolo

Query Match 40.8%; Score 6419; DB 2; Length 4868;
Best Local Similarity 43.8%; Pred. No. 0;
Matches 1339; Conservative 517; Mismatches 845; Indels 354; Gaps 51;

Qy 4 AEGGASBQDDVVSFLTEDMVCLSTYAT-----GERVCLAABEGGNRCFLIENTAD-KNIPP 58
Db 2 AEGGEVE-DEIQFLRTDDEVVLQCTATITHEQRKFLAAEGIGNRLCFLEPSEAKYVP 60
Qy 59 DLSQCVPIEQLSVRALQELV--TAASFTGKSGSGHRTLLVGNATILRLNSDMYLA 116
Db 61 DLTCLNFWLEQSLSRALQEMLANITANGNBASQGGHRTLLYGHATILRHSFSGMYLT 120
Qy 117 CLTSSS--QDKLAFDVLGQHSQGEACWMTLLPASKORSBEGKRVVGGDLILVYATERY 175
Db 121 CLTISRSLTDKAPFVGLQDPTATGSAWMTTHIPAKQSSBEGKRVVIGDILLIVSSERY 180
Qy 176 LHTTKENEVS--TVASHTVHWSVQPYGTGISRKRYGVGYFGDVLRFPHGDECLTTP 233

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181 LHLISNGMNIQVDASFMQTLNWHPTCGSSVSER--GYLLGSHVVRPFHGDDECLTP 238
QY 234 STWTXOGGONI VVYEGGSVMSOARSJLWRLBARTKMGAFINNYHPRIRHITTTGRYLG 293
DB 239 STDPAAQHRKATYENAGAGIRARSJLWRLBARTKMGAFINNYHPRIRHITTTGRYLG 298
QY 294 NDONEVLYVSREBATTASCAFCLROEKDOKOYLBEDKLEVIAGAPIIKYDSTVIYVHSE 353
DB 299 TEOQGLVLODRAVSDTSSAFCFRASKEDLSV-PKRDIDQMGVAIEIKYDSCIFIQHVD 357
QY 354 TGLMYSKYETKKKGVKVEKQALIHGKRDODGIDFSRQSEBSEKTAARVIRKCSLFP 413
DB 358 SGMLTYKQADATARAGPL-KRRAIILQHSHMDGDTLQCKQHSEBQARIRNTTGLP 416
QY 414 TKRINGLETLQENRBRHSMFPASVNLGEMWMLBEDIYVPAOPDEMBHEKONKPRALRN 473
DB 417 SOTISDLSLTGNRRITTAVALPIEBEVOTLODLIYFOPREBDEHEKONKLSLKN 476
QY 474 RODLFQEEGILNLILBAIDKINVTYSGPLAGPLAGDSQSWMISGYLYOLLAIIKNG 533
DB 477 ROLNPFREBGMALVTLNCTIDRLNYSASAHFABII-GEKAGPAMKEILNLFYBLAALIRG 535
QY 534 NHTNCAQFANSNRLNMLPSRLSGOAGEGTMLDYHLCVILDBPBAIIMKRDHIKITYIS 593
DB 536 NRSNCAQF--SYNLDMLISILBRLER--SSGILEVLHSHIIESPBEALNLIIEKHIRSVIS 591
QY 594 LLEKHGDPRKVLVYLSLGVNGVAVASGNNICDYLPGKNLILLOALDVHVSVPNI 653
DB 592 LLDKHGNVYKVLVYLSLGVNGVAVATNQNOLICDNLPRRDLLOLRLVNDVTSKPN 651
QY 654 FVGRVEGSAVYRKMYFEVTDHIEKTHMMR-HLRIGMANTTGYVYPGGEGKKGNGV 712
DB 652 FLGVAOSAGYKMYFEMIIDQVDPYLTREPTHARVOMASTSGAPRPGGBEGMGNGV 711
QY 713 DDLYSGFDGAYLMSGGRKTPVNRTHABERYIRKQDVTGALDITVPIINFMNGVAVTG 772
DB 712 DDLFSYGFDDGLHMSG--RVPRVAVASNOHLIASDQVASCCLDLGVPISIFRINQCPVQG 769
QY 773 SFNPNLEGMFPFVPGSSKLSGRFLGSHGHLRYAAREGVAFLVYSLLPQOILSLERP 832
DB 770 MFPNPFTEGLFPFVAVSPSAGVKAFLGSHGHEKFLPFRAGVAPCYEALIPKEKMRREVP 829
QY 833 FYEGNLSK--RALAGPRLVODDTAFVPTPVDTLOITLPTVYEQIRDLAKAENIEMWAMK 890
DB 830 KEKRCDEGVRDLGTHPLSQAISFICPDIQSOIVLPHLEKIRDLAKAENIEMWAMK 889
QY 891 IBAGMAYGDOREDLAKIHPLVPEERLPPAKRYDOLAVOTLKTIIALGYI--SLDKP 948
DB 890 IELGMIYGVKVRDNKRQHPCLVPSKLPETEKYNNLOMSTETLKTLLALGCLIVHSHQTA 949
QY 949 PAIRIRVRLPNEPRMONGYKPARLDLSAVTLTPPKMBELVDOLAKENHIMABERIOQGM 1008
DB 950 BENIKKVKLPKN-YMNSNGYKPARLDLSAVTLTPPKMBELVDOLAKENHIMABERIOQGM 1008
QY 1009 TYGLNEDSDHMSRPHLVPRKVDALIKKANRDTASFTVTLIYGVMLDPPESQHEAL 1068
DB 1009 TYGLQODLKKKKRPLVLYALDBERTKSNRDSLEAVNRTFIGGYNIRERPDQELTDMT 1068
QY 1069 LBASKOKQADFRTRYAEKNAVASSGKMYFEFEIITAGPMEVMAHADMAFGMLGODENS 1128
DB 1069 SRVSIDK--IRFRVEGTYAVKTKGVYFEFEVVTGDMVGMARPTCRPDLIELGADRA 1125
QY 1129 WADGVYBEKYSGNTSPKQMAVGNVGVFDLITKITSPLSANGILLDALGGETPA 1188
DB 1126 FVEEG-SRGOCMNGSSPFGMNGPQGVVSMINLIDKSMIFTLNGBELLTNOGSELAFA 1184
QY 1189 DVQODN-FVPACTGVGOKARLTGYQDVNTLKYFTTGLOGEVPPFCNNKRDVTHYTK 1247
DB 1185 DPELENGFVYCSGLQIGRMNGKQASFTKTYTNGCLOGBGPQVAVNNRREAVAMFSK 1244
QY 1248 DQPIENTDEMDITRIDVTRIPAGSDTRPCKISHNTPEKMEKANWE--FLRLSLPVICH 1305
DB 1245 RLFPFVVPK-DHPIEIVTRKDGTVBIRPCLKVTHTKFGT-QNSNEDMICRSLMPVEFH 1302

QY 1306 NEFIIDEAKARRWVEIKDROQILMKEAVEAOHPAHIDQIMRSGFTWNDIKGLHYEDNOSE 1365
DB 1303 SAVINE----- 1308
QY 1366 LPSSKMKRLPSRPPRKGSMTRGVTTQNYNNLDQGVNGHRSISEMAKYDLGAGLTP 1425
DB 1309 -----BNF----- 1311
QY 1426 DDKDKRGRSPFAKFRSKEGSDRAKSRKSTPDPSPTEVSPERGARRPNQIKVQA 1485
DB 1312 -----QKRNQLOD----- 1319
QY 1486 NORVNGMARPSKTNLYGSOVLNMAPTQDRKOMTSTLAOSATETVGNELPDACELKI 1545
DB 1320 -----ASHTTTL----- 1327
QY 1546 INEYFGVRIYPCQDPTHYIGWTTQYHLKSDPNQSKYTKSSVLTIDDYRVENVNR 1605
DB 1328 ---YYSVRIFAQODPSSVWVGWVTPDYHFSNFDLSKCTVTVTLGDERGVHBSVYK 1384
QY 1606 QSCMTRADELVNEWABAATAKASQ-GWPIGGSVDTSGSVSFTCEGKDTSEFKPMRE 1664
DB 1385 SMCYMWGGDL---STGSQSRGSNVDDIGGLVLAIGLSFTANGKDLGTCYQVEPN 1440
QY 1665 TKLPRAIPYBATSKEILQIBLGRSATSPLSAVLTPTSDKRVLPQPPRLKYQCLKPHOV 1724
DB 1441 TKLPRAVPLQPTSTNLFOFBLGKLKNTMPLLSAIPKSEBKNPVSQCPRLVDGTITPVLW 1500
QY 1725 ARVPNOSLOVHALKSDINGMSMLCEDAVSMALHIPEEDRCIDILPEIEMDKLSFPHSH 1784
DB 1501 SRMPNMFUKVETERVBERGWMVVOCLBPLQMLAHIPEENRCIDILIELSEBODLMKFNHY 1560
QY 1785 TLTLYALCYQSVYRAAHLCTHVQKOLLYAIOQSYMGSPRLQGFYDLIALHLSHAT 1844
DB 1561 TLTLYAVCALGNRRVAHALCSHVDSQLLYTTIDNOYLPRLSGFNNLISITYLSAKX 1620
QY 1845 TMEACKNEFYPLGPRLKALYEBPDWG--HSLRSL-QTESVPRPOMKMTDIAESIT-EISN 1900
DB 1621 GKLMMNNEFTIPTDTRKIRLFPDESXKHGLPGVBSRSTCKSDMLFTAPCFVLTJBERQ 1680
QY 1901 LYSPPPLVAREFVQALABAVETNOVNRDPVGSNNELPLIKLYDRLLVGMKRD 1960
DB 1681 QHGPETIPVDLISKALISMTEAVQSGDHIRDPVGKABEQFVPLKLTATLLIMGVFED 1740
QY 1961 EDVEXKLLIMNPEPTWPSRDKGKDNH-----KGLIHM 1994
DB 1741 EDVROQILLIDPVNFGDHKEBEKENGKEDVAQIEBKAVAGEKPTRDAKAPAKGLQ 1800
QY 1995 KMAEGAKLOMCTYLOHLNIDOLHRYEALIAFAHDFVGLDQTLRRYTEIKOS-DLPSA 2053
DB 1801 RLPEBYKLOMCELLIAPCCBCLKGRVESIYABDKYVSLQVNOXKRYNEMIALMMSAA 1860
QY 2054 VAAKTRBPRCPREBOMNALSFKHLEBEDKENCPCGBELIARNEPHDTLMAHVSIALH 2113
DB 1861 LTAKTREBFSPQBOQINMLNFQOMQES-----PCPEBTRIDLUEFHEDLLHICG--- 1912
QY 2114 QSEDAENQPRPAKPAFGCLYNIINTVYK---ELEBEAKAIEBPPKTPBEKRYVLIOT 2170
DB 1913 --PLEBEOEBEOTSWT-GTLRSLVYKIKRPAEEOAPQEEB--EKSP-TTLKEILSOT 1966
QY 2171 IYVMAESQIETPKLVREMSPLLVROYDAVGEILIRALEKTYVNAKTKLDVAEMVYGLSQ 2230
DB 1967 MYVMAQEDHIODELVRIRMSFLRLQYDSDGELLRLMKRTYITSAASVEDTITMLASIGQ 2026
QY 2231 IRALLPVONSQSEBELMRKRLMTLVNNHTYFQHPDILRVLRVHENVMAVMNNTLGERBAQ 2290
DB 2027 IRSLISVBMKEBEREMIMIDELADIMNNKYVYQRPMLRVLGMEBETVMEVAVDVLAGN-KS 2085
QY 2291 QSDAQSOSQVVAADSKEKOTSHENVVAACCFRLCYFCTRGONOKAMFHDHDFLENSNLI 2350
DB 2086 QOAIAPF-----RMVASCCRFLEYCFRISRONKAMFELHAYLLENSSVG 2129

QY 2351 USRPSLRSTPLDVAVYSSMLMENTELALALREHYLEKIAVILSRGCLGNSLSEVKGYPDL 2410
 Db 2130 LASPKRSTPLDVAASVMDNNELALALQEDLEKVTYVLAAGCLGSLMLIRTKGYDI 2189
 QY 2411 GMDPLPESGRYDPLFLFCVWVNGESVEENANVILRLIRPRECLGPALGE-GEGLTKAIV 2469
 Db 2190 GMPLEGERYLSFLAFPAFVNCESVEENASVVKLLIRPECFPSLGBEGNGILNAAQ 2249
 QY 2470 DANKSEIRADRKRKLREMEQEGDVNFHPLPESEDEDEDYDTGAALNFCTVLVLLGRC 2529
 Db 2250 EAINISENDPLDLPEQGYQR-----VVEEDEEERIEVHGNALIMFSYALIDLLGRC 2302
 QY 2530 APDAVIALGKRESLRARAILRLSLVPLDLOGVLSLRTLNNPAAGERP--KSDMPSGL 2587
 Db 2303 APEPRLIAGKEAELIRAILRLSLPTDLVGLIISIPKLT--PAPNKGTVEEDMASF 2360
 QY 2588 IPGHNSVGLFLERYYGIETDELFYKLEEAFLPLRAATMLDRNDGCESMALSMRYI 2647
 Db 2361 CPDHKAPVLFIDRRYGIKDSGLHLHLVAFPLDPLRASLDLNASLVTMALALNRYI 2420
 QY 2648 GNSILPLLIRKAAVFNBEANVASLIDATLHTVYRLSKRMCLKGREAVSDFVALTSAM 2707
 Db 2421 CSAVPLTLTRQPLFSGEHTHAALDSTLHTLIRLSKRSRLTKQRDRIEELCLISCHM 2480
 QY 2708 QPSMLKLRLKLTVDVSKLSEYTTVALRLTLHYERCAKTYGSGAGQAFGASDEER 2767
 Db 2481 RPSMLQQLRLRLVPEVPLISEYCKMPLKLTLTNHYEQCKRY-CLPSCGSGYGLASBEELH 2539
 QY 2768 LTMMLFSNIPDLSIMQDEPELFGKALPLCLALGCLPDDVSLSKNDVDEYRGEQAAD 2827
 Db 2540 LTELKFWGIFPSLSHKYDAELFRMCPLSLNAGALPPD-----VTRIKATPEKOMS 2594
 QY 2828 LD-NPOYDPOPINTSSVALNDLNTIYQFSEHYHDAAASHRIENGWYVSGMSDSOKTH 2886
 Db 2595 VDAEENPFPKVTNANLTLPEKLBYIVNKPFAHSHDKAAVYKGLNSGMKTYGTLTIDENYKSH 2654
 QY 2887 PLKPYNMLNDEKERYEPVRESIKALLAIGMSYEH-S-EVDIPSNNSRMSROKSGGR 2945
 Db 2655 FLTPFPKTLAEKEKRIYWPRIRESYKTMALIGMSYERKEGEALALHRENEKMS----- 2709
 QY 2946 PPEIYTSBATEPDVNPHPVDMTNLTLSEMONMAERLADNADIMAKKKEELVT 3000
 Db 2710 ----ISQTSQNGNGYTPVPIDLSNVLSRELQGVEMVAENYHNIMWAKKXKRLDET 2760

RESULT 12
 S27272
 Ryanodine receptor, brain - rabbit
 C|Species: Oryctolagus cuniculus (domestic rabbit)
 C|Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C|Accession: S27272
 R|Hakamata, Y.; Nakai, J.; Takehima, H.; Imoto, K.
 FEBS Lett. 312, 228-235, 1992
 A|Title: Primary structure and distribution of a novel ryanodine receptor/calcium release
 A|Reference number: S27272; MUID:93050200; PMID:1330694
 A|Accession: S27272
 A|Molecule type: mRNA
 A|Status: preliminary
 A|Residues: 1-4872 <HAK>
 A|Cross-references: UNIPROT:O9T533; UNIPARC:UPI00001101C5; EMBL:X68650
 C|Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homoid

Query Match 40.7% Score 6413; DB 2; Length 4872;
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 Matches 1333; Conservative 508; Mismatches 844; Indels 382; Gaps 52;

QY 4 AEGGASBDDVSLFRTEDMVCISCTAT-----GERVCLAAEGFGRNHGLENIAD-KNIIP 58
 Db 2 AEGGCGSDLEIQLFRTEDDEVLLQCIATVHKGRKCLAAEGGLGRKLCGLFPTSSAKPIIP 61
 QY 59 DLSQCVFPIEDALSVRALQELVTAAGSETGKT--GSGHRTLLIGNAILRHLSNDMYLA 116
 Db 62 DLVCNFPYLEOSLSVRALOEMLANTGENGCGAAGCGGHRTLLVGHAILLHSPSGMYLT 121

QY	117	CLUSTSSQ-DKLAFPVQIQNSQSAQMWTLHPAKQNSBGRKVPVGDLLIVSATERY	175
Db	122	CLTYSRSQTDKLAFPVGLREHATGSAQWTLHPAKQNSBGRKVRIGDILLIVSSERY	181
QY	176	LHTTKENSVSYNASFHTWHSVQYGVGI SHMKVGVYFGVDVLPFFHQDECLTIPST	235
Db	182	LHSTISNQNIDVASFMQTLMMVHTCGSSIEE--GYLLGGHVRLPFGHDECLTIPST	239
QY	236	WTKQGGONIVYEGGSVMSQASBLRLELARTKAGGFINWHPMRIRHTTGRVYGVND	295
Db	240	DQNSQOHRIFEAGAGTARASLRVBPRLISMGSNIRMQOAFRLRHLTGHYALALZE	299
QY	296	QNEVLVSREEXTTASCAFLROEODDQOV--LEDKOLEVGAFLIKXGDSFTVYQHSB	353
Db	300	DOGLLDQGRKADYTSIFSRPSKETEKDLDSHKRDI EBGWVEIKKGDSVCFYQHLA	359
QY	354	TGLMLSYKS YETKKKGAVKEKQALHEBGMDDGLDFSRQSEBSRTARVIRKCSLPE	413
Db	360	SGLWTVYKAOAKTSRLGPLRK--VILHQEGMDGLTLQRCQRESSQAARIIIRNTALF	418
QY	414	TKPINGLETLQENRHSMFPASVNLGEMVNCLEDLINTPAQODEDEMEHEKONKPRALAN	473
Db	419	SOVPSG-----NNRPAAP--VTLPIBEVYQLTHDIAAFOQPEBEMQHDKONKRSLNK	471
QY	474	RODLPQEEGILNLLIEADKINVTYSOGFLAGFLAGDSQSGEMMISGYLOLMAI IKG	533
Db	472	RQNLFKBEGMLALVINCIDRLNITVNSVAHPAG-IARESGMAMKEVLSLTYLMAAL IKG	530
QY	534	NHTNCAQFANSNRNLMLFSLRGSQASGSGCTGMDLVLCYLDISPALNMRDEHIKYTIS	593
Db	531	NRNTCAQF--SNNDLMLISKDLRUES--SGGLEVLHCLILSPALNMAEGHISIIIS	586
QY	594	LLEKHGRPKYLDVLCSLCVGNGVAVRSSONNICYLLPGKYLLOTLAVDHVSSVRPI	653
Db	587	LIDKHGRHKYLDVLCSLCICNGAVARANOLICNLPRLRYLLQTRLINDVTSIRPI	646
QY	654	FVGRVSGSAVRKMYFEVYMDHI EKTTHMP--HLRI GANTTGYVYPGSGEKGNGVG	712
Db	647	FLGVNESAQYKKWFELIIDQVDPFLTAEPHLTAVGWASSGVA PPGSGEKGNGVG	706
QY	713	DDIVSYGDDGAVLWSSGGRKTPVNRHAEPRYIRKQDVGCLDLVPIINFMNGRVVG	772
Db	707	DDIVSYGDDGLHWSG--RIPAVASINQHLKSDVVASCCDLDAVPSISFRINGPVG	764
QY	773	SFTNFNLGEMFPFVYISCSKSLSCRLGEGHGRLYAAPREGYSLPVESHLPOOLISLEBC	832
Db	765	MFENNTDGLFPFVWSPSAGVKVRRLMGGRGEPFLPPSGVAPCYEALLPCKQRIEYV	824
QY	833	FFYGNLSK--RALGCPPLVODDTAFVPPVDTLOITLPTVYEQIADKLAENIHEMMANXK	890
Db	825	KEYKRDAGVNDLGTTOFLSQASEPCIPIDTSQVALLPHELEKIDRLAENIHEIMGNK	884
QY	891	IEAGMMYDQREDDLHKIRPLVFPFRLPAEAKRYVIOAVOTLKLITLALGYTISLDPKA	950
Db	885	IELGTFBGRKDDNKGRQHPCLVBSKLPETEKENYLNQSTETLKLILALGCHIAHVPNA	944
QY	951	R--IRNVLPNEBPFMSNGYKPAPLDLSAVTLTPRDELVQDLAENTANLMARERIQQSM	1001
Db	945	BEEDLKVYLPKN--YMSNGYKPAPLDLSADVCLLPOBILIVDGLAENAHVMAKRIKQW	1001
QY	1009	TYGLANBDBMRSPLVYPKYVDALIKRANDDTASERTYRTLLVGYTMLDPPFGQDEHALL	1061
Db	1004	TYGQIQODLKNRNPFLVYALLDETCKSNDSLSLEAVRTFVGYGNIIRPSQDELADPAV	1061
QY	1069	LEASQKQADERTYAEKNAVSSGKMYFEEFILLAGEMRVGMALADMAPGMMLGODENS	1122
Db	1064	EKVSIDK---IRPFRVRSYAVRSKMYFEFEEVTVGDMRVGMARPGCRDIEIGMTKP	1122
QY	1129	WAFQDYNBKYSGNTBSPQKMAVGVYGFLLIDKTISSLANGELIMDLGSETTFA	1188
Db	1121	LCLNAG--ASVGTKVGVILGVPMQGVAVGCINIDDA SMFTTLNGELLITTKGSLAPA	1177

QY 1189 DVQGDN-FVPACTLGVGQAKRLTYGDVNTLKIPTTCGLOGBEPCVNNKRDVTHMYTK 1247
 DB 1180 DYEIENGFPVPCISIGLSQIGRMNIGTDASTFKFYTMGLOGBEPFAVNNNRDVAWMSFK 1239
 QY 1248 DOIIFENTDMIDRIVTIRIPAGSDPPCLKISHNTPEFM-EKANNFPLRLSPVICHN 1306
 DB 1240 RLPTFVNVPR-DHPHLEVNRI DGTMDSPCLKVTHKFTGTONSANNIYCLSLSPVCHS 1298
 QY 1307 EPIDEAKARWWEIKDROQILMKEAVEAQWPAHIDQIMRSGFTMNDIKGLHYEDNOBEL 1366
 DB 1299 SF----- 1300
 QY 1367 PSSKMKKLPSRPPKSGMTRGVTTIQNNYNTLQPGVNGMBSTSEAKNATYDLGAQGLTPD 1426
 DB 1301 ----- 1300
 QY 1427 DKDKDKGRSPPKFRSGRESSDPAKSRKSTPPRPSDTEVSPRGARRPPOIKVSOAN 1486
 DB 1301 -----SHSPCLDSEA----- 1310
 QY 1487 QRYNGMNAAPSRRTLYGSGVGLMNAATPTDPRKOWTSTLAQSAETGVNBIFDAECLKLI 1546
 DB 1311 -----FOKKOH-QSILSHTT-----QC----- 1328
 QY 1547 NEYFYGVRIYPGODPTHVYIGWTTGYHLSKDNOSKVTYSVITDDYDRVENVNRQ 1606
 DB 1329 ---FYSIRIFAGODPSGVWGVWTPDYHLYSEKFDLNKNCTVYITLDEBGRVHESYKRS 1385
 QY 1607 SCYTMRADELNYEMATAKASQGMFIGSVDTSVTSVGSFTEBGDTSFKPRMEERTK 1666
 DB 1386 NCTWVGWGDV---VASSORSRSNVDELIGCLVDLNGMLSFSAANGELGTCYQVEBNTK 1442
 QY 1667 LFPALFVBEATSKELIOLDEGRSATSPLSAVALPTSDKHVYIPOPRLKATYQCLPHQMAR 1726
 DB 1443 VFPALFQPTSTSLFQELGKLNAMPLSAHIFKSEKPNVPOCPRLDVOTIOPVIMSR 1502
 QY 1727 VPNOQLQVHALKCLDIRGWSMLCEDAVSMALHPIBEDRCIDILEPIEMDKLSPHSHTL 1786
 DB 1503 MPNSPLKVEITERVERSERHGMVVOCLEPLQWMAHNIPEENRCVDILEQOEBDMGFHTL 1562
 QY 1787 TLYAALCYOSNYRAAHLCTHVDOKLLYAIQSOYMGPLRQGYDILLALHESAHATTM 1846
 DB 1563 RLTSAYCALGNSRYAVALCSHVLDLSQLFHAIIDNKYLGGLRSGYDILLISHLANAKERK 1622
 QY 1847 EACKNBEVITPLGPELK--ALYEBPMGMSLSLSJOTES--VRPOMGMDIASSIT-EISNLY 1922
 DB 1623 LMKNEVITITSTTRNIRIYPRDESKKRGLPVGPRCTLKRGFEFSPPCFVNVNEEROKQ 1682
 QY 1903 SPYFPLEVAREFVQALAEAVETQVANDRPVGSNENLFLPLIKLVDRLLLVGMREDD 1962
 DB 1683 SPEIPEILMKKLSMLTEAVOCGAHIRDPVGSVFEFOVPVAKLVGTLLVMGVPCDD 1742
 QY 1963 VEKLLIINTPEBTM-DPSFD-KEGDEHR-----KGLIMK 1995
 DB 1743 VRQILLIDISVFGESADTEBGAKEEVSQVEBEKAVEAGEKTSKARKKAPVAGLLQTR 1802
 QY 1996 MARGAKLQWICYLLOHNDIQARHVEVATIAFANDPVODLQDQRRYTEIKOS-DLESAV 2054
 DB 1803 LPSVYKLOMCELSYLDCBEOHNEVAIVAFGDIYVEKTLANOQFRNEMLOALNMSAAL 1862
 QY 2055 AAKTRFRCPRPRONNAIISFKLBEEDKENCPGSELTARMBFHDTLMAHYSALAQ 2114
 DB 1863 TAKTRFRSPPOQIMMLNF-----QGENCPCPEIRBELVDHEDLLVHGV----- 1913
 QY 2115 EPDAENQEPBAKGAFGKLYNINTVKELEBEAKAIEBPBKTPPEEK-----FRKVL 2167
 DB 1914 --PLEEBEEBEDSWTKLRTLYYKI-----KBPKEKEOPTEEBEEBCPTTLKELI 1964
 QY 2168 IOTVNAABESQITPTVLNEMFSLIVROYDAVGLIRALEKTYVINAKTKLDVAEMWVG 2227
 DB 1965 SQMIRNAQBDQIDAEIVRMFPLLRQYDSIGELQALRKTYTISHASVSDTINILAA 2024
 QY 2228 LSGIRALLPVQMSQEBEELMKRLMKLVNNTTFQHPDILIRVLVHENVMAVMNNTLGRR 2287

DB 2025 LSGIRSLSLVRMGREBELMINGIDIMNKNVYQHPNLMRVLGMHETVNEVWNVLG-- 2082
 QY 2288 AQAQSDAPSSQPAEDSKESKOTSHENVVAVCCFLCYFCRTGRONQKAMPDHEPDLLENS 2347
 DB 2083 -----TEKQIAFPKRVASCFCFLCYFCRTGRONQKAMPDHEPDLLENS 2126
 QY 2348 NILLSRSLNGSTPLDVAVASLMENTELALAREHYLEKIAVYLSRGCQOSNELVEKGY 2407
 DB 2127 SVGLASPSKMGSTPLDVAVASVMDNNEALGLBEEDLEKVTYIAGGQGLSCMPLAKGY 2186
 QY 2408 PDLGMDPVGEERTYLDLRFCEVWVNGSEVENNALVIRLLIRREPCGLPARGE-GBELK 2466
 DB 2187 PDVGWMPIDEBERYLSFLRFVAVFVNSSEVENNASVWGLLRREPCFEPALRGGMGLLA 2246
 QY 2467 AIVDANKSERIADRRRLRMEBOGDVNFSPHPE-SDEEDYIDTGAALINFCTYVLD 2525
 DB 2247 AMOGALIKISESPA-----LDLPSQG--YREYVDEDEEBEELVHMGNALMSFTSALIDL 2298
 QY 2526 LGRCAPDAGVIALGKNESELARAILNSLVLEBLOGLVSLRFTLNNPAGEBEPKS--DM 2583
 DB 2299 LGRCAPBEMHILQTKGKALIRSLRSLVPTEDLVGISLPLKL--PSLNKDSVSSEPM 2356
 QY 2584 PSGILPEHQSGVGLFERVYGTQSLFYKLLEBAFLPDLRAATMLDRNDGCSDMALSM 2643
 DB 2357 AANFCPDHKAPMVLFDRVYGIKDTFLHLLEVGFLPDLRASASLDLVALSTTESALAL 2416
 QY 2644 NRYTNGSILPLIKHAFYVBEAENVASILDATLHTVYRLSKNMLTKGOREAVSDPVAL 2703
 DB 2417 NRYTCSAVPLLRCAPLFEGTEHTYSLIDSTQITRYLSKGSLSLRAQDTEIECLAL 2476
 QY 2704 TSAQPSMLKLRLKLVDSKLSSEYTVVALRLTLHYERCAKYGSTGAQGAFGASD 2763
 DB 2477 CNHLPBMLQQLRLRLVDFVDPOLNDYCKMPLKLLTNHFBQCMKKY-CLPSGWSYGLAVE 2535
 QY 2764 BEKRLTMFLFSNIFDSISKNDYBEFLFKALPCLLAIACALPPDY-----SLSKYDD 2816
 DB 2536 BEHLTEKLPWGIJFDSISHKKYDPDLFRMSLPCLISALAGLAPDYLDTRITATLEK---- 2591
 QY 2817 EYFKEDQAGDLDNPQVDPQIINTSSVALNNDNTIYQKSEHYHDAMARKIENGWVG 2876
 DB 2592 -----QVSADAG-NDPPPIVINTINSLEPKELIYTKAEHSHDMACKESQSGMKY 2644
 QY 2877 EGMDSQKTHPRILKPYMNLANDYERKYEPRRESIKLALIGSVSEH-----VDIPSN 2931
 DB 2645 ISLDENYKTHPLRPFYTLTRKEKEIYRWARSLSKTMALVGMTVEKTBGALVQAREN 2704
 QY 2932 NRSSMRQSKSGRPREIYVDSATPPDYNHPVDMNTLSREMNNABERLADNADIWA 2991
 DB 2705 EKLSRVQSQTGN-----SYNAPADLSNVLSRELQGVAVVAENYHNIWA 2751
 QY 2992 KKKKEEL 2998
 DB 2752 KKKKEEL 2758

RESULT 13

147214
 probable brain tyrodine receptor - pig (fragment)
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
 R/Accession: 147214
 R/Author: M.W.; Pretner, J.K.; Louis, C.F.; Michelson, J.R.
 A/Title: Tyrodine distribution of tyrodine receptor isoforms and alleles determined by r
 A/Reference number: A55660; MUID:95081095; PMID:7969322
 A/Accession: 147214
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-163 <LEID>
 A/Cross-references: UNIPROT:Q28954; UNIPARC:UP1000008799; EMBL:U15975; NID:9562099; PT
 C/Superfamily: tyrodine receptor; transcription initiation factor sigma region 1 homol.

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Query Match      3.4%; Score 538; DB 2; Length 163;
Best Local Similarity 61.7%; Pred. No. 1.8e-26;
Matches 103; Conservative 31; Mismatches 29; Indels 4; Gaps 2;

Qy    510 DESGASHEMISGVLYOALLAIIKGNHTNCAOPANSNRNLMTFSRLGSQASGETGMVDLV 569
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db     1 EESGMAKELINLTKLAALIRGRNNACQF--SNLDWLISKDLRLES--SSGLEVL 56
       ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Qy    570 HCVILDSPEALNMNRDEHIKYITISLEKHGRDPKVLVDVCSLCVGNGVAVRSSQNNICDY 629
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db     57 HCLIESPALNLIAEGHKISITSLDKHGRHXKVLVDVCSLCVGAVRANQNLICDN 116
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Qy    630 LLEPKNLLQTALVDHVSVSRPNIFVGRVEGSAVTRKYFEVTMDHI 676
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db     117 LERRNLLQTRLINDVYSIRNPFLGVAEESQAQYKKMYFELLIDGV 163
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 14
147213
cardiac muscle ryanodine receptor - pig (fragment)
Cispecies: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C/Accession: I47213
R/Ledbetter, M.W.; Preiner, J.K.; Louis, C.F.; Mickelson, J.R.
J. Biol. Chem. 269, 31544-31551, 1994
A>Title: Tissue distribution of ryanodine receptor isoforms and alleles determined by re
A/Reference number: A55660; PMID:95081095; PMID:7989322
A/Accession: I47213
A>Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-162 <LED>
A/Cross-references: UNIPROT:Q28953; UNIPARC:UPI0000087898; EMBL:g562097; PIR
C/Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homoid
C/Keywords: cardiac muscle; heart

Query Match      3.3%; Score 520; DB 2; Length 162;
Best Local Similarity 65.2%; Pred. No. 2.4e-25;
Matches 101; Conservative 29; Mismatches 21; Indels 4; Gaps 2;

Qy    523 LVOLLAIIRKGNHTNCAOPANSNRNLMTFSRLGSQASGETGMVDLVHCVILDSPEALNM 582
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db     7 LHELLNALIRGNRNCAQFSGS--LDWLISR--ERLEASSGLEVLHCVLSPPALNI 62
       ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Qy    583 MRDEHIKVITISLEKHGRDPKVLVDVCSLCVGNGVAVRSSQNNICDYLTPKNLLQTAL 642
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db     63 IKRGHKISITSLDKHGRHNKVLVDVCSLCVGAVRANQNLICDNLPGRDLLQTRL 122
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Qy    643 VDHVSVPENIIVGRVEGSAVTRKYFEVTMDHI 677
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db     123 VNHSVMRPNIPLGVSEGAQYKKMYELMDYTE 157
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 15
T31431
inositol 1,4,5-trisphosphate receptor, localized in plasma membrane - Panulirus argus
Cispecies: Panulirus argus
C>Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C/Accession: T31431
R/Munger, S.D.; Ache, B.W.; Greenberg, R.M.
Submitted to the EMBL Data Library, March 1998
A>Description: Plasma membrane localization of an olfactory inositol 1,4,5-trisphosphate
A/Reference number: Z21030
A/Accession: T31431
A>Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-2783 <MUN>
A/Cross-references: UNIPROT:O77089; UNIPARC:UPI00000773B6; EMBL:AF055079; NID:g360666;
C/Superfamily: inositol-trisphosphate receptor

Query Match      2.1%; Score 327; DB 2; Length 2783;
Best Local Similarity 17.9%; Pred. No. 6.5e-11;
Matches 520; Conservative 416; Mismatches 980; Indels 990; Gaps 136;
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QY	5	EGAGSEODDVSFLRTEDMVCSC--TATGERVCLAAEGGNHCELE-NIADKNIP-DL	60
Db	4	EGSA-----SFLHMGDIYSLAEGSVSG--FISTGLGVADRCVYNPEAGDLSIPPKKF	54
QY	61	SOCCVYV-----EQLSVRLQELVTNAGSETGKTSSGHR----	96
Db	55	RDCLFSPCSNRYSAOKQFWKAAKHSNSTDPSSLNLRHDAKTEKQNEASKXMG	114
QY	97	TLLYGNALILRLHNSDMYIAC-LSTSSODKLAPVGHQOHSQGEACWMTTLPAKORSE	155
Db	115	VYNGVITTLQHLHKSNTKLVNKKRLPALLERKAMVYLDANG-NEGSMFYINPYTKLRNP	173
QY	156	GERKVEGDLLILVAVATERYHTTKEN-----EVSIVNASFHVTHWSVQPYGTGIS	206
Db	174	GDNVVVGKVIILSPVNAQQQLHVSSTHDLRHPCKEYVNVLSNN---TCWKISLFLHKE	230
QY	207	RKKYGVYFGGDVLAFFHHGDEBCLTIPSTWTKDGGQNIYVYEGS---SWNSQASLWRL	262
Db	221	NLE--GVLKGGDVNRLFHAEQEKFLTMDYKKK--QHVFLLRTGTTTAAATSSKALWEV	286
QY	263	ELAR--TKWAGFYNVYHMPRIKHTITGTYLVGNQDNEIYLVSRBEATYASCAFLGRQED	321
Db	287	EYVQHDPSRGAGAHNSLFRKHATGYLAEIDDD-----PRPD	327
QY	322	DQKQVLEKDD--LEVIAPL-----IKYGDST-----VYVQSHSETGLW	357
Db	328	FRTRLRDPNGOPVQVLSVPLSNDIASIFELEPTTLIRGDSMVQSSVYRLRHLCSTW	387
QY	358	LSYKSY---ETKKGKGVKRV-----EKKQAL--LHEGKMDDGLDPSQSQEBEEXTA	403
Db	388	VHSTISPIDKBEDKFWMSKVCAPIKEDKEAFSLVPYHAKVRD--LDFADASB-----	440
QY	404	RYIRKCSLTFKJFINGLETTQENRHSWFASVNLGEBWMCLEDLINFPAQDEBMEHEE	463
Db	441	VLAKHAK--KLEKGSITQAEFR-----SLMLLLDLILYTTA-----EKHBQ	480
QY	464	KONKFRAL-----RNRQDLFOEBEGLIHLLEAIDKINVTSGGFLAGLADGEG--	513
Db	481	NKSESLALAEVTPNPNRQRLKREQSILKQIFKTL-RAPFLTEQGQGGPILRIDELNDP	539
QY	514	--QSMEMISGVLVQYLLAAITKGNHTNCQAFNSNRKMLFBRLSQASGEGTMLDYLHC	571
Db	540	RHSAKYNLFRLCYRLRLRAOQGYRKNDBHIA--OHFGFMQOIGIDILAEET-----ITA	592
QY	572	VLIDPEALAN-MDEHFKVILISLEK--HQRDPVLDVLVLSLGCNGVAVRASSONNI-CD	628
Db	593	LHNNRKLLEHITATLETETVGLYRKNMKMDRFLDYLVYLCISNNQALPRYDELLICK	652
QY	629	YLLPEKN--LLIQTALVDHVSVAENIFVGEVGEASAVYRKWYFEVYMDHIKETTMMPHL	686
Db	653	SVFSKKNODILIELRLVBEDEIEVYN-----VEGSC-----PMLAIRDEEV--	695
QY	667	RIGMAN--TTGYPPYFGGGEKKMGANGVGDLLYSTGFGAYLMSGGRKTPVNRKTAEBPY	743
Db	696	-LTYNGBECSKSIYELASRAONLDSQGBE-----RLILE--Y	731
QY	744	IRKGDVISCALDLVPIINFMENGVRVLTGSPTFNPLBGMFP-----PVISCSKLSGRF	797
Db	732	YRH-----MDDL-----FSMNCBDRQYLAIRPLSLLIKINMLKCM-	767
QY	798	LLGGEHGRLYAADEGVSPLVESL-----LPQOILS-----LEBCFPFGNLSKRAL	843
Db	768	---EERTLAVDLNAAFRLMHNHNDCEPEEMVTPVYKATYARLWSBIOHMSIADYDKIA-	822
QY	844	AGPFLVDDDTAFVTPVDTLOITLPTVYEQJRDCLAEINHEMMAMNKLIEAGMWTGDQRED	903
Db	823	---AMHSTAAETTFDVIYVFEYELCANVDIM-----WSPSDCON	861
QY	904	LHKIHPCLVPERLRPAEKRYDIOGLAOTKLTITALGYIISLDKPARIRVRLPNBEFM	963
Db	862	-----KLTBE-----VYKLARYLLYFGFGYSND-----	884
QY	964	QSNQYKAPALDLSAVTILPKMDELVDOLAENTHMLMARERIQQGWTGLNEDSDMHSRPH	1023

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Db      885 -----LRLTKLLSLID-----YSPDTSKY-----906
Qy      1024 LVPEPKVDALKKANRPTASBTWTLTVGYMLDPTGBOHALLBASQKQADPRTYR 1083
Db      907 -----FNSNIPQSTASAKGVNLSJLDMGAUV-----933
Qy      1084 AEKRYAVSSGKMYEFELITAGPMRVGMADNAPGMMLQODENSNAPDGENEKVYSGN 1143
Db      934 --TNLALGTR-----MGF-RLG-----GSSSPKKKVG 959
Qy      1144 TBSFGKQAVGVVGLDLIDKTI SPLSNGELMLDAGETTFADVQGNFPACTLV 1203
Db      960 TB--KEDTL--VMDTKIIR-ILFLLVRL-----DYRISCLSI 996
Qy      1204 GQARLRYGGDVNLTAKFTTCGLQEGVBPVNMKRDVTHMYTKQPIFENTDMIDTRI 1263
Db      997 PKCE-----SDENP-SSLTGBISQGLK-----NKVENIWAQOSIFBETS-----1037
Qy      1264 DVTRIPAGSDTPPCLKIS-----HNTPEMKEANWEPRLSLPVI CHNEFIDEAKARWV 1319
Db      1038 GGLGVSSSQKRPBLOSTSCBENSJLDDBEGCKKFLRVLLHLMH-----1083
Qy      1320 EIKDROQILMKEAVEAQMRAHIDQIMSGFTMNDIKGLHYEDNGELPSSKMKRLPBRPP 1379
Db      1084 -----EYPLVSRSLQLLFR-----HFSQREVLQNFQVQL-----1115
Qy      1380 RKSGMTRGVITIQNNYIOPQOVNMGHSTSEAMAKYDLGAQSLTPDDCKDKGRSPPK 1439
Db      1116 ----LVQDGVESYKQIKEDS-DDRLNLVSKSELWV-----KRSSTDEDCGKTKK 1162
Qy      1440 FRKRGSSDRAKSRKSTPDP-----FSDTEVSPERGARRPMPQIKVSOANQRY 1489
Db      1163 KKKKDDDEDDALSKPKPRPKLTADQKESALDGLGPRLEBQADNYKRIQIILVRM 1222
Qy      1490 NGM-----NAPSRF-----NLVSGOYGLMATTPTODRKO-MTSTSLAOSATE---1531
Db      1223 NKLCVTSQSHGNLSPKKNBOQLNMGHSHVLELQIPYDRKDKKMNELIBLAHQFLQ 1282
Qy      1532 --TVGNEIFDAECLKLINEFYGVRIYFG-----ODPNHV-----YIG 1567
Db      1283 NPGCGDANQALLYKSIDLF-----LNPGLBAKTCAVFPKNSHLSEVSERVIOFII 1337
Qy      1568 WYTTQ--YHLSKDFNOSKVTSSVITTDYRVVENVNRQSCVWRADE---LYNEVMA 1622
Db      1338 CIETHGHVQYKFLQITIVAKSGOPLRSQDIVQOR-----LVNAGEVDLVFYNE---1387
Qy      1623 EATAKGAQCMFJGC-----SVDTSTGS-----VSPTCEKDTSPFKQME---1662
Db      1388 ----RASPMFIEMKADNRMDPDDSPLRVHIBLVKLACTEKGKNASTEIKCHSL 1442
Qy      1663 -----PETKLPALFV-----BATSKEIIQ-----IELGR 1667
Db      1443 PLDDIVAMVEHKDCIPEVKEAYINFLNHCYIDTEVEKEIYNSHHWSLEPKSFLLVDMGR 1502
Qy      1688 SATSLP-----LSAAYL-----PTSDKHVLPORPRLKVQCKLRQMAR 1726
Db      1503 VATAPEPRRIADKALENYVINSIMTITTFPNSPSPDOSQTIQTRQPVQVQL--HAAYR 1560
Qy      1727 VPNOQLVHALKLDIRGWSMLCEDAVSMLAHIPEEDRCIDILEPIEMD-KLISFHSHT 1785
Db      1561 V-SQAVVGHQ-----RNVENCIKITL-----EVARKNHISIPVDLEAQVVMGORT 1606
Qy      1786 LTYAALCYGNSYRAAIA-----LCTHVQKOLLVAIQSYMSGRLRGFYD 1832
Db      1607 TSIMTRTASKWSNATRRDASSSSLSGRMDHVLIEODFNSVAVLBAELR--PLVAABLS 1664
Qy      1833 LIALHLESH-----ATTWACKN-BFVLPGLPELKALYEEPRMGSLRSJOTESVPRQ 1885
Db      1665 VLVDILYQPHRLFPDSEBASIKCKNGGFIISRLIHCEKLEEBDEKLCIOVLYKT--LKDM 1722
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GenCore version 5.1.7
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(without alignments)
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Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1	COS94804	15606 bp	DNA	linear	PAT 02-FEB-2004
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DEFINITION	COS94804				
ACCESSION	COS94804.1	GI:41651849			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM	Drosophila sp.				
	Drosophila sp.				
	Bukariyola; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;				
	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
	Ephydroidea; Drosophilidae; Drosophila.				
REFERENCE	1	Venter, J.C., Adams, M., Li, P.W. and Myers, R.W.			
AUTHORS					
TITLE		Detection of kites, such as nucleic acid arrays, for detecting the			
		expression of 10,000 or more Drosophila genes and uses thereof			
JOURNAL		Patent: WO 0171042-A 22562 27-SEP-2001;			
		PR Corporation (NY) (US)			
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Best Local Similarity	73.9%	Pred. No. 0;			
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RESULT 4
OCRR 15361 bp mRNA linear MAM 10-MAR-2001
LOCUS Rabbit skeletal muscle mRNA for ryanodine receptor.
DEFINITION X15750
ACCESSION X15750
VERSION X15750.1 GI:1709
KEYWORDS calcium binding protein; channel protein; receptor; ryanodine receptor.
SOURCE Oryctolagus cuniculus (rabbit)
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 15361)
Takehime, H., Nishimura, S., Matsumoto, T., Ishida, H., Kangawa, K., Minamino, N., Matsuo, H., Ueda, M., Haraoka, M., Hirose, T. and Numa, S. Primary structure and expression from complementary DNA of skeletal muscle ryanodine receptor Nature 339 (6224), 439-445 (1989)
2 (bases 1 to 15361)
Takehime, H., Nishimura, S., Nishi, M., Ikeda, M. and Sugimoto, T. A brain-specific transcript from the 3'-terminal region of the skeletal muscle ryanodine receptor gene FEBS Lett. 322 (2), 105-110 (1993)
3 (bases 1 to 15361)
Numa, S.
Direct Submission
Submitted (05-MAY-1989) Numa S., Kyoto University, Dept of Medical Chemistry and Molecular Genetics, Faculty of Medicine, Yoshida Sakyo-ku, Kyoto 606, Japan
*Source: pRR72, pRR203, pRR308, pRR359, pRR451, pRR616. see X15749 for ryanodine receptor gene 5' end; X15749 and X15750 seqs are shown as a compiled one in [1]
Data kindly reviewed (27-AUG-1989) by Numa S.
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RESULT 5
OCRYAN LOCUS
DEFINITION O.cuniculus mRNA for skeletal muscle ryanodine receptor.
ACCESSION X15209
VERSION X15209.1 GI:1713
KEYWORDS ryanodine receptor.
SOURCE Oryctolagus cuniculus (rabbit)
ORGANISM Oryctolagus cuniculus
Bkayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha;
Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 15823)
Takehima,H., Nishimura,S., Matsumoto,T., Ishida,H., Kangawa,K.,
Minamino,N., Matsuo,H., Ueda,M., Hanaoka,M., Hirose,T. and Numa,S.
TITLE Primary structure and expression from complementary DNA of skeletal
muscle ryanodine receptor
JOURNAL Nature 339 (6224), 439-445 (1989)
PUBMED 2725677
AUTHORS Numa,S.
2 (bases 1 to 15823)
TITLE Direct Submission
JOURNAL Submitted (05-MAY-1989) Numa S., Kyoto University, Dept of Medical
REFERENCE Chemistry and Molecular Genetics, Faculty of Medicine, Yoshida,
Sakyo-ku, Kyoto 606, Japan
JOURNAL Location/Qualifiers
FEATURES
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polysignal 15799. .15804

Query Match 26.2%; Score 785.8; DB 4; Length 15823;
Best Local Similarity 56.7%; Pred. No. 1.9e-163;
Matches 1699; Conservative 0; Mismatches 1182; Indels 114; Gaps 9;

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DEFINITION	Homo sapiens mRNA for ryanodine receptor 1 (skeletal) variant		
ACCESSION	AB209425		
VERSION	AB209425.1		
KEYWORDS	cDNA, human		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

REFERENCE	1	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
AUTHORS		Totoki, Y., Toyoda, A., Takeda, T., Sakaki, Y., Tanaka, A., Yokoyama, S., Ohara, O., Nagase, T., and F. Kikuno, R.
TITLE		None Title
JOURNAL		Published Only in Database (2005)
REFERENCES	2	(bases 1 to 6266)
AUTHORS		Totoki, Y., Toyoda, A., Takeda, T., Sakaki, Y., Tanaka, A., Yokoyama, S., Ohara, O., Nagase, T., and F. Kikuno, R.
TITLE		Direct Submission
JOURNAL		Submitted (22-MAR-2005) Ogamu Ohara, Kazusa DNA Research Institute, Department of Human Gene Research; 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan (E-mail:cdnainfo@kazusa.or.jp), URL: http://protein.gsc.riken.go.jp/, Tel: 81-438-52-3930, Fax: 81-438-52-3931)
COMMENT		This work was supported in part by the National Project on Protein Structural and Functional Analysis, Ministry of Education, Culture, Sports, Science and Technology of Japan. Totoki Y, Toyoda A, Takeda T, Sakaki Y, Tanaka A, Yokoyama S. RIKEN Genomic Sciences Center, 1-7-22 Suehiro-cho, Tsurumi, Yokohama 230-0045, Japan. e-mail: aktanaka@postman.riken.go.jp URL: http://protein.gsc.riken.go.jp/.
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Homnidae; Homo.
REFERENCE
AUTHORS Abbas, A., Clark, H., Ouyang, W., Williams, M.P., Wood, W.I. and Wu, T.D.
TITLE Compositions and methods for the treatment of immune related
diseases
JOURNAL Patent: WO 2005016962-A 1367 24-FEB-2005;
Genentech, Inc. (US)
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DEFINITION CS035785
ACCESSION CS035785
VERSION CS035785.1 GI:60733700
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
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REFERENCE
Abbas, A.; Clark, H., Ouyang, W., Williams, M. P., Wood, W. I. and Wu, T. D.
ATTHORS
TITLE
Compositions and methods for the treatment of immune related
diseases
JOURNAL
Patent: WO 2005016962-A 5291 24-FEB-2005;
Genentech, Inc. (US)
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Beet Local Similarity 56.5%; Pred. No. 2.3e-159;
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 ORGANISM
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 Homidae; Homo.
 REFERENCE
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 AUTHORS Abbas, A., Clark, H., Ouyang, W., Williams, P. M., Wood, W. I., and Wu, T. D.
 TITLE Compositions and methods for the treatment of immune related
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Homnidae; Homo.
REFERENCE 1
AUTHORS Abbas, A., Clark, H., Ouyang, W., Williams, P. W., Wood, W. I. and Wu, T. D.
TITLE Compositions and methods for the treatment of immune related diseases
JOURNAL Patent: WO 2005019258-A 5291 03-MAR-2005;
Genentech, Inc. (US)
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ORIGIN

Query Match 25.2%; Score 756.2; DB 6; Length 15345;
Beet Local Similarity 56.3%; Pred. No. 6.4e-156;
Matches 1685; Conservative 0; Mismatches 1178; Indels 132; Gaps 9;

38 TGAAGCCCAAGATATGACAGAAAATGGAACAATGCGGACGCTAGAGAGAGATCT 97

DG 9791 TGGGGCTCCCAACAGTGTGAGAGAGATGTGTCGCCAGATCCCGGTGCTGAGCCGCTCA 9850
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RESULT 12
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LOCUS Human ryanodine receptor mRNA, complete cds.
DEFINITION J05200
ACCESSION J05200.1 GI:337721
VERSION
KEYWORDS ryanodine receptor; skeletal muscle sarcoplasmic reticulum Ca+2 release channel.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 15346)
Zorzato,F., Fujii,J., Otten,K., Phillips,M., Green,N.M., Lai,F.A., Melsener,G., and MacLennan,D.H.
AUTHORS Molecular cloning of cDNA encoding human and rabbit forms of the Ca2+ release channel (ryanodine receptor) of skeletal muscle sarcoplasmic reticulum

JOURNAL J. Biol. Chem. 265 (4), 2244-2256 (1990)
PUBMED 2298749
COMMENT Original source text: Human (adult) muscle, cDNA to mRNA, and DNA.
Draft entry and printed sequence for [1] kindly submitted by
D.H.MacLennan, 30-NOV-1989.

FEATURES
Location/Qualifiers

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EBEKTEKKTAKISQSAQTYDPRBGYNPQPLDSAVTLISREIQMAAEALAEVHTWG

ORIGIN 648 bp upstream of SalI site; chromosome 19 proximal long arm.

Query Match	25.2%	Score 756.2	DB 8	Length 15346
Best Local Similarity	56.3%	Pred. No. 6.4e-156		
Matches 1685	Conservative 0	Mismatches 1178	Indels 132	Gaps 9
QY 38	TGGAAGCCCAAGACATTAATGCAAGAAAATGAAACAATGATGCCGACGCTGAGACATCT	97		
Db 9791	TGGGGCTCCCAACAGTGTGAGAGAGATGTGTCGACATCTCCGCTGTGAGCGGCTCA	9850		
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LOCUS CS071082 245 from Patent WO2001032927.
DEFINITION CS071082
ACCESSION CS071082
VERSION CS071082.1 GI:63088486
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
1 Sornasse, T., Selthamer, J. J. and Watson, G. A.
TITLE Tissue specific genes of diagnostic import
JOURNAL Patent: WO 2001032927-A 245 10-MAY-2001;
Incyte Genomics, Inc. (US)
FEATURES
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ORIGIN
Query Match 25.2%; Score 756.2; DB 6; Length 15355;
Beech Local Similarity 56.3%; Pred. No. 6.4e-156;
Matches 1685; Conservative 0; Mismatches 1178; Indels 132; Gaps 9;

Qy 38 TGAAGCCCAAGACATATGACAGAAAATGAAACAATGATGCGACGCTAGAGACGATCT 97
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VERSION AF009345.1 GI:4102116
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Noctuidae; Noctuidae; Heliothinae; Heliothis.
REFERENCE
AUTHORS Puente, R., Sumer, M., Evans, A. D., McCaffery, A. R. and Windass, J. D.
TITLE Identification of a polymorphic ryanodine receptor gene from
Heliothis virescens (Lepidoptera: noctuidae)
JOURNLS Heliothis virescens. Mol. Biol. 30 (4), 335-347 (2000)
PUBMED 10727900
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AUTHORS Puente, R. and Windass, J. D.
TITLE Direct Submission
JOURNLS Submitted (18-JUN-1997) Biologie et Pathologie Digestive, INSERM
U151, Institut Louis Bugnard, CHU Rangueil L3, Toulouse 31403 CEDEX
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GenCore version 5.1.7
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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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SUMMARIES

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4	15550.5	98.7	5142	US-10-668-767-2	Sequence 2, Appl
5	15475	98.3	5100	US-10-668-767-146	Sequence 146, App
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10	12460.5	79.1	5109	US-10-668-767-10	Sequence 10, Appl
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; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Guttridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: B1513 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 128
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; FEATURE:
; OTHER INFORMATION: PXL-Hv7
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DB 841 RALAGPPLVODDDAFVPTPVDTLOITLPTVVEQIRDLAENHEMMANMKIEAGMYGQD 900
QY 901 REDLHKIHPLCVFEBRLPRAEKRYDLOAVQTLKTIILAGYIISLXKPPAIRINVLPE 960
DB 901 REDLHKIHPLCVFEBRLPRAEKRYDLOAVQTLKTIILAGYIISLXKPPAIRINVLPE 960
QY 961 PFMQSNQYKPAPLDLSAVTLTPQMDLIVQDLAENTHLMARERIIOGWTYGLNEDSDMR 1020
DB 961 PFMQSNQYKPAPLDLSAVTLTPQMDLIVQDLAENTHLMARERIIOGWTYGLNEDSDMR 1020
QY 1021 SPLHVPYPKVDDAIKKANDPTABETVTTLVGYMDLPTGEOHEALLLEASKOKADR 1080
DB 1021 SPLHVPYPKVDDAIKKANDPTABETVTTLVGYMDLPTGEOHEALLLEASKOKADR 1080
QY 1081 TYRAEKQYAVSSGKWT FEEFELITAGPMRVGMADADAPGMMLQODENSNAFDGYNEKY 1140
DB 1081 TYRAEKQYAVSSGKWT FEEFELITAGPMRVGMADADAPGMMLQODENSNAFDGYNEKY 1140
QY 1141 SGNTSEFGQMAVGVVGFVLDLIDXTISFLNGELLMALGSETTFADYQGNFVPACT 1200
DB 1141 SGNTSEFGQMAVGVVGFVLDLIDXTISFLNGELLMALGSETTFADYQGNFVPACT 1200
QY 1201 LGVGOQARLTYGQDVNTLKYFTTCGLOEGYEPFCVMKGDVTHWYTKQDPIFENTDEMD 1260
DB 1201 LGVGOQARLTYGQDVNTLKYFTTCGLOEGYEPFCVMKGDVTHWYTKQDPIFENTDEMD 1260
QY 1261 TRIDVTRIPAGSDTPCLKISHNTFETMEKANEFLRLSLPVI CHNEFIDEAEKARWTE 1320
DB 1261 TRIDVTRIPAGSDTPCLKISHNTFETMEKANEFLRLSLPVI CHNEFIDEAEKARWTE 1320
QY 1321 IKDROOILMKEAVEAQMPAHIQIMRSGFTMDIKGLHYEDNOBELPSSRMKRLPSRPPR 1380

DB 1321 IKDROOILMKEAVEAQMPAHIQIMRSGFTMDIKGLHYEDNOBELPSSRMKRLPSRPPR 1380
QY 1381 KGSMTGVTI QNNNNLOPGOVNGHRSSTSAEBAKXDLGAGQLTPDDKXKRGSPKXF 1440
DB 1381 KGSMTGVTI QNNNNLOPGOVNGHRSSTSAEBAKXDLGAGQLTPDDKXKRGSPKXF 1440
QY 1441 RSRKGS SDRAKSRKSKTDPFSDTEVSPERGARRPNPOLKYSQANQRYNGMARPSTN 1500
DB 1441 RSRKGS SDRAKSRKSKTDPFSDTEVSPERGARRPNPOLKYSQANQRYNGMARPSTN 1500
QY 1501 LVGSOGLMATAPTQORKQNTTSTLAQSAETETGNETFPAECLKLINEYGYRITPGQD 1560
DB 1501 LVGSOGLMATAPTQORKQNTTSTLAQSAETETGNETFPAECLKLINEYGYRITPGQD 1560
QY 1561 PTHVYIGWTTQVHLHSKQFNOSKMYKSSVYIINDVDVRYVENNRQSCVYWRADLEYNEV 1620
DB 1561 PTHVYIGWTTQVHLHSKQFNOSKMYKSSVYIINDVDVRYVENNRQSCVYWRADLEYNEV 1620
QY 1621 MABATKAGASQGMFICSDYDTSTGVSFTCEGKOTSFKFPMBETKLPALFVEATSKEI 1680
DB 1621 MABATKAGASQGMFICSDYDTSTGVSFTCEGKOTSFKFPMBETKLPALFVEATSKEI 1680
QY 1681 LQIELGRSATSPLSLAAVPTSPKXVIPOPPRLKYOCLKPHOMARVPNOSLOVHALKLS 1740
DB 1681 LQIELGRSATSPLSLAAVPTSPKXVIPOPPRLKYOCLKPHOMARVPNOSLOVHALKLS 1740
QY 1741 DIRGSMLECEDAVSMALAIPEEDRCIDILEPEMDKLSFHSHTLTLYAALCYQSNYRA 1800
DB 1741 DIRGSMLECEDAVSMALAIPEEDRCIDILEPEMDKLSFHSHTLTLYAALCYQSNYRA 1800
QY 1801 AAHALCTHVDOQOLLYAIOGYMSGPLRQGFYDLLALHLSHAATTMEACKNEFVILGPE 1860
DB 1801 AAHALCTHVDOQOLLYAIOGYMSGPLRQGFYDLLALHLSHAATTMEACKNEFVILGPE 1860
QY 1861 LKALYEEPMGHSIRLSLOTESVRPQMKMTDIABSTIEINLSPYPLVYARFPVQALA 1920
DB 1861 LKALYEEPMGHSIRLSLOTESVRPQMKMTDIABSTIEINLSPYPLVYARFPVQALA 1920
QY 1921 EAVETQVNRDPVGGSENLEFLPLIKLYDRLLLVGMMDDEVEKLLIMTNPETMPSFD 1980
DB 1921 EAVETQVNRDPVGGSENLEFLPLIKLYDRLLLVGMMDDEVEKLLIMTNPETMPSFD 1980
QY 1981 KEGKDEHRKGLHMKABEAGKLQMCYLLQHLNDIQLRHVEAIIAFAHDFVGDLOTDQAR 2040
DB 1981 KEGKDEHRKGLHMKABEAGKLQMCYLLQHLNDIQLRHVEAIIAFAHDFVGDLOTDQAR 2040
QY 2041 RYTEIKQSDLPBAVAAKTRBEPCPREQMAILSFKHLSEBDKXKCPGGBELIAAMNEF 2100
DB 2041 RYTEIKQSDLPBAVAAKTRBEPCPREQMAILSFKHLSEBDKXKCPGGBELIAAMNEF 2100
QY 2101 HDTLMAHVSILALOEPDAENOEPEAKPGAFGLVNIINTVBLEBEAKAIEBPPKCTE 2160
DB 2101 HDTLMAHVSILALOEPDAENOEPEAKPGAFGLVNIINTVBLEBEAKAIEBPPKCTE 2160
QY 2161 EKEFRKVLQTIIVNMAEESQIETPKLVREMFSLVQYDAVGEILRALKETYVINAKTXLD 2220
DB 2161 EKEFRKVLQTIIVNMAEESQIETPKLVREMFSLVQYDAVGEILRALKETYVINAKTXLD 2220
QY 2221 VABEMVGLSOLRALLPVQMSQSEEBELMRKWLNNHTFFQHPDLIRLARVHENMAYM 2280
DB 2221 VABEMVGLSOLRALLPVQMSQSEEBELMRKWLNNHTFFQHPDLIRLARVHENMAYM 2280
QY 2281 NMTLGRBAQOASDAPSSQPVABEDSKXOTSHEMVVACCRFLCYFRTORQOKAMFDFE 2340
DB 2281 NMTLGRBAQOASDAPSSQPVABEDSKXOTSHEMVVACCRFLCYFRTORQOKAMFDFE 2340
QY 2341 DFLSNSNITLSRPSLRGSTPLDVAVYSSIMENTELALAREHYLEKIAVYLSRCSQSN 2400
DB 2341 DFLSNSNITLSRPSLRGSTPLDVAVYSSIMENTELALAREHYLEKIAVYLSRCSQSN 2400
QY 2401 ELVEKGYPLGMDPVJGERIYLDPLRCPVWNGESVBEANLVITRLIRPBCGLPALRGE 2460

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Db      2401 ELVENGYDPLGMDPVEGERYLDPLRPECVWNGESVEENMLVTIRLLIRREPECIGPALRGE 2460
Qy      2461 GEGILKAIYDANKMSERIRADRRLRAREMEODGVNFSHPLESDDEBDYIDTGAAILNFCY 2520
Db      2461 GEGILKAIYDANKMSERIRADRRLRAREMEODGVNFSHPLESDDEBDYIDTGAAILNFCY 2520
Qy      2521 TLVDLGRCAPDAGVIALGKNSLSRARAILRSVPLEDLQGVLSLRFTLNPAAGEBRK 2580
Db      2521 TLVDLGRCAPDAGVIALGKNSLSRARAILRSVPLEDLQGVLSLRFTLNPAAGEBRK 2580
Qy      2581 SPMPSGLIPGHKOSVGLFLERVYGIETQELFYLLSEBAPFDLRAATMLDRNDGCSDMA 2640
Db      2581 SPMPSGLIPGHKOSVGLFLERVYGIETQELFYLLSEBAPFDLRAATMLDRNDGCSDMA 2640
Qy      2641 LSNMRIRIGSILPLIKHAFYVNEAENVASILDATHTVYRLSKNMLTGOREAVSDFL 2700
Db      2641 LSNMRIRIGSILPLIKHAFYVNEAENVASILDATHTVYRLSKNMLTGOREAVSDFL 2700
Qy      2701 VALTSAMPMLKILRKLTVDSKLSYTTVALRLTLHYERCAKYGSTGAGQAFGA 2760
Db      2701 VALTSAMPMLKILRKLTVDSKLSYTTVALRLTLHYERCAKYGSTGAGQAFGA 2760
Qy      2761 SSDEERLITMMLFSNIPDSLSKMDYBEPFLFKALPCLIAIGCALPPDYLSKRYDDEFPYG 2820
Db      2761 SSDEERLITMMLFSNIPDSLSKMDYBEPFLFKALPCLIAIGCALPPDYLSKRYDDEFPYG 2820
Qy      2821 KEOAGADLNDPOVDPOPINTSSVALNNDNTIYOKFSEHYHDMASRKIENGWYVYEGMS 2880
Db      2821 KEOAGADLNDPOVDPOPINTSSVALNNDNTIYOKFSEHYHDMASRKIENGWYVYEGMS 2880
Qy      2881 DSOCTHPLKPYMLNDYKERYKEPVRBSLKALAIKMSVESHBYDIPSNNSSMRQOS 2940
Db      2881 DSOCTHPLKPYMLNDYKERYKEPVRBSLKALAIKMSVESHBYDIPSNNSSMRQOS 2940
Qy      2941 KSGGRPEPIVTDATSPDYVPHVDMTNLTLSREKONMAERLADNAHDIWAKKKEBELVT 3000
Db      2941 KSGGRPEPIVTDATSPDYVPHVDMTNLTLSREKONMAERLADNAHDIWAKKKEBELVT 3000

RESULT 2
US-10-668-767-130
Sequence 130, Application US/10668767
Publication No. US2004017114A1
GENERAL INFORMATION:
APPLICANT: Caesar, Timothy
APPLICANT: Cordova, Daniel
APPLICANT: Guttridge, Steven
APPLICANT: Rauh, James
APPLICANT: Smith, Rejane
APPLICANT: Tao, Yong
APPLICANT: Wu, Jihong
TITLE OF INVENTION: Isolation and Use of Ryanodine Receptors
FILE REFERENCE: B15133 US NA
CURRENT APPLICATION NUMBER: US/10/668,767
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: 60/412,795
PRIOR FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 60/427,324
PRIOR FILING DATE: 2002-11-18
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PatentIn version 3.1
SEQ ID NO 130
LENGTH: 5134
TYPE: PRT
ORGANISM: Heliothis virescens
FEATURE:
OTHER INFORMATION: PKL-Hv2
US-10-668-767-130

Query Match      99.7%; Score 15693.5; DB 4; Length 5134;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2992; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

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Qy      1 MABEAGSASEQDDVSFLRTEDVCLSCITATGERVCLAAEGFGRNCFLENIADKXIPDL 60
Db      1 MABEAGSASEQDDVSFLRTEDVCLSCITATGERVCLAAEGFGRNCFLENIADKXIPDL 60
Qy      61 SOCVPIEQLSVRALQELVTAAGSETGKTSGHRTLLYGNAILLRHNSDMWYLAJLST 120
Db      61 SOCVPIEQLSVRALQELVTAAGSETGKTSGHRTLLYGNAILLRHNSDMWYLAJLST 120
Qy      121 SSSODKLAPDVGLQOHSQGEACMWTLHPASKORSEBEKRVGDLLIVVATERVLAHTTK 180
Db      121 SSSODKLAPDVGLQOHSQGEACMWTLHPASKORSEBEKRVGDLLIVVATERVLAHTTK 180
Qy      181 BNEVSIVNASFVYTHNSVOPYGTGTSIRMKYGVYFGDYLRFPHGDECLTIPSTTKOG 240
Db      181 BNEVSIVNASFVYTHNSVOPYGTGTSIRMKYGVYFGDYLRFPHGDECLTIPSTTKOG 240
Qy      241 GQNIIVYEGGSVMSQARSIMRLLELATKWAAGFINNYHMPRLRHITTTGYLVGNDDNELY 300
Db      241 GQNIIVYEGGSVMSQARSIMRLLELATKWAAGFINNYHMPRLRHITTTGYLVGNDDNELY 300
Qy      301 LYSREBATTAASCAFLCROEKDQKQVLEBDKLEVIAPITIKYGDSTVIYQHSBTGLMLSY 360
Db      301 LYSREBATTAASCAFLCROEKDQKQVLEBDKLEVIAPITIKYGDSTVIYQHSBTGLMLSY 360
Qy      361 KSYETKKGVKVEKROAILHEBGKMDGLDPSRQSEBSRTARVIRKCSLFTKFINGL 420
Db      361 KSYETKKGVKVEKROAILHEBGKMDGLDPSRQSEBSRTARVIRKCSLFTKFINGL 420
Qy      421 EITQERHRISMPPASVNLGEMWCLDLINYPADPDEMEHEKOKFALRYRQDLFOE 480
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Qy      481 EGIINLILEAIDKINITYSOGFLAGFLAGDESQSEMIISGYLYQLAAIKGNHTNCAQ 540
Db      481 EGIINLILEAIDKINITYSOGFLAGFLAGDESQSEMIISGYLYQLAAIKGNHTNCAQ 540
Qy      541 PANSNRLNMLFSRLGSQASGEGTMDVLHCVLIDSPEALNMWRDEHIKVIISLEKGR 600
Db      541 PANSNRLNMLFSRLGSQASGEGTMDVLHCVLIDSPEALNMWRDEHIKVIISLEKGR 600
Qy      601 DPEYLDVLCSLCYNGGVAVRSSQNNICDYLLPGRKILLQTLAVDHTSSVRPNI FVGRVGE 660
Db      601 DPEYLDVLCSLCYNGGVAVRSSQNNICDYLLPGRKILLQTLAVDHTSSVRPNI FVGRVGE 660
Qy      661 SAYYRKWYFEVMTDHIKTTTHMPLIRIGNANTGYVYPYGGGKKGVNGVDLVSYGF 720
Db      661 SAYYRKWYFEVMTDHIKTTTHMPLIRIGNANTGYVYPYGGGKKGVNGVDLVSYGF 720
Qy      721 DGAYLWSGRKTPVNRTHAEPYIRKGDVIGCALDLTVPIINMFNGVAVTSGFTFNPLE 780
Db      721 DGAYLWSGRKTPVNRTHAEPYIRKGDVIGCALDLTVPIINMFNGVAVTSGFTFNPLE 780
Qy      781 GMEFPVISCSSKLSGCPFLGGEHGLRYAAPGYSPVBSLLPQOLLSJEPCCYFGNLK 840
Db      781 GMEFPVISCSSKLSGCPFLGGEHGLRYAAPGYSPVBSLLPQOLLSJEPCCYFGNLK 840
Qy      841 BALAGPVLVODDPAFPTPVDTQITLPTVVEQIRPKLAENIHEMAMKIBAGMYGDO 900
Db      841 BALAGPVLVODDPAFPTPVDTQITLPTVVEQIRPKLAENIHEMAMKIBAGMYGDO 900
Qy      901 REDLAKIHPLCLVFERPLPAEKRYDIQLAVQTLKTLIALGYIISLDPKPARINVL PNE 960
Db      901 REDLAKIHPLCLVFERPLPAEKRYDIQLAVQTLKTLIALGYIISLDPKPARINVL PNE 960
Qy      961 PFMQSNGYKPAPIJLSAVTLTPPMDELVDQLAENTNMLAREETIOGWTYGLNEDSDMR 1020
Db      961 PFMQSNGYKPAPIJLSAVTLTPPMDELVDQLAENTNMLAREETIOGWTYGLNEDSDMR 1020
Qy      1021 SPHLVYPKVDADIKKANRDTASVYRTLLVGYMDLPTGBOEALLLEASAKOXADFR 1080
Db      1021 SPHLVYPKVDADIKKANRDTASVYRTLLVGYMDLPTGBOEALLLEASAKOXADFR 1080
Qy      1081 TYBAKRYAVSSGKMYFBEPIILTAGPMRVGMADNA PGMLLQGDENSMAPDGYNEBKVY 1140

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RESULT 3
US-10-668-767-144
; Sequence 144, Application US/10668767
; Publication No. US2004017114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutierrez, Steven
; APPLICANT: Raun, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Mu, LiHong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA

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/ CURRENT APPLICATION NUMBER: US/10/668.767
/ CURRENT FILING DATE: 2003-09-23
/ PRIOR APPLICATION NUMBER: 60/412.795
/ PRIOR FILING DATE: 2002-09-23
/ PRIOR APPLICATION NUMBER: 60/427.324
/ PRIOR FILING DATE: 2002-11-18
/ NUMBER OF SEQ ID NOS: 149
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 144
/ LENGTH: 5142
/ TYPE: PRT
/ ORGANISM: Heliothis virescens
/ FEATURE:
/ OTHER INFORMATION: pXL-Hv3
US-10-668-767-144

Query Match      99.4%; Score 15655.5; DB 4; Length 5142;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2988; Conservative 5; Mismatches 7; Indels 9; Gaps 2;

QY      1 MABEAGASBODVSPFLRTEDMYCLSTATGERVCLAAEGFNHCFLENIADKNIPDL 60
DB      1 MABEAGASBODVSPFLRTEDMYCLSTATGERVCLAAEGFNHCFLENIADKNIPDL 60
QY      61 SQCVPIEOLSVRALQELVTAAGSET----GKGTSGHRTLLYGNAILLRHNSDMYL 115
DB      61 SQCVPIEOLSVRALQELVTAAGSETGKENTLGKGTSGHRTLLYGNAILLRHNSDMYL 120
QY      116 ACISTSSODKLPDVGLOHSGEACWTLHPASKORSEGEKRVGDDLLIVSVATERY 175
DB      121 ACISTSSODKLPDVGLOHSGEACWTLHPASKORSEGEKRVGDDLLIVSVATERY 180
QY      176 LHTTKNEYSIVNASFHVTHMSVOPGTGTSRMKXVGVYFGSDVLPFPHGSDCLTIPST 235
DB      181 LHTTKNEYSIVNASFHVTHMSVOPGTGTSRMKXVGVYFGSDVLPFPHGSDCLTIPST 240
QY      236 WTKDQGNIVYVEGGSYMSQARSLMRLTLARTKAGGFIMYHPMRIRHITTTGRYLVND 295
DB      241 WTKDQGNIVYVEGGSYMSQARSLMRLTLARTKAGGFIMYHPMRIRHITTTGRYLVND 300
QY      296 QNELYVSRREATTASCAPCLRQKDDQKYLEDKOLEVIGAPIIKKGDSIVYVHSETG 355
DB      301 QNELYVSRREATTASCAPCLRQKDDQKYLEDKOLEVIGAPIIKKGDSIVYVHSETG 360
QY      356 LMTSYSEYETKKKGVGVKEBKQALIHBEKMDGLDERSOEBESRTARIYRKCSSLFTK 415
DB      361 LMTSYSEYETKKKGVGVKEBKQALIHBEKMDGLDERSOEBESRTARIYRKCSSLFTK 420
QY      416 FINGLETLOENRHSMPFASVNLGEMVCLLDLINTYPAQPEDDMHEHEKQNKFRALNRQ 475
DB      421 FINGLETLOENRHSMPFASVNLGEMVCLLDLINTYPAQPEDDMHEHEKQNKFRALNRQ 480
QY      476 DLFOEBGILNLILEADKINVTISQGFPLAGFLAGDESGSWEMISGYLYOLLAAIYKGN 535
DB      481 DLFOEBGILNLILEADKINVTISQGFPLAGFLAGDESGSWEMISGYLYOLLAAIYKGN 540
QY      536 TNCQAPANSRLMLPBRGLSOSGEGTGLDVLVHCTLIDSPRALNMREBEHKVIIISL 595
DB      541 TNCQAPANSRLMLPBRGLSOSGEGTGLDVLVHCTLIDSPRALNMREBEHKVIIISL 600
QY      596 EKEGRDPKVDVLCSLCVGNGVAVRSSQNNICDYLTPGKILLQTLALVDHVSVPNIPV 655
DB      601 EKEGRDPKVDVLCSLCVGNGVAVRSSQNNICDYLTPGKILLQTLALVDHVSVPNIPV 660
QY      656 GRAVEGASVYRKMTPEVTMDHI EKTTHMPHLRIGMANTTGYVYPGGGEKMGANGVDDL 715
DB      661 GRAVEGASVYRKMTPEVTMDHI EKTTHMPHLRIGMANTTGYVYPGGGEKMGANGVDDL 720
QY      716 YSYGPDAAVYMSGGRKTPVNRTHABBPYIRKGVYIGALDLYVTIINPMNGRVYVSSFT 775
DB      721 YSYGPDAAVYMSGGRKTPVNRTHABBPYIRKGVYIGALDLYVTIINPMNGRVYVSSFT 780
QY      776 NPNLEGMFPVIVGSSKSLSCRFLLGGBHRLRYAAPGYSPLVESLLPQOILSLPFCYF 835

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DB      781 NPNLEGMFPVIVGSSKSLSCRFLLGGBHRLRYAAPGYSPLVESLLPQOILSLPFCYF 840
QY      836 GNLSKRALAGPPLVODDTAFVPTPVDTLOITLPTVEQIRDKLAENIHMMANNKIEAGV 895
DB      841 GNLSKRALAGPPLVODDTAFVPTPVDTLOITLPTVEQIRDKLAENIHMMANNKIEAGV 900
QY      896 MYGDQREDLHKHPCLVPEERLPPAEKRYDIOALVOTLTITIALGYIISLDEKPARIRV 955
DB      901 MYGDQREDLHKHPCLVPEERLPPAEKRYDIOALVOTLTITIALGYIISLDEKPARIRV 960
QY      956 RLPNRPFMSNGKPARPLDSAVTLTPKDELDVDOALAEVTHNMMAERIOQGTGLAND 1015
DB      961 RLPNRPFMSNGKPARPLDSAVTLTPKDELDVDOALAEVTHNMMAERIOQGTGLAND 1020
QY      1016 SDMHRSPHLVVPYKVDALIKKANDTASEVTRTLIVGYMLDPTTGEQHEALLLEASOK 1075
DB      1021 SDMHRSPHLVVPYKVDALIKKANDTASEVTRTLIVGYMLDPTTGEQHEALLLEASOK 1080
QY      1076 QADFRTRYABKNYAVSSGKMYEFEBILTAGPMKVGNAHADMAPGMMLGODENSWAFDGYN 1135
DB      1081 QADFRTRYABKNYAVSSGKMYEFEBILTAGPMKVGNAHADMAPGMMLGODENSWAFDGYN 1140
QY      1136 BEKVYSGNTSFGKQAVGVGVFVFDLIDKTSFSLNGBELMDALGGETTFADVGDNF 1195
DB      1141 BEKVYSGNTSFGKQAVGVGVFVFDLIDKTSFSLNGBELMDALGGETTFADVGDNF 1200
QY      1196 VPACTLVGQKALTYGQDVNTLKYFTTCGLQEGYPCVNNMGRDVTHWYTKQPIFENT 1255
DB      1201 VPACTLVGQKALTYGQDVNTLKYFTTCGLQEGYPCVNNMGRDVTHWYTKQPIFENT 1260
QY      1256 DEMIDTRIDVTRIPAGSDTPEPCLKISHNTFETMEKANWELRLSLPVI CHNEPIDEAKA 1315
DB      1261 DEMIDTRIDVTRIPAGSDTPEPCLKISHNTFETMEKANWELRLSLPVI CHNEPIDEAKA 1320
QY      1316 RRMWEIKDRQOILMKEAVEAOMPBAHIDQIRSGFTNMDIKGLHYBNQDELPSSKMRKL 1375
DB      1321 RRMWEIKDRQOILMKEAVEAOMPBAHIDQIRSGFTNMDIKGLHYBNQDELPSSKMRKL 1380
QY      1376 SRPFRKSGMTGVTIONYNNLQGOVNGMHRSTSEABMAKYDGAQGLFPDDKKDKRGRS 1435
DB      1381 SRPFRKSGMTGVTIONYNNLQGOVNGMHRSTSEABMAKYDGAQGLFPDDKKDKRGRS 1440
QY      1436 PPKFPRSKGESSDRASKRSKTPDPFSDTEVSPERGARPNQIRVSOANORVNGNAR 1495
DB      1441 PPKFPRSKGESSDRASKRSKTPDPFSDTEVSPERGARPNQIRVSOANORVNGNAR 1500
QY      1496 PSRTNLYGSOVGLAN---NATPQDRKONTSTLQASATETVGNBIFDAECLKLINBYFY 1551
DB      1501 PSRTNLYGSOVGLANMAATPQDRKONTSTLQASATETVGNBIFDAECLKLINBYFY 1560
QY      1552 GVRITYGQDPDTHYIGMTVTOYHLHSKDPFMSKVTSVYITDDYRVVENVRQSCYV 1611
DB      1561 GVRITYGQDPDTHYIGMTVTOYHLHSKDPFMSKVTSVYITDDYRVVENVRQSCYV 1620
QY      1612 RADELINWEAABATAGASQWFTIGCSVDTSVSFTCEGKDTSEFKNEPTELPAI 1671
DB      1621 RADELINWEAABATAGASQWFTIGCSVDTSVSFTCEGKDTSEFKNEPTELPAI 1680
QY      1672 FVEATSEKILQIELGASATSLPLSAAVLPSTDGHVTPQPPRLKVQCLKPHQARVPNOS 1731
DB      1681 FVEATSEKILQIELGASATSLPLSAAVLPSTDGHVTPQPPRLKVQCLKPHQARVPNOS 1740
QY      1732 LOYHALKLSDIRGMSWLCEDAVSMALHHPERBCDILIEPIMDKLASHSTLTLYAA 1791
DB      1741 LOYHALKLSDIRGMSWLCEDAVSMALHHPERBCDILIEPIMDKLASHSTLTLYAA 1800
QY      1792 LCTQSNYRAAHALCTHVQKOLLAYATQSQYMSGPLRQGFYDLLIALHLSHATTMEACN 1851
DB      1801 LCTQSNYRAAHALCTHVQKOLLAYATQSQYMSGPLRQGFYDLLIALHLSHATTMEACN 1860
QY      1852 EBYIPLGPEIKALYBEPDMGHSIRSLQTSVSRPQMKTTDIASTITRISNYSYFPLEVA 1911

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Db 1861 EFVIFPGPELKLAYEPPDMGHSLSRLQTESVRPQMKTIDIAESITETISNYSPPLELV 1920
Qy 1912 REFVMOALAEAVETNOVNRDPVGSNENLFLPLIKLVDRLLVGNMDEDEKLLIMTN 1971
Db 1921 REFVMOALAEAVETNOVNRDPVGSNENLFLPLIKLVDRLLVGNMDEDEKLLIMTN 1980
Qy 1972 PETWDSFPKGGDERKGLIHKMAEGACLQMCYLLQHLNDIQLHRYEALIIAPADPV 2031
Db 1981 PETWDSFPKGGDERKGLIHKMAEGACLQMCYLLQHLNDIQLHRYEALIIAPADPV 2040
Qy 2032 GDLQTOQLRRYTEIKOSDLPAAVAAKKEFRCPPEONMAIISFPHLEEDKENCPCG 2091
Db 2041 GDLQTOQLRRYTEIKOSDLPAAVAAKKEFRCPPEONMAIISFPHLEEDKENCPCG 2100
Qy 2092 ELIARNNEFHDTLMHVSLHALQEPDAENQEPAAFGKLYNINTVKELEBAKA1 2151
Db 2101 ELIARNNEFHDTLMHVSLHALQEPDAENQEPAAFGKLYNINTVKELEBAKA1 2160
Qy 2152 BEPPKKTPEBKPRKVLIOITVMAESQIETPKLVEMSGSLVROYDANGELIRALEKTY 2211
Db 2161 BEPPKKTPEBKPRKVLIOITVMAESQIETPKLVEMSGSLVROYDANGELIRALEKTY 2220
Qy 2212 VINAKTKLVAAEMWVGLSOIRALLPVQMSQEEBELMRKLMKLVNHTTFQHPDLIRVLR 2271
Db 2221 VINAKTKLVAAEMWVGLSOIRALLPVQMSQEEBELMRKLMKLVNHTTFQHPDLIRVLR 2280
Qy 2272 VHENVAVAMNTLGRBAQASDAQSPVABDSKEKOTSHENVVACSRFLCYFCRTGRQ 2331
Db 2281 VHENVAVAMNTLGRBAQASDAQSPVABDSKEKOTSHENVVACSRFLCYFCRTGRQ 2340
Qy 2332 NOKAMDHDFLLNENIILSRPSLFGSTPLDVAYSLSMENTELALAEHILEKAVYL 2391
Db 2341 NOKAMDHDFLLNENIILSRPSLFGSTPLDVAYSLSMENTELALAEHILEKAVYL 2400
Qy 2392 SRGLOSNELEVEKGYPDGMPDVEGERLUDFLRFQWNGESVEENANLVIRLRRE 2451
Db 2401 SRGLOSNELEVEKGYPDGMPDVEGERLUDFLRFQWNGESVEENANLVIRLRRE 2460
Qy 2452 CLGPAIRGEGEGLIKAVDANKMSERLADRRKLRREMGQDVNFSPHLPESDEDEDYDT 2511
Db 2461 CLGPAIRGEGEGLIKAVDANKMSERLADRRKLRREMGQDVNFSPHLPESDEDEDYDT 2520
Qy 2512 GAAILNFYCTIYDLGRCAPDAGVIALGKNEISRAAIIIRSLVPLEDLOGVSLKRTTLN 2571
Db 2521 GAAILNFYCTIYDLGRCAPDAGVIALGKNEISRAAIIIRSLVPLEDLOGVSLKRTTLN 2580
Qy 2572 PAAGEBRPKSDMPSGLIPGHKOSVGLFERVYGIETQELFYKLLEBAFLPDLRAATMLR 2631
Db 2581 PAAGEBRPKSDMPSGLIPGHKOSVGLFERVYGIETQELFYKLLEBAFLPDLRAATMLR 2640
Qy 2632 NDGCESDMALSMNRYIGNSILPLLIKHAIFYNEAENYASILDATLHTVYRLSKNMLTKG 2691
Db 2641 NDGCESDMALSMNRYIGNSILPLLIKHAIFYNEAENYASILDATLHTVYRLSKNMLTKG 2700
Qy 2692 QBEAVSDFLVALTSAMQPSMLKLRKLVVDVSKLSEYTTVALRIITLHYERCAKTYGT 2751
Db 2701 QBEAVSDFLVALTSAMQPSMLKLRKLVVDVSKLSEYTTVALRIITLHYERCAKTYGT 2760
Qy 2752 GAGGQAFGASDEBEKRLTMWLFNSNIFDSLSKMDYBELFGKALPCLIAIGCALPPDYS 2811
Db 2761 GAGGQAFGASDEBEKRLTMWLFNSNIFDSLSKMDYBELFGKALPCLIAIGCALPPDYS 2820
Qy 2812 KNYDDEFYGEQQAAGLDNDPOYDPOPIINTSSVALNNDLNTIVOKSEHHDAMASRKEN 2871
Db 2821 KNYDDEFYGEQQAAGLDNDPOYDPOPIINTSSVALNNDLNTIVOKSEHHDAMASRKEN 2880
Qy 2872 GMYVYBGWSDQKTHPRKPYMMLNDYERKYEKPEPRESLKALLAIGMSVEHSEVDIPSN 2931
Db 2881 GMYVYBGWSDQKTHPRKPYMMLNDYERKYEKPEPRESLKALLAIGMSVEHSEVDIPSN 2940
Qy 2932 NNSNRROGSGGRRPEIYTDSATPFYDNPYDMNLTLSRBOMMARLADNADHWA 2991
Db 2941 NNSNRROGSGGRRPEIYTDSATPFYDNPYDMNLTLSRBOMMARLADNADHWA 3000

Qy 2992 KKKKEELVT 3000
Db 3001 KKKKEELVT 3009

RESULT 4
US-10-668-767-2
; Sequence 2, Application US/10668767
; Publication No. US2004017114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Guteridge, Steven
; APPLICANT: Raul, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 5142
; TYPE: PRT
; ORGANISM: Heliothis virescens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1755)..(1755)
; OTHER INFORMATION: Xaa = Ser
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (4250)..(4250)
; OTHER INFORMATION: Xaa = Thr
US-10-668-767-2

Query Match 98.7%; Score 15550.5; DB 4; Length 5142;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 2966; Conservative 12; Mismatches 22; Indels 9; Gaps 2;

Qy 1 MAEAGGASBODDVFELRTEDMVCISCTATGRVCLABGFGRNRCPLENTADKNIPPL 60
Db 1 MAEAGGASBODDVSILRTEDMVCISCTATGRVCLABGLGNRRHCFLENTADKNIPPL 60
Qy 61 SQCFVIEQALSVRALQELVTPAGSET-----GKGTSQGHRTLLYGNAILLRHLSNDWYL 115
Db 61 SQCFVIEQALSVRALQELVTPAGSETKENNGKGTSGYRLLYGNAILLHLSNDWYL 120
Qy 116 ACLTSSSQDCLAFVGLQCHSQGEACWTLHPASKORSEGEKRVGDDLIVSVATERY 175
Db 121 ACLTSSSQDCLAFVGLQCHSQGEACWTLHPASKORSEGEKRVGDDLIVSVATERY 180
Qy 176 LHTTBENSVITNASFHTHNSVOPYGTGISMKYVGVFGSDVLRPFHGGDECLTTPST 235
Db 181 LHTTBENSVITNASFHTHNSVOPYGTGISMKYVGVFGSDVLRPFHGGDECLTTPST 240
Qy 236 WTKDGGQNIIVYEGGSVNSQARSILMRLELATTKNAGCFINWYPMRIRHITTRGYLVND 295
Db 241 WTKDGGQNIIVYKGSVNSQARSILMRLELATTKNAGCFINWYPMRIRHITTRGYLVND 300
Qy 296 QNELYLVREATATASCFCIRQEKDQKQVLEDKQLEVIQAPIIKYGDSTVIYVQHSSTG 355
Db 301 QNELYLVREBETATASCFCIRQEKDQKQVLEDKQLEVIQAPIIKYGDSTVIYVQHSSTG 360
Qy 356 LMLSVKSYETKKKGKGVKEKQALIHGSKMDGGLDPSRSQEESERTARVIRKGSGLFTK 415
Db 361 LMLSVKSYETKKKGKGVKEKQALIHGSKMDGGLDPSRSQEESERTARVIRKGSGLFTK 420

QY 416 PINGLETQENRHRSHFASVNLGEMVCLIEDLLINYPAQPEDMEHEBKONKFRALRNQ 475
DB 421 PINGLETQENRHRSHFASVNLGEMVCLIEDLLINYPAQPEDMEHEBKONKFRALRNQ 480
QY 476 DLFOEBGILNLIIBADKINVTISOGFLAGFLAGDSSGQWEMI SGVLVOLLAAI IKGN 535
DB 481 DLFOEBGILNLIIBADKINVTISOGFLAGFLAGDSSGQWEMI SGVLVOLLAAI IKGN 540
QY 536 TNCQANSNRLNWLPSRLGSOASGSGTGM DLVLCVLIDS PRALNMMRDEHIKVIISLL 595
DB 541 TNCQANSNRLNWLPSRLGSOASGSGTGM DLVLCVLIDS PRALNMMRDEHIKVIISLL 600
QY 596 EKHGRDPKVL DVLCSL CVNGVA VRSSQNNI CDYLLPGKULLQTLV DHSVSSVRNPIFV 655
DB 601 EKHGRDPKVL DVLCSL CVNGVA VRSSQNNI CDYLLPGKULLQTLV DHSVSSVRNPIFV 660
QY 656 GRVGSAYVRKMYFEVYTMDEI EKTTHM PHLRIGMANTTGYVY PGGGEKMGANGVDDL 715
DB 661 GRVGSAYVRKMYFEVYTMDEI EKTTHM PHLRIGMANTTGYVY PGGGEKMGANGVDDL 720
QY 716 YSYGPDGAYLMSGGRKTPVNRTHABEPIRKGDVIGCALDLTVPIINFMNGVRYVGSFT 775
DB 721 YSYGPDGAYLMSGGRKTPVNRTHABEPIRKGDVIGCALDLTVPIINFMNGVRYVGSFT 780
QY 776 NPLBGMFPFVLS CSSKLS CRFLGSGHGLRYAAEGYS PLVESILLPOQILSLBECFYF 835
DB 781 NPLBGMFPFVLS CSSKLS CRFLGSGHGLRYAAEGYS PLVESILLPOQILSLBECFYF 840
QY 836 GNLSCALAGPRLVODDTAFVPTPVDTLQITLPTTYEQIRDKLAENIHEKMANNKI EAG 895
DB 841 GNLSCALAGPRLVODDTAFVPTPVDTLQITLPTTYEQIRDKLAENIHEKMANNKI EAG 900
QY 896 MNGDQBEDLHKHPCVPERLPAKRYDIO LAVOTLKTILAGYIISDKRPAPIRNY 955
DB 901 MNGDQBEDLHKHPCVPERLPAKRYDIO LAVOTLKTILAGYIISDKRPAPIRNY 960
QY 956 RLPNEBFMOSNGYKPA PLDSAVTLTPKMDLVOLAE NTHNIMABERLOCGWTYGLNED 1015
DB 961 RLPNEBFMOSNGYKPA PLDSAVTLTPKMDLVOLAE NTHNIMABERLOCGWTYGLNED 1020
QY 1016 SDMHRSPHLYPYKVDDAIKKANRDTASEVTRTLVGYMLDPTGBOHEALLLEBSKOK 1075
DB 1021 SDMHRSPHLYPYKVDDAIKKANRDTASEVTRTLVGYMLDPTGBOHEALLLEBSKOK 1080
QY 1076 QADFRYRAEKYNAVSGKYPFEBILTAGPMKVGMAHADMAPGMMLGQDENS WAFDGYN 1135
DB 1081 QADFRYRAEKYNAVSGKYPFEBILTAGPMKVGMAHADMAPGMMLGQDENS WAFDGYN 1140
QY 1136 BEKYVSGNTESFGKQNAVGDVGVPLDLIDKTI SFSLNGELMDALGSETTPADVOGDNF 1195
DB 1141 BEKYVSGNTESFGKQNAVGDVGVPLDLIDKTI SFSLNGELMDALGSETTPADVOGDNF 1200
QY 1196 VPACTIGVGKALTYGQDVNTLKYFTTCGLQSGYBFCVNMKRDVTHWYTKOPIFENT 1255
DB 1201 VPACTIGVGKALTYGQDVNTLKYFTTCGLQSGYBFCVNMKRDVTHWYTKOPIFENT 1260
QY 1256 DEMIDRIDVTIRIPASGDPFPCIKISHTNTEMEKANMEFLRLSLPTCINERIDAEKKA 1315
DB 1261 DEMIDRIDVTIRIPASGDPFPCIKISHTNTEMEKANMEFLRLSLPTCINERIDAEKKA 1320
QY 1316 RARVETIKDROQILMKEAVEAQMPAHI DOIKRSGFTMNDIKGLHYBDQBELPSSKMKRLP 1375
DB 1321 RARVETIKDROQILMKEAVEAQMPAHI DOIKRSGFTMNDIKGLHYBDQBELPSSKMKRLP 1380
QY 1376 SRPFRKSGMTRGYTIQYNNYLQPGQVNGMHRSTSEAMATYDGAQGLTPDDKDXGRS 1435
DB 1381 SRPFRKSGMTRGYTIQYNNYLQPGQVNGMHRSTSEAMATYDGAQGLTPDDKDXGRS 1440
QY 1436 PRFPFRSGKSSDRAASRKSCTPDPSDTEVSPERABRPNOIKYSQANORVYNGNAR 1495
DB 1441 PRFPFRSGKSSDRAASRKSCTPDPSDTEVSPERABRPNOIKYSQANORVYNGNAR 1500

QY 1496 PSRTNLYGSQVGLN---MATPQDRKQMTTSTLQASATETVONETIPDABCLKLINEYF 1551
DB 1501 PSRTNLYGSQVGLN---MATPQDRKQMTTSTLQASATETVONETIPDABCLKLINEYF 1560
QY 1552 GVRITPGQDPHTYVIGMWTTOYHNSKDPNOSKVTSYVITDDYRVAENVNRQSCYNY 1611
DB 1561 GVRITPGQDPHTYVIGMWTTOYHNSKDPNOSKVTSYVITDDYRVAENVNRQSCYNY 1620
QY 1612 RADELVNEVMAEATAKAGASQGFICGSVDSTGVS VFTCEKQDTSFKPKQMBETKLPPI 1671
DB 1621 RADELVNEVMAEATAKAGASQGFICGSVDSTGVS VFTCEKQDTSFKPKQMBETKLPPI 1680
QY 1672 FVBATSKELIOLBELGSAFSLPSAAVLPSTDKHYVPOPPRILKVOCLKPHQABRPNOS 1731
DB 1681 SVEATSKELIOLBELGSAFSLPSAAVLPSTDKHYVPOPPRILKVOCLKPHQABRPNOS 1740
QY 1732 LOVHALKSDIGMSWLCEDAVSMALNHPBEBRCIDILEPTEMDGLSFHSHTLTLTYA 1791
DB 1741 LOVHALKSDIGMSWLCEDAVSMALNHPBEBRCIDILEPTEMDGLSFHSHTLTLTYA 1800
QY 1792 LCYQSNYRAAHALCTHVDQKOLLYAIOQYMSGPLRQGEYDILLALHLSHATTMBAKRN 1851
DB 1801 LCYQSNYRAAHALCTHVDQKOLLYAIOQYMSGPLRQGEYDILLALHLSHATTMBAKRN 1860
QY 1852 EFVITPLGPELKLAYEEDMGHSIRSIQTESVRPQMKMTDIABSIITISNYSYFPLEVA 1911
DB 1861 EFVITPLGPELKLAYEEDMGHSIRSIQTESVRPQMKMTDIABSIITISNYSYFPLEVA 1920
QY 1912 REFVMOALAEVETNOVNRDPVGSNENLPLRLGVRLILVGMARDBDVKLLIMTN 1971
DB 1921 REFVMOALAEVETNOVNRDPVGSNENLPLRLGVRLILVGMARDBDVKLLIMTN 1980
QY 1972 PETWDSFKGEGDEHRRKGLIHKMAEAGAKIQMCYLLQHLNDIQLSHRVEALIAFADHFV 2031
DB 1981 PETWDSFKGEGDEHRRKGLIHKMAEAGAKIQMCYLLQHLNDIQLSHRVEALIAFADHFV 2040
QY 2032 GDIQTDQLRRYTRIKOSDLP SAAVAKTBRFCRPREQONAIISFNLBEBDEKNCPCGE 2091
DB 2041 GDIQTDQLRRYTRIKOSDLP SAAVAKTBRFCRPREQONAIISFNLBEBDEKNCPCGE 2100
QY 2092 ELIABNNEFHDTLMAVSLHAIQEPDAENQBEAARGA FGKLYNIIINWYKLEBEEKAI 2151
DB 2101 ELIABNNEFHDTLMAVSLHAIQEPDAENQBEAARGA FGKLYNIIINWYKLEBEEKAI 2160
QY 2152 BEPCKTPEBEKFKVLIQITIVNABESQIETPLVABEMFSLVRODAGELIRALEKTY 2211
DB 2161 BEPCKTPEBEKFKVLIQITIVNABESQIETPLVABEMFSLVRODAGELIRALEKTY 2220
QY 2212 VINAKTKLDVAEMWVGLSQIRALLPVQMSQEBEELMRKLMKLVNNHTFPQHPDLIRVLR 2271
DB 2221 VINAKTKLDVAEMWVGLSQIRALLPVQMSQEBEELMRKLMKLVNNHTFPQHPDLIRVLR 2280
QY 2272 VHENVNAVMMNTIGRAQAOQSDAQBSSOPVABESKCKOTSHENVVACCPFLCFCTGTGRQ 2331
DB 2281 VHENVNAVMMNTIGRAQAOQSDAQBSSOPVABESKCKOTSHENVVACCPFLCFCTGTGRQ 2340
QY 2332 NOKAMFHDPEFLLENSNIIILSRPSLKGSTPLDVAYSLSMENTELALAREHYLEKIAVYL 2391
DB 2341 NOKAMFHDPEFLLENSNIIILSRPSLKGSTPLDVAYSLSMENTELALAREHYLEKIAVYL 2400
QY 2392 SRCGLQSNBELVEKGYPDLGMPDVGBERYLDLRFPCVWNGSVBENANLVIRLLIRRPE 2451
DB 2401 SRCGLQSNBELVEKGYPDLGMPDVGBERYLDLRFPCVWNGSVBENANLVIRLLIRRPE 2460
QY 2452 CLQPALRGSEGLLKAIVYANKKSERIADRRKLRMEQSGDVNFSHPLPSSDDEBYIDT 2511
DB 2461 CLQPALRGSEGLLKAIVYANKKSERIADRRKLRMEQSGDVNFSHPLPSSDDEBYIDT 2520
QY 2512 GAAILNFYCTVLDLGRCAPDAGVIALGKNESIRABAILRSVLPLBDLQGVSLRFTLNN 2571
DB 2521 GAAILNFYCTVLDLGRCAPDAGVIALGKNESIRABAILRSVLPLBDLQGVSLRFTLNN 2580
QY 2572 PAAGBBRPKSDMPSGLIPGHKQSVGLFLBRVYGIETQELPYKLLBEAFPLDLRAATMLDR 2631

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Db 2581 PAAGERRPKSDMPSGLTGHKQSVGLFAGVYGLTQVLEFYLKLEBAFLDLRAATMLDR 2640
Qy 2632 NDCESDMALSMNRYYIGNSILPLIIKAYFENEANYASLLDATTHTVRLSKRM/LTKG 2691
Db 2641 NDCESDMALSMNRYYIGNSILPLIIKAYFENEANYASLLDATTHTVRLSKRM/LTKG 2700
Qy 2692 QREAVSDPLVALTSANOPSM/LKLRGLTVDSKLSYTTVALRLTLHYERCAKYYGST 2751
Db 2701 QREAVSDPLVALTSANOPSM/LKLRGLTVDSKLSYTTVALRLTLHYERCAKYYGST 2760
Qy 2752 GAGQAFGASDDEKRLTMM/LPSNIPDSLSKMDYEPRLPGKALPC/LIAGCALPPOYSLS 2811
Db 2761 GAGQAFGASDDEKRLTMM/LPSNIPDSLSKMDYEPRLPGKALPC/LIAGCALPPOYSLS 2820
Qy 2812 KNYDDEFGKEQAAGLDNPDQYDPOPIINTSSVALNNDLNTIYOKFSEHYHDAMASRKIEN 2871
Db 2821 KNYDDEFGKEQAAGLDNPDQYDPOPIINTSSVALNNDLNTIYOKFSEHYHDAMASRKIEN 2880
Qy 2872 GWYVGGWSDSQKTHPLKPYNMLNDYERKRYEPRESIKALLAIGMSVSESEVDI PSN 2931
Db 2881 GWYVGGWSDSQKTHPLKPYNMLNDYERKRYEPRESIKALLAIGMSVSESEVDI PSN 2940
Qy 2932 NRSSMRQSKSGRPPEIYVDSATPPDYNPHPYDMLNTLSREMONAERLADNADIVA 2991
Db 2941 NRSSMRQSKSGRPPEIYVDSATPPDYNPHPYDMLNTLSREMONAERLADNADIVA 3000
Qy 2992 KKKKEELVT 3000
Db 3001 KKKKEELVT 3009

RESULT 5
US-10-668-767-146
; Sequence 146, Application US/10668767
; Publication No. US2004017114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutierrez, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BBI53 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 146
; LENGTH: 5100
; TYPE: PRT
; ORGANISM: Heliocheila virescens
; FEATURE:
; OTHER INFORMATION: PXL-Hv6
US-10-668-767-146

Query Match 98.3%; Score 15475; DB 4; Length 5100;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 2958; Conservative 4; Mismatches 5; Indels 38; Gaps 3;
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Db 121 ACISTSSODKLAFDVGLQOHSGBAQWTLHPASQORSEGEKVRVGDILLVSATERY 180
Qy 176 LHTTKENEYSIVNASHYVTHMSVOPVGTGTSRKRYGYVPGGVNARFPHGDECLTIPST 235
Db 181 LHTTKENEYSIVNASHYVTHMSVOPVGTGTSRKRYGYVPGGVNARFPHGDECLTIPST 240
Qy 236 WTKDQGNITVVEGGSVMSQARSMLRLBELARTKAGGFINWYPMRIRHTTGRYGVND 295
Db 241 WTKDQGNITVVEGGSVMSQARSMLRLBELARTKAGGFINWYPMRIRHTTGRYGVND 300
Qy 296 QNELYIVSBEATTASCAFLAQEKDQKQVLEDKLLEYIYAPRIKYGSTVIYVHSETG 355
Db 301 QNELYIVSBEATTASCAFLAQEKDQKQVLEDKLLEYIYAPRIKYGSTVIYVHSETG 360
Qy 356 LMTSYSTYETKKKGKVKREKQALHBEKMDGDLPSHSQBEESTARYIRKCSLFTK 415
Db 361 LMTSYSTYETKKKGKVKREKQALHBEKMDGDLPSHSQBEESTARYIRKCSLFTK 420
Qy 416 FINGELTLOENRRHSWFASVNLGEMVCLBDLINYFAQPDDEMEHEBKONFRALRNQ 475
Db 421 FINGELTLOENRRHSWFASVNLGEMVCLBDLINYFAQPDDEMEHEBKONFRALRNQ 480
Qy 476 DLFOEBGILNLLLEAIDKINVTISQGLAGFLAGDESQGSWEMISGYVQLAAIIKGNH 535
Db 481 DLFOEBGILNLLLEAIDKINVTISQGLAGFLAGDESQGSWEMISGYVQLAAIIKGNH 540
Qy 536 TNCAPFANSNRLNMLFSRLGSOASGEGTGMVLVHCVLIDSPALNMRDEHIXVILSL 595
Db 541 TNCAPFANSNRLNMLFSRLGSOASGEGTGMVLVHCVLIDSPALNMRDEHIXVILSL 600
Qy 596 EKHGRDPKVLDTYLSLGVNGVAVRSONNICDYLLPGKLLQLRLVHVSVRNIYF 655
Db 601 EKHGRDPKVLDTYLSLGVNGVAVRSONNICDYLLPGKLLQLRLVHVSVRNIYF 660
Qy 656 GRVBSAVYRKMYFEVYMDHIEKTHMPHLRIGMANTGYVYPGGEKMGNGVGDLL 715
Db 661 GRVBSAVYRKMYFEVYMDHIEKTHMPHLRIGMANTGYVYPGGEKMGNGVGDLL 720
Qy 716 YSYGPDGATVLSGSKRTPNRTHABEPTIRKQDVGICALDLTVPIINFPNGRYVTGST 775
Db 721 YSYGPDGATVLSGSKRTPNRTHABEPTIRKQDVGICALDLTVPIINFPNGRYVTGST 780
Qy 776 NFNLEGMFPFVYSCSSKSCRFILGGBHGRLEYAAPBGVSPVBSLLPQOILSLBPCF 835
Db 781 NFNLEGMFPFVYSCSSKSCRFILGGBHGRLEYAAPBGVSPVBSLLPQOILSLBPCF 840
Qy 836 GNLKRALAGPPLVODDTAFVPTPVDTLOITLPTVYBQIRDKLAENIHEMAMANKLEAG 895
Db 841 GNLKRALAGPPLVODDTAFVPTPVDTLOITLPTVYBQIRDKLAENIHEMAMANKLEAG 900
Qy 896 MYGDQREDLHKTHPCVLPPEERLPAPAKRYDOLAVQTLKTIYALGYISLDRPARIRV 955
Db 901 MYGDQREDLHKTHPCVLPPEERLPAPAKRYDOLAVQTLKTIYALGYISLDRPARIRV 960
Qy 956 RLPNRPFQOSNGYKAPLDLSAVTLPKMDLVDOLAENTHNLMAERIQOQMTYGLAND 1015
Db 961 RLPNRPFQOSNGYKAPLDLSAVTLPKMDLVDOLAENTHNLMAERIQOQMTYGLAND 1020
Qy 1016 SDMHSRPHLVYPKYVDALIKKANRDYASBYVTLTVYGYMLDPPTGBOHEALLLEASOK 1075
Db 1021 SDMHSRPHLVYPKYVDALIKKANRDYASBYVTLTVYGYMLDPPTGBOHEALLLEASOK 1080
Qy 1076 QADFTTYAEKXVAVSSGKWTFFEBIILTAGPMRVGMADMAFGMLGODENSMAFDGYN 1135
Db 1081 QADFTTYAEKXVAVSSGKWTFFEBIILTAGPMRVGMADMAFGMLGODENSMAFDGYN 1140
Qy 1136 BEKYVSGMTESFGKQWAVGVVGVFLDILDKTISLNGELMDLAGEFTTADVOGDNF 1195
Db 1141 BEKYVSGMTESFGKQWAVGVVGVFLDILDKTISLNGELMDLAGEFTTADVOGDNF 1200
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QY 1196 VPACTLGVGQARLTYGQDVNTLKYFTTQGLQEGYEPFCVNNKRDVTHMYTKDQIPFENT 1255
DB 1201 VPACTLGVGQARLTYGQDVNTLKYFTTQGLQEGYEPFCVNNKRDVTHMYTKDQIPFENT 1260
QY 1266 DEMIDTRIDVTRIPAGSDTPCLKISNHTFETMECANWELSLPVCYCHNEFTDEAKA 1315
DB 1261 DEMIDTRIDVTRIPAGSDTPCLKISNHTFETMECANWELSLPVCYCHNEFTDEAKA 1320
QY 1316 RRMVETIKORQOILMEBAVEAQAQPAHIDQIMRSGFTMNDIKGLHYDNQBELPSSKMKRLP 1375
DB 1311 RRMVETIKORQOILMEBAVEAQAQPAHIDQIMRSGFTMNDIKGLHYDNQBELPSSKMKRLP 1380
QY 1376 SRPPEKSGWTRGVTTQNYNNLQPGVNGMHRSTSEMAKYDLAGQGLTPDDKDKRGGS 1435
DB 1381 SRPPEKSGWTR-----GQVNGMHRSTSEMAKYDLAGQGLTPDDKDKRGGS 1428
QY 1436 PFKFRSRKGSBSSDAKSKKSTPPSPSTEVSPERGARRPVPQIKVGOANRNYGMAR 1495
DB 1429 PFKFRSRKGSBSSDAKSKKSTPPSPSTEVSPERGARRPVPQIKVGOANRNYGMAR 1481
QY 1496 PBRNTLYSOGVGLNMAPTPODRKQMTSTLAQSATETVGNELFDAECLKLINEFYGYRI 1555
DB 1482 -----NATPTQDRKQMTSTLAQSATETVGNELFDAECLKLINEFYGYRI 1527
QY 1556 YPGQDPTHYIGWTTQYHLHSKDFNQSRYTKSVYITDDYDRVVENVNRQSCYVNRDE 1615
DB 1528 YPGQDPTHYIGWTTQYHLHSKDFNQSRYTKSVYITDDYDRVVENVNRQSCYVNRDE 1587
QY 1616 LYNEVMAEATKAGASQGMFICGSVDTSTGVSFTEBGKDTSEFKPMPEPTKLPFAIPVEA 1675
DB 1588 LYNEVMAEATKAGASQGMFICGSVDTSTGVSFTEBGKDTSEFKPMPEPTKLPFAIPVEA 1647
QY 1676 TSKEILOIBLGSASISPLSAVLPSTDHVIPOPPRLKVQCLKPHQARPNQSLQVH 1735
DB 1648 TSKEILOIBLGSASISPLSAVLPSTDHVIPOPPRLKVQCLKPHQARPNQSLQVH 1707
QY 1736 ALKSDIDIGMSMLCEDAVSMALAHIPEDRCIDILEPIEMDKLSFHSHTLLTYALCYO 1795
DB 1708 ALKSDIDIGMSMLCEDAVSMALAHIPEDRCIDILEPIEMDKLSFHSHTLLTYALCYO 1767
QY 1796 SNYRAAHLCTHVQKOLLYAIOQOYMSGRLQGFYDLIALHLSHAATMCAKXBEFY 1855
DB 1768 SNYRAAHLCTHVQKOLLYAIOQOYMSGRLQGFYDLIALHLSHAATMCAKXBEFY 1827
QY 1856 PLGPELKLAYERPDHSHLSRSIQTESVPRQMKOTIDABSITISNLYSYFFLEBVARFV 1915
DB 1828 PLGPELKLAYERPDHSHLSRSIQTESVPRQMKOTIDABSITISNLYSYFFLEBVARFV 1887
QY 1916 MOALAEAVSTQVNRDPVGSNENLFLPLIKLVDRLLVGMNRDEBVEKLLINTNPETW 1975
DB 1888 MOALAEAVSTQVNRDPVGSNENLFLPLIKLVDRLLVGMNRDEBVEKLLINTNPETW 1947
QY 1976 DPGFDKGEKDEHRKGLLHMKMAEGAKLQNCYLLQHLNDIQLRHVEALIAFAHDFVGDIO 2035
DB 1948 DPGFDKGEKDEHRKGLLHMKMAEGAKLQNCYLLQHLNDIQLRHVEALIAFAHDFVGDIO 2007
QY 2036 TDOLRKYTEIKOSDIPSAVAACKTREFRCPREBQMAIISFYLHEBEDKENCPCGEBELIA 2095
DB 2008 TDOLRKYTEIKOSDIPSAVAACKTREFRCPREBQMAIISFYLHEBEDKENCPCGEBELIA 2067
QY 2096 RMRNEFDITMAHVSILALOEPRDAERQEBKAFGAKLYNINTVKELEBBAKAIIEBP 2155
DB 2068 RMRNEFDITMAHVSILALOEPRDAERQEBKAFGAKLYNINTVKELEBBAKAIIEBP 2127
QY 2156 KKTPEKFRKVLIOITVMAESQIETPKLVREMFSLVROYDAVELIRALEKTYVINA 2215
DB 2128 KKTPEKFRKVLIOITVMAESQIETPKLVREMFSLVROYDAVELIRALEKTYVINA 2187
QY 2216 KTKLDVAEAMVVGISQIRALLPVOMSBEBELKAKLYNNTHTFQHDLLRVLRVHEN 2275
DB 2188 KTKLDVAEAMVVGISQIRALLPVOMSBEBELKAKLYNNTHTFQHDLLRVLRVHEN 2247
QY 2276 VMAVMNNTLGRBAQASDAQPSQPAEDSKKUTSHEMNVACSRFLCYFCRTGRQNGKA 2335

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DB 2248 VMAVMNNTLGRBAQASDAQPSQPAEDSKKUTSHEMNVACSRFLCYFCRTGRQNGKA 2307
QY 2336 MEDHDFLENSNITLSPRLSGSTPLDVAVSSLMENTELALAREHYLEKIAVYLSRCG 2395
DB 2308 MEDHDFLENSNITLSPRLSGSTPLDVAVSSLMENTELALAREHYLEKIAVYLSRCG 2367
QY 2396 LOSNSELVEKGYPDLGMDPVEGERYDLRFQVWNGSVEBANLVIRLLIRREDCGP 2455
DB 2368 LOSNSELVEKGYPDLGMDPVEGERYDLRFQVWNGSVEBANLVIRLLIRREDCGP 2427
QY 2456 ALRGEGBELKAIYDANKSERIADRCLREMEQGDVNPBHPLEPESBEDDYIDTGAII 2515
DB 2428 ALRGEGBELKAIYDANKSERIADRCLREMEQGDVNPBHPLEPESBEDDYIDTGAII 2487
QY 2516 LNFYCTLVLDLGRCPADGAVIALGNESLBARAIIRSIPLLEDLOGVLSLFTLNNPAAG 2575
DB 2488 LNFYCTLVLDLGRCPADGAVIALGNESLBARAIIRSIPLLEDLOGVLSLFTLNNPAAG 2547
QY 2576 BERPSPDMPGSLIPGHKQSVGLFLERVYGIETQELFYKLEBEAFLPDLRATMLDRNDGC 2635
DB 2548 BERPSPDMPGSLIPGHKQSVGLFLERVYGIETQELFYKLEBEAFLPDLRATMLDRNDGC 2607
QY 2636 ESDMALSNMRYIGNSILPILLIKHAYFYNEAEVYASILDATHTYRLSKNRLTGORBA 2695
DB 2608 ESDMALSNMRYIGNSILPILLIKHAYFYNEAEVYASILDATHTYRLSKNRLTGORBA 267
QY 2696 VSDFLVALTSAMPQSMMLKLRKLVQVYSKLYSEYTVVALRLTLHYERCAKYSGTAGQ 2755
DB 2668 VSDFLVALTSAMPQSMMLKLRKLVQVYSKLYSEYTVVALRLTLHYERCAKYSGTAGQ 2727
QY 2756 GAFGASDEBEKRLTMMLFNSIFDSLSKMDYEBELFGKALPCIIAIGCALPDYSLSKND 2815
DB 2728 GAFGASDEBEKRLTMMLFNSIFDSLSKMDYEBELFGKALPCIIAIGCALPDYSLSKND 2787
QY 2816 DEFYKEQDAGDLNPQYDPOPIINTSVYALNNDLNTIYQKSEHYHDMAASKIENGWY 2875
DB 2788 DEFYKEQDAGDLNPQYDPOPIINTSVYALNNDLNTIYQKSEHYHDMAASKIENGWY 2847
QY 2876 GEGWSDQKTPHRLKPYMNDLYEKERYKEPREBSLKALLAIGWSESEVDYIPSNRSS 2935
DB 2848 GEGWSDQKTPHRLKPYMNDLYEKERYKEPREBSLKALLAIGWSESEVDYIPSNRSS 2907
QY 2936 MRQSGSGRPEIYTDATPEPDYNPHVDMTNLTLSMEMQMAERLADNADIAKXXX 2995
DB 2908 MRQSGSGRPEIYTDATPEPDYNPHVDMTNLTLSMEMQMAERLADNADIAKXXX 2967
QY 2996 BELVT 3000
DB 2968 BELVT 2972

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RESULT 6
 US-10-668-767-8
 ; Sequence 8, Application US/10668767
 ; Publication No. US2004017114A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Caspar, Timothy
 ; APPLICANT: Cordova, Daniel
 ; APPLICANT: Gutierrez, Steven
 ; APPLICANT: Rauh, James
 ; APPLICANT: Smith, Rejeane
 ; APPLICANT: Tao, Yong
 ; APPLICANT: Wu, Lihong
 ; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
 ; FILE REFERENCE: B01533 US NA
 ; CURRENT APPLICATION NUMBER: US/10/668,767
 ; PRIOR FILING DATE: 2003-09-23
 ; PRIOR APPLICATION NUMBER: 60/412,795
 ; PRIOR FILING DATE: 2002-09-23
 ; PRIOR APPLICATION NUMBER: 60/427,324
 ; PRIOR FILING DATE: 2002-11-18
 ; NUMBER OF SEQ ID NOS: 149

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 5127
; TYPE: prt
; ORGANISM: Pterginius maldis
; FEATURES:
;   NAME/KEY: misc_feature
;   LOCATION: (416)..(416)
;   OTHER INFORMATION: Xaa = Ile
US-10-668-767-8

Query Match      80.9%; Score 12738; DB 4; Length 5127;
Beet Local Similarity 80.5%; Pred. No. 0;
Matches 2446; Conservative 236; Mismatches 278; Indels 78; Gaps 24;

QY      1  MAEAGSASEQDDVFLRTEDMVCISCTATGERVCLAAEGFGRRCFLENIDAKNIPDL 60
DB      1  MADSSGG-SEQDDVFLRTEDMVCISCTATGERVCLAAEGFGRRCFLENIDAKNIPDL 59
QY      61  SQCFVIEQALSVRALQELVTAAAGSETGKGSGHRTLLYGNAIILRHLSDMYLACLS 120
DB      60  STCFVIEQALSVRALQELVTAAAGSEBKGSGHRTLLYGNAIILRHQNSDMYLACLS 119
QY      121  SSSQOKLAFVGLQOHSGCEACWTLHPASKORSSEGEKRVGDDILVSVATERLHATTK 180
DB      120  SSSNDKLSFVGLQEHSGCEACWTVHPASKORSSEGEKRVGDDILVSVATERLHATTK 179
QY      181  ENEVASIFVATMNSVQPYGTGISRMKTVGVFGDYLRFPHGDECLTIPSTWTKOG 240
DB      180  ENDSLIVASIFVATMNSVQPYGTGISRMKTVGVFGDYLRFPHGDECLTIPSTWSEAP 239
QY      241  GQNIIVYEGGSVMSQARSIMLELARTKAGGFIMWYHPMRIHATITGGRYLGANDQNEL 300
DB      240  GQNIIVYEGGSVMSQARSIMLELARTKAGGFIMWYHPMRIHATITGGRYLGANNELH 299
QY      301  LVSRREATTASGAFGLRQEKDQKOVLEBKDLVIGAPRIKKGDSVTIVYHSEGLMST 360
DB      300  LIVREATTALSAFCLRQEKDQKVLBDKLEVGAPRIKKGDSVTIVYHSEGLMST 359
QY      361  KSYETKKKGKGVKEEKQAILHEBGMDDGLDPSRQSEESRTARYIRKSSLFTEKINGL 420
DB      360  KSYETKKKGKGVKEEKQAVLHEBGMDDGLDPSRQSEESRTARYIRKSSLFTEPKXGL 419
QY      421  ETLQENRHSMPFASVNLGEVMVCLIEDLIINYPAQDEDEMEHEKONKFRALRNRODL 480
DB      420  ETLQVNRHSMLFCATVNLNEMVCLIEDLIINYPAQADMEHEKONFRALRNRODLQOE 479
QY      481  EGIINLILIEAIDKINVTISQGLAFGLAGDBSGQWEMI SGYLYQLLAAIIRKNTNCAQ 540
DB      480  EGIINLILIEAIDKINVTISQGLFVS-LAGDBSGQWMIISGYLYQLLAAIIRKNTNCAQ 538
QY      541  FANSNRILNMLFSRLQSQASGEGTGM,DVLAHCVLIDSPALNMNRDEHIKVIISLEKGR 600
DB      539  FANSNRILNMLFSRLQSQASSEGTGM,DVLAHCVLIDSPALNMNRDEHIKVIISLEKGR 598
QY      601  DPKVL,DVLCSLCVNGGVAVRSSQNNICDYLPGKNLLQTLVYHVS SVRPNI FVGRVEG 660
DB      599  DPKVL,DVLCSLCVNGGVAVRSSQNNICDYLPGKNLLPOTQLVDHVASVRNIFGRVVG 658
QY      661  SAVYRKWFFETTMHIEKTTMMPHLIRIGMANTTGYVYRGGGEKMGNGVGDLLYSTGF 720
DB      659  SAVYQKWFEEVYTMHIEQTHMTPLIRIGMANTSYVYRGGGEKMGNGVGDLLYSTGF 718
QY      721  DGAYLMSGKRTPVNRTAABEPIYRKGDVIGCALDLPYIINFMNGVAVTSGFTNPLB 780
DB      719  DGAYLMTSGKRTCV-LPHATEPIYKGDVIGVSLDLTPYIITFSNGSPINGCFRDEYD 777
QY      781  GMFPFVISCSSKLGCRFLGSEHGRLRYAABEGVSPLYESSLPQOILSEBQCFYFGLNSK 840
DB      778  GMFPFVISCSSKLGCRFLGSEHGRLRYAABEGVSPLYESSLPQOVLISIDPCFFGGLNSK 837
QY      841  RALAGRPVYODDTAFVPTPVDTLQTLTPTVYEQIRDKLAENIHHEWMANKIEAGMAYDQ 900
DB      841  RALAGRPVYODDTAFVPTPVDTLQTLTPTVYEQIRDKLAENIHHEWMANKIEAGMAYDQ 900
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DB      838  CVLSGPWTVEDDTAFVPTPVDTTKVLSPNYIESIRDKLAENIHHEWMANKIEAGMFGEK 897
QY      901  REDLAKIHPCLVFPERLPPAEKRYDIOAVOTLKTILAGYYSIDKDPARIRNRLPNE 960
DB      898  RDDIRKHFCLIQFQLPPEAKRYDSQIAVOTLKTILAGYIITNDKPPSRKTRILPNE 957
QY      961  PFMQNGYKPAPLDISAVTLTPKDELVDQLAENTHNLWABERRIQGWTYGLNEDSMIR 1020
DB      958  PFMQNGYKPAPLDLTALSLTPKDELVDQLAENTHNLWAKERRIQGWTYGLNEDSMIR 1017
QY      1021  SPHLVYPRKDDALIKKARODTASEVTRTLTYGYNLDPPTGHOHALILKASKQOAPDR 1080
DB      1018  SPHLVYPRKVDALIKKARODTASEVTRTLTYGYNLDPPTGHALALAEASRLQOTHR 1077
QY      1081  TYRAEKNTAVSSGKVFEEFELITAGPMKVGNVAHMDMAGMMLGDENSMAFPGVNEKY 1140
DB      1078  TYRAEKNTAVTTGKVFEEFELITAGPMKVGNVARSQCPGSQLGNDYSHADGFBNEKY 1137
QY      1141  SGNTESPGQNAVGDVGVFLDLIDKTI SFSLNGBELMDALGETTPADVOGDNFVPACT 1200
DB      1138  LGTGESFGQMOVGDVGVFLDLIDHTWSFSLNGBELMDALGETSPADVOGESFVPAFT 1197
QY      1201  LGVQKALITYGQDVNTLKYTTGCLQEGYRPPCYNMKRDYTHWTKQPIFENTDEMID 1260
DB      1198  LGVQKALITYGQDVNTLKYTTGCLQEGYRPPCYNMKRAVYTYTKDPIFENTDEYAD 1257
QY      1261  TRIDVTRIPASDTPPCCLKISHTFETMEKANMEFLRLSLVYI CHNEPFI DEAEKARWVE 1320
DB      1258  SRIDVTRIPASDTPPCCLKISHNLFSMEKANMEFLRLSLVYI CHISFPIBSBKARKOE 1317
QY      1321  IKDRQOILMKEAVEAQMPAHIDQIMRSGFTNNDIKGLH--YEDN-----QEBLPSK 1370
DB      1318  IRIQHRLLVBA-DQTPFAHMEQIMKSGLSMSDIKGLHRSYEDAVEADMMMQSTPTTK 1376
QY      1371  MK-RLPSRPPKSGMTGRTVITQNTNLDQGVNG-----MHRSTSEAKYKYLGAAGL 1423
DB      1377  SKMOPSRPPKSGISLR-----NEDPMINSLGEGSKNRSTSLDRLRYNADLQN- 1427
QY      1424  TPDDKDKRGSRPKFPRSKGSESSDRAKSKSTPPDPSTVEPSERGARPN-----P 1478
DB      1428  DKDDK-KRGSPRFRPSRGRBAENR--SKAASPEBNSMMDRGMGSGSHMMKTP 1484
QY      1479  QIKVSQANQRYGNMABRSRTNLVGSQVGLMATPTQDRKQMTSTLAQSAATEVGNIEF 1538
DB      1485  TVKTAAPMKVLPETI-PERSNM-----PKQMTGAPLSGSGIESVGNIEF 1528
QY      1539  DABCLKLINEFYGVRIYRQDPTHVYTGWTTQYHLKSDQFNOSKTKSVIITDDYDR 1598
DB      1529  DGECLKLINEFYGVRIYRQDPTHVYGVWYTTQYHFFANEFNOSKVRKVTVHTLDESR 1588
QY      1599  VVENVNRQSCYMAVADDELVNEVMAEATAKASQGMPTGCSVDSTGVSPTCEGKDTSEK 1658
DB      1589  VNESVDNOSCYMAVADDELVNEVTMDSSGKASQGMPTGCFDAATGYISPTCEGKETSHK 1648
QY      1659  FKMEPETKLPFAIFVEATSKELIQIELGRSATSLPLSAVALPTSDKHVLPQPPRLKYQC 1718
DB      1649  FKMEPETKLPFAIFVEATSKELIQIELGRSTITLPLSAVALQNSBRHVNPQPPRLKYQC 1708
QY      1719  LKPHQMARVPNQSIOVALALKSDIRGWSMLCEDAVSMALAHIPREDCIDILPEPMK 1778
DB      1709  LKPHQMARVPNVSIOVALALKSDIRGWSMLCEDPMSMALAHIPREDRIDILBIEIEMK 1768
QY      1779  LSFASHTLTYAALCYOSNRYAALACHYVQOKOLAVALGOSNGSPRGOSFYDILLALH 1838
DB      1769  LSFASHTLTYAALCFPSNRYAALACHYVQOKOLAVALGOSNGSPRGOSFYDILLALH 1828
QY      1839  LESHATTMEACKNEFVILPGLBELKALYBBDMGHLSLQTESVRPQMKMTDIA----- 1892
DB      1829  LESHATTMEACKNEFVILPGLBELKALYBBDMGHLSLQTESVRPQMKMTDIA----- 1888
QY      1893  ESTEISNLSPYPRPLEVABEFVQALAEAVETNOVNRDPVGSNENRPLPLKLDVRL 1952
DB      1889  EVDVINRSLVSPQPLDVVDVFWAALDEAVQINQLHNRDPVGSNENRYFLPLKLDVRL 1948
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QY 1953 LTVGMEDEBVEKLLIMTNPETWDSFDKEGDEHRKGLIMKKAEGAKLQMCYLLOHLN 2012
1949 LTVGLMDGDVWKLLIMFSPETWDAFEPKODGDEHRKGLIMKKAEGAKLQMCYLHLHY 2008
QY 2013 DIOQRHVEAIIAFAHPFVGLDQDRLRYTEIKQSDIPSAVAAKTRREFCPREQMA 2072
2009 DIOQRHVEAIIISFVDFVGLQSDQDRLRYTEIKQSDIPSAIAKTRREFCPREQMA 2068
QY 2073 ILSPKHLBEBDEKENCPCGBELIARMNEPHDTLMAHVSILHAIQOEADA-NOEPRAKGAF 2131
2069 ILGFKNLBEGDIENPCGBELIRKLNSTFHEKLMKVSILHAIQOESEBASAEBVKKPVAL 2128
QY 2132 GKLNIINTVKELEEBEAKAIEBPKTPEEKFRKYLQITIVNMAESQIETPKLVREMS 2191
2129 NRIUNFNAVKELEBETQIEBEPKTPPEIFRVLSTIYKMEBETQIEBEPKLVREMS 2188
QY 2192 LTVQYAVAGELIPIALEKTYVINAATKLDVABMVGSLQIPALLPVQMSQEEBELMKRL 2251
2189 LTVQYDTVGBELIPIALGKTYVINSKTDODALMMVGLSQIPALLPVQMSQEEBELMKRL 2248
QY 2252 WKLVNHTPPHPLIIVLPHENVAVMMNTLGRBAQOSDAPPSQPVABDEKEDTS 2311
2249 WKLVNHTPPHPLIIVLPHENVAVMMNTLGRBAQOSDAPPSQPVABDEKEDTS 2308
QY 2312 HENVVACCRFLCYFCRTGRQOKAMFDHFDLLENSNILLSRPSLRGSTPLDVAVYSSIME 2371
2309 HENVVACCRFLCYFCRTGRQOKAMFDHFDLLENSNILLSRPSLRGSTPLDVAVYSSIME 2368
QY 2372 NTEIATLALREHYLEKIAVILSRGSLQSNSELVEKGYDPLGMDPYEGERYDPLRFCVAVN 2431
2369 NTEIATLALREHYLEKIAVILSRGSLQSNSELVEKGYDPLGMDPYEGERYDPLRFCVAVN 2428
QY 2432 GSEVENANVITRLIRREPELGALGEGGLKALIVDANKMERLADRKCLREMDEG 2491
2429 GSEVENANVITRLIRREPELGALGEGGLKALIVDANKMERLADRKCLREMDEG 2487
QY 2492 D---VNSHPLESEDEDEDYIDTGAALNFCYCTVLDLGRCAPAGVIALGKNSLRARA 2548
2488 TTMVMEHBPPESEDEDEDYIDTGAALNFCYCTVLDLGRCAPAGVIALGKNSLRARA 2547
QY 2549 ILRLSVLEBDLQVLSLRFLLANPAGGERPKSDMPGSLIPGHKQSVGLFLERYVGIETQ 2608
2548 ILRLSVLEBDLQVLSLRFLLANPAGGERPKSDMPGSLIPGHKQSVGLFLERYVGIETQ 2607
QY 2609 ELFPKLIBEAFPLPURAATMLDRNDGCSDMALSNRTYIGNSIIPLIKAYFPYNEABY 2668
2608 ELFPKLIBEAFPLPURAATMLDRNDGCSDMALSNRTYIGNSIIPLIKAYFPYNEABY 2667
QY 2669 ASLIDATLITVYRLSKRMKLTGOREAVSDPLVALTSMOPSMILKLRKLTUVUSLSE 2728
2668 ASLIDATLITVYRLSKRMKLTGOREAVSDPLVALTSMOPSMILKLRKLTUVUSLSE 2727
QY 2729 YTTVALRLTLHYERCAKYGTGAGOGAFGASDEEKLRLTMMFLFSNIFDLSKMDYEP 2788
2728 YTTVALRLTLHYERCAKYGTGAGOGAFGASDEEKLRLTMMFLFSNIFDLSKMDYEP 2786
QY 2789 LFGKALPCLIAIGCALPPDYSLSKNYDEBYG-KBOAAGDLNFOYDOPQINTSSVALNN 2847
2787 LFGKALPCLIAIGCALPPDYSLSKNYDEBYG-KBOAAGDLNFOYDOPQINTSSVALNN 2845
QY 2848 DLANITVQKFSRHNDANASRLKENGWYGEBSQSKTHPRKLYNNMLNDY----EKER 2902
2846 DLANITVQKFSRHNDANASRLKENGWYGEBSQSKTHPRKLYNNMLNDY----EKER 2905
QY 2903 YKEPVBESLKAIIAGMSVSEBVDIPSNRRSSMRQSGSGRPPEIYTDSATFPDYPH 2962
2906 YKEPVBESLKAIIAGMSVSEBVDIPSNRRSSMRQSGSGRPPEIYTDSATFPDYPH 2960
QY 2963 PVDMTNLTLSREKQNMARLADNADHDIWAKKKKEBLVT 3000
2961 PIDMTNLTLSREKQNMARLADNADHDIWAKKKKEBLVT 2998

RESULT 7
US-10-668-767-122
; Sequence 122, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutierrez, Steven
; APPLICANT: Rauch, James
; APPLICANT: Smith, Rejeane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, LiHong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: B1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ. ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 122
; LENGTH: 5127
; TYPE: PR
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: g1 17352469
US-10-668-767-122
Query Match 79.5%; Score 12516.5; DB 4; Length 5127;
Best Local Similarity 78.8%; Pred. No. 0;
Matches 2387; Conservative 263; Mismatches 312; Indels 67; Gaps 21;
QY 1 MAAEAGASRODDVSFRTEDMVCLSTATGERVCLAAEGGNHCLNENIADKXIPDL 60
DB 1 MAAEAG-SEDDVSFRTEDMVCLSTATGERVCLAAEGGNHCLNENIADKXIPDL 59
QY 61 SQCFVIEQALSVALLDELTAAGSEFGKGSRRFLVGNALLRHNSDMVLACST 120
DB 60 SQCFVIEQALSVALLDELTAAGSEFGKGSRRFLVGNALLRHNSDMVLACST 119
QY 121 SSQDKLAFVGLQOHSQGEACMWTLPASKORSEKRVGDDLLIVSVATERYLAHTTK 180
DB 120 SSQDKLAFVGLQOHSQGEACMWTLPASKORSEKRVGDDLLIVSVATERYLAHTTK 179
QY 181 ENEVSIVNASFHTVMSVOPVGTGISRMKVYGVFGDVLRFHGDDECLTIPSTWTKG 240
DB 180 ENEVSIVNASFHTVMSVOPVGTGISRMKVYGVFGDVLRFHGDDECLTIPSTWTKG 239
QY 241 GQNTIVVEGGSVNSQASLWELIARFKWAGGPIWTHPMKRIHTTGRYGVNDONELY 300
DB 240 GQNTIVVEGGSVNSQASLWELIARFKWAGGPIWTHPMKRIHTTGRYGVNDONELY 299
QY 301 LVSREATYASCAFCRROEDDQOVLEDDLRYIGA.PIKYGDSYIVHSENGMLSY 360
DB 300 LVSREATYASCAFCRROEDDQOVLEDDLRYIGA.PIKYGDSYIVHSENGMLSY 359
QY 361 KSYETKKKGVKVEKQALIHBEKMDGLDFSSQSEESRTAVIRKCSLFTFKFINGL 420
DB 360 KSYETKKKGVKVEKQALIHBEKMDGLDFSSQSEESRTAVIRKCSLFTFKFINGL 419
QY 421 ETLQENRHSNFPASVNLGEMVCLDLINFAOPDEDMHEBKONKFRALRNQDLFOE 480
DB 420 ETLQENRHSNFPASVNLGEMVCLDLINFAOPDEDMHEBKONKFRALRNQDLFOE 479
QY 481 EGIINTLLEADIKNTVTSOGFLAGFLAGSGSWMISGYLQOLAAITKGNHTCAQ 540
DB 480 EGIINTLLEADIKNTVTSOGFLAGFLAGSGSWMISGYLQOLAAITKGNHTCAQ 539
QY 541 FANSNRLNMTLSRIGSQASGEGTMDVLHCVLIDSEALNMWDEHIKVIISLEKGR 600

Db 540 FANSNRNLNMLPSRLGSGASBSGMLDVLCVLDSPBALNMRDEHIIKVIISLEBGR 599
QY 601 DPKYLDVLCSLCVNGNVAVSSONNICDYLLPGKNLLQTLVDHSSVBPNI FVGEV 660
Db 600 DPKYLDVLCSLCVNGNVAVSSONNICDYLLPGKNLLQTLVDHSSVBPNI FVGEV 659
QY 661 SAYVRKYFVYMDHIEKTHMPLHIGANTGVYPRGGGKMGNGVDLYSGF 720
Db 660 SSMQKMYFEVYMDHIEKTHMPLHIGANTGVYPRGGGKMGNGVDLYSGF 719
QY 721 DGAYLMSGRKTPVNRTHAEPYIRKGDVIGCALDTPVPIINFMFNGRVTSFTNNLE 780
Db 720 DGAFILMIGRKTLVVDALPEEPYIRKGDVIGVALDLVPITTFPNEGVRKGRSDNLD 779
QY 781 GMEFPVISCSSKLSGRLGGBHRLYVAAPGYSPLVESILLPOOILSLBPCFYGNLSK 840
Db 780 GMEFPVISCSSKLSGRLGGBHRLYVAAPGYSPLVESILLPOOILSLBPCFYGNLSK 839
QY 841 BALAGPVLVDPTAFVPTVDTLOITLPTVVEQIRDLCLANIHMMAMNKTIEAGMYGQ 900
Db 840 NVLAGPVLIEDDTAFVPRVDITGVTLPSVSDQIKELAEINHEMMLNKIEAGMYG 899
QY 901 REDLHKHPCLVPERLPBAEKRYDQIAVQTLKTIILAGYIISLDKPRIRVRLPNE 960
Db 900 RDYHHRHPCLTHERPKPAEBEKYDQIAVQTLKTIISLGYYITMDKPRIRVRLPNE 959
QY 961 PEMQNGYKPAPLDLSAVTLTPKMDLVOLAENTHNLMBERIIOGQTYGLNEDSMR 1020
Db 960 IFMQNGYKPAPLDLSAVTLTPKMBELVDOLAENTHNLMBERIIOGQTYGLNEDSMR 1019
QY 1021 SPLHVPYKVDIAIKKANRDTASSTVTLVYGMIDLPPTGEGHEALLBASOKODFR 1080
Db 1020 SPLHVPYKVDIAIKKANRDTASSTVTLVYGMIDLPPTGEGHEALLBASOKODFR 1079
QY 1081 TYBAEKYAVSSGMYFEFELLTAGPMRVGMADNAPGMMIGODENSMAPDGNBKY 1140
Db 1080 TYBAEKYAVSSGMYFEFELLTAGPMRVGMADNAPGMMIGODENSMAPDGNBKY 1139
QY 1141 SGNTEFSGKQMAVGVVVEFLDIDKTIISFLNGELMDALGGETTPADY--OGDNFPA 1198
Db 1140 GGVSEFSGKQCPGDIYGVFLDLADHTISFLNGELMDALGGETTPADYTAGVGVPA 1199
QY 1199 CTIGVGOKALTYGQVNTLYKFTTQCLQEGYEPFCNMKRDYTHWTKOPIFENTDEM 1258
Db 1200 CTIGVGOKALTYGQVNTLYKFTTQCLQEGYEPFCNMKRDYTHWTKOPIFENTDEM 1259
QY 1259 IDTRIDVTRIPAGSDTPPCIKISHTNPETMEKANMEFLRLSLPYICNEPIDEAKRMY 1318
Db 1260 PDCRIDVTRIPAGSDTPPCIKISHTNPETMEKANMEFLRLSLPYICNEPIDEAKRMY 1319
QY 1319 VEIKDQOILMKEA-VEAQN-----PAHIDQIMRSGFTMNDIKGLHYE-DNOBELPSKM 1371
Db 1320 DEIKNQYRLMREAEIAAQWQVTOQAHDHMLKGFNNMDIKGLTRNFBHADAEADM 1379
QY 1372 KALPSRPPRGSGTTRGVITONNNLOPGVNGHRSISEMAKYDLGAQGLTPDDKCK 1431
Db 1380 MRPKNPPRRGSLTRNIT---FETDMSALDEMQRSTS-----VLDMNGLGBEMDCK-K 1430
QY 1432 RGRSPKPFPSKSGSSDRAKSRKSTPDPFSDTEVSPERGARPNOIKVQANORNG 1491
Db 1431 RGRSPKPFPSKSGSSDRAKSRKSTPDPFSDTEVSPERGARPNOIKVQANORNG 1488
QY 1492 MNAPSRMYLGSQVGLNATPTQDRKOMTSTYLAOSATETVNEIFDAECLKLINEYF 1551
Db 1489 AEIPSPV-----PQPKQJSGSNLGGQPVETSDENFADACLINIEYF 1534
QY 1552 GYRIYFGQDPTTHYIGWTTQYHLKSDPNQSKYTKSSVITTDYDRVAVENVNRQSCY 1611
Db 1535 GYRIYFGQDPTTHYIGWTTQYHLKSDPNQSKYTKSSVITTDYDRVAVENVNRQSCY 1594
QY 1612 RADELNEWMAEATAGASQGMFISGVSTSGSVSFTSGKOTSPFKIMEPEPKLPPAI 1671
Db 1595 RADELNEWMAEATAGASQGMFISGVSTSGSVSFTSGKOTSPFKIMEPEPKLPPAI 1654

QY 1672 FEATSKETIIQIEIGRSATSLPLSAAVLPTSDKHVIFQFPRLKVQCLKPHQMARVPO 1731
Db 1655 FEATSKETIIQIEIGRSATSLPLSAAVLPTSDKHVIFQFPRLKVQCLKPHQMARVPO 1714
QY 1732 LOYHALKLSIDIRGMSMCEDAVGMLAHIEEDRCIDILPIEMDKLSPSHSLTYAA 1791
Db 1715 LOYHALKLSIDIRGMSMCEDAVGMLAHIEEDRCIDILPIEMDKLSPSHSLTYAA 1774
QY 1792 LCVSNYRAAHAACTHVQKQLYALQSOYMSGRLPGFYDLALALHESHAATMEACKN 1851
Db 1775 LCVSNYRAAHAACTHVQKQLYALQSOYMSGRLPGFYDLALALHESHAATMEACKN 1854
QY 1852 EFVYPLGPELKLAYEEDPKHSIRSLQTESVPRQMKTTDI-----ASITE 1897
Db 1835 EFVYPLGPELKLAYEEDPKHSIRSLQTESVPRQMKTTDI-----ASITE 1894
QY 1898 ISNLSYSPFPLVABERVMQALAEAVTNOVNRDPGGSNENFLPLICLVDRLLVGM 1957
Db 1895 IDQYSPKPEPLVABERVMQALAEAVTNOVNRDPGGSNENFLPLICLVDRLLVGM 1954
QY 1958 MRDEVEKLLIMTNPETWDSFDKEGDEBRKGLHMKMAEGAKLQWICYLLOHLNDQLR 2017
Db 1955 LTBEDVQRLVMTIDPETMQAFREBGDEBRKGLHMKMAEGAKLQWICYLLOHLNDQLR 2014
QY 2018 HRVEALIAFANDFVGLQTDQLRYYTEIKQSDLPASAVALKTRBFRCPREQNNALISFK 2077
Db 2015 HRVEALIAFANDFVGLQTDQLRYYTEIKQSDLPASAVALKTRBFRCPREQNNALISFK 2074
QY 2078 HIEEDKENCPCGEBELIARNEFHDTLMAVSHALQEPRAENOE-PEAKRPAFGCLN 2136
Db 2075 HIEEDKENCPCGEBELIARNEFHDTLMAVSHALQEPRAENOE-PEAKRPAFGCLN 2134
QY 2137 IINTVKELEBEAKAIEBPCKTPEBEKRYLQIOTVNMABESQIETPKLVREMFSLVRQ 2196
Db 2135 IINTVKELEBEAKAIEBPCKTPEBEKRYLQIOTVNMABESQIETPKLVREMFSLVRQ 2194
QY 2197 YDAVGEILRALEXTVYINAKTKLDVAMWVGLSQIRALLPVQMSOEBEELMRKMLCN 2256
Db 2195 YDAVGEILRALEXTVYINAKTKLDVAMWVGLSQIRALLPVQMSOEBEELMRKMLCN 2254
QY 2257 NHTFQHPDLIRLRAHENVMAVMNTLGRBAQSDAOPSQPVAE--DSKEDTSHEN 2314
Db 2255 NHTFQHPDLIRLRAHENVMAVMNTLGRBAQSDAOPSQPVAE--DSKEDTSHEN 2313
QY 2315 VVACRFLCYFCGTRONQKAMPDFPFLNENIILSRPSLGSPTLDAVAYSIMENTE 2374
Db 2314 VVACRFLCYFCGTRONQKAMPDFPFLNENIILSRPSLGSPTLDAVAYSIMENTE 2373
QY 2375 LALALREHYLEKIAVYLSRQGLQSNSELEVEKGYPDLGMPVEGERYLDPLFCVMVNGS 2434
Db 2374 LALALREHYLEKIAVYLSRQGLQSNSELEVEKGYPDLGMPVEGERYLDPLFCVMVNGS 2433
QY 2435 VEENANLVRLIRRECEGPAIRGSEGLKRAYANAMKSERIARRKILREHQBQDV- 2493
Db 2434 VEENANLVRLIRRECEGPAIRGSEGLKRAYANAMKSERIARRKILREHQBQDV- 2492
QY 2494 --NFSHPLPESDEDEYIDTGAAILNFCTLYDLRCAPIADGVIAMGNKESLRARAILR 2551
Db 2493 GNFHTPLPESDEDEYIDTGAAILNFCTLYDLRCAPIADGVIAMGNKESLRARAILR 2552
QY 2552 SLVPLEDLQGVLSLRTLNNPAAAGEBRPKSDPESGLIPGHKQSVGLFLERVYIETQELF 2611
Db 2553 SLVPLEDLQGVLSLRTLNNPAAAGEBRPKSDPESGLIPGHKQSVGLFLERVYIETQELF 2612
QY 2612 YKLEBAFLPDLRAATMLDRNGCESDMLSNMRYIGNSILPLILKHAFTYNAEYASL 2671
Db 2613 YKLEBAFLPDLRAATMLDRNGCESDMLSNMRYIGNSILPLILKHAFTYNAEYASL 2672
QY 2672 LPAATHTVYRLSGNRRLTGOREBAVSDPLVALTSANQPSMLKRLKLTVDVKSLEYTT 2731
Db 2673 LPAATHTVYRLSGNRRLTGOREBAVSDPLVALTSANQPSMLKRLKLTVDVKSLEYTT 2732

2733 VALRLTLHYERCAKYGSTGAGOGAFGASDBEKKLTWMLPSNIPDSIKMDYBEELG 2791
2733 VALRLTLHYERCAKYGSTGAGOGAFGASDBEKKLTWMLPSNIPDSIKMDYBEELG 2791
2733 VALRLTLHYERCAKYGSTGAGOGAFGASDBEKKLTWMLPSNIPDSIKMDYBEELG 2791
2792 KALPCLIAIGCALPPYISISKYVDEFFYKEQAAGLDNPOYDPOIINTSSVALNDIAT 2851
2792 KALPCLIAIGCALPPYISISKYVDEFFYKEQAAGLDNPOYDPOIINTSSVALNDIAT 2851
2792 KALPCLIAIGCALPPYISISKYVDEFFYKEQAAGLDNPOYDPOIINTSSVALNDIAT 2851
2852 IYOKSEHHDAMASRKIRNGWYEGWSDOKTHRLKPYNNMLNDYKERYKPYRESL 2911
2852 IYOKSEHHDAMASRKIRNGWYEGWSDOKTHRLKPYNNMLNDYKERYKPYRESL 2911
2850 LVOKSEHHDAMASRKIRNGWYEGWSDOKTHRLKPYNNMLNDYKERYKPYRESL 2909
2912 KALLAIGWSEHSEVDIPSNRRSMBROSQSGRPPEI--VYDSATPPDYNPHVPVMTL 2969
2912 KALLAIGWSEHSEVDIPSNRRSMBROSQSGRPPEI--VYDSATPPDYNPHVPVMTL 2969
2910 KGLLAIAGWYHSEHSEVVALNHRGSTRQSK-----PQINEPQNEGSPFYNNPHVPVMSL 2964
2970 TLRSEKQNAERLADNADIMAKKKEEL 2998
2965 TLRSEKQNAERLADNADIMAKKKEEL 2993

RESULT 8

US-10-668-767-121
Sequence 121, Application US/10668767
Publication No. US2004017114A1
GENERAL INFORMATION:
APPLICANT: Casper, Timothy
APPLICANT: Cordova, Daniel
APPLICANT: Guttridge, Steven
APPLICANT: Rauh, James
APPLICANT: Smith, Rejane
APPLICANT: Tao, Yong
APPLICANT: Wu, LiHong
TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
FILE REFERENCE: BB1533 US NA
CURRENT APPLICATION NUMBER: US/10/668,767
CURRENT FILING DATE: 2003-09-23
PRIOR FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 60/412,795
PRIOR FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 60/427,324
NUMBER OF SEQ ID NOS: 149
SOFTWARE: Patentin version 3.1
SEQ ID NO 121
LENGTH: 5113
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: g1 17352467
US-10-668-767-121

Query Match 79.3%; Score 12489.5; DB 4; Length 5113;
Beat Local Similarity 78.8%; Pred. No. 0;
Matches 2376; Conservative 271; Mismatches 315; Indels 53; Gaps 20;

1 MABEGSAGBODVSLRTEDMVCLSCTATGSRVCLAAFGNRHCFLEINADKNPDL 60
1 MABEGSAGBODVSLRTEDMVCLSCTATGSRVCLAAFGNRHCFLEINADKNPDL 59
61 SOCVFPIEALSVRALQELVTAAAGSETGKGTSGHRTLLYGNAILRLHNSDMYLA 120
61 SOCVFPIEALSVRALQELVTAAAGSETGKGTSGHRTLLYGNAILRLHNSDMYLA 120
60 SOCVFPIEALSVRALQELVTAAAGSETGKGTSGHRTLLYGNAILRLHNSDMYLA 119
121 SSGODKLAFDVGIQHSQSGACWTLHPASKORSEBKVAVGDDLLVSVATERYHTTK 180
121 SSGODKLAFDVGIQHSQSGACWTLHPASKORSEBKVAVGDDLLVSVATERYHTTK 180
120 SSSNDKLSFDVGIQHSQSGACWTLHPASKORSEBKVAVGDDLLVSVATERYHTTK 179
181 ENEVSVVNSFHTVHSVOPVNGISRMKYGVVPGDVLVRFPHGDECLTIPSTWKG 240
181 ENEVSVVNSFHTVHSVOPVNGISRMKYGVVPGDVLVRFPHGDECLTIPSTWKG 240
180 ENEQSVVNSFHTVHSVOPVNGISRMKYGVVPGDVLVRFPHGDECLTIPSTWKG 239
241 GQNIIVYEGSVNSQARSIMRLRLATKAGGFINNYHPIRSHITTTGRTLVNDQNEL 300
241 GQNIIVYEGSVNSQARSIMRLRLATKAGGFINNYHPIRSHITTTGRTLVNDQNEL 300

240 GQNIIVYEGSVNSQARSIMRLRLATKAGGFINNYHPIRSHITTTGRTLVNDQNEL 299
301 LVSRBATTASCAFCIRJOEKDOKOVLBDKLEVIQAPITIKYGDSTVIYQHSSETGLMSY 360
301 LVSRBATTASCAFCIRJOEKDOKOVLBDKLEVIQAPITIKYGDSTVIYQHSSETGLMSY 360
300 LVKKBASIAITTFCLRQEKDEKVLBDKLEVIQAPITIKYGDSTVIYQHSSETGLMSY 359
361 KSYETKKKGKGVKYEKOAILHEGRKDDGLDPSRQSEBSRTARVIRKCSLFTPEINCL 420
361 KSYETKKKGKGVKYEKOAILHEGRKDDGLDPSRQSEBSRTARVIRKCSLFTPEINCL 420
360 KSYETKKKGKGVKYEKOAILHEGRKDDGLDPSRQSEBSRTARVIRKCSLFTPEINCL 419
421 ETLQSRRRSMTFPASVNLGEMVCLBDLINTPAQDPEDMEHEKONKFPALNRDOLPES 480
421 ETLQSRRRSMTFPASVNLGEMVCLBDLINTPAQDPEDMEHEKONKFPALNRDOLPES 480
420 ETLQSRRRSMTFPASVNLGEMVCLBDLINTPAQDPEDMEHEKONKFPALNRDOLPES 479
481 EGLIHLILEALIKINIVTSQGLAGFLAGDESGQSEMIISGLYOLLAIIKSNHTNCAQ 540
481 EGLIHLILEALIKINIVTSQGLAGFLAGDESGQSEMIISGLYOLLAIIKSNHTNCAQ 539
480 EGLIHLILEALIKINIVTSQGLAGFLAGDESGQSEMIISGLYOLLAIIKSNHTNCAQ 539
541 FANSNRNLMTFSLRGSQASGBGTGMLDVLAHCVLIDSPBALNMRDEHIIKVIIISLEKGR 600
541 FANSNRNLMTFSLRGSQASGBGTGMLDVLAHCVLIDSPBALNMRDEHIIKVIIISLEKGR 600
540 FANSNRNLMTFSLRGSQASGBGTGMLDVLAHCVLIDSPBALNMRDEHIIKVIIISLEKGR 599
601 DKPVLDVLCSLCVGNGAVNRSSQNNICDYLRLGKNTLLQTLAVDVHVSVRPIFYGRVAG 660
601 DKPVLDVLCSLCVGNGAVNRSSQNNICDYLRLGKNTLLQTLAVDVHVSVRPIFYGRVAG 660
600 DKPVLDVLCSLCVGNGAVNRSSQNNICDYLRLGKNTLLQTLAVDVHVSVRPIFYGRVAG 659
661 SAVYGRKVEYTMMDHEKTHMMPHLRIGMANTTGVVPYGGGKKMGVGDOLYSYGF 720
661 SAVYGRKVEYTMMDHEKTHMMPHLRIGMANTTGVVPYGGGKKMGVGDOLYSYGF 720
660 SSMYQKMFYEVTMDHIEQTHMMPHLRIGMANTTGVVPYGGGKKMGVGDOLYSYGF 719
721 DCAVILMSGGRKTPVNRTHABRPYIRKGVIGCALDLYVPIINFMNGVRVTSPTNFNLE 780
721 DCAVILMSGGRKTPVNRTHABRPYIRKGVIGCALDLYVPIINFMNGVRVTSPTNFNLE 780
720 DCAVILMSGGRKTPVNRTHABRPYIRKGVIGCALDLYVPIINFMNGVRVTSPTNFNLE 779
781 GMPPIYSCSSYLCSCFPLGSHGRVYAPRGVSEVLESLLPQOILSLBPCFYGNLSK 840
781 GMPPIYSCSSYLCSCFPLGSHGRVYAPRGVSEVLESLLPQOILSLBPCFYGNLSK 840
780 GMPPIYSCSSYLCSCFPLGSHGRVYAPRGVSEVLESLLPQOILSLBPCFYGNLSK 839
841 BALAGPVLVODDTAFVPPVVDLTQITLPTVYQIDBKLENTHBMAMNKIEAGMNYGDO 900
841 BALAGPVLVODDTAFVPPVVDLTQITLPTVYQIDBKLENTHBMAMNKIEAGMNYGDO 900
840 BALAGPVLVODDTAFVPPVVDLTQITLPTVYQIDBKLENTHBMAMNKIEAGMNYGDO 899
901 RBDLKHHPCLVFERLPABKRYDIQLAVQTLKTYIALGYIISLDKPARIRNVLPE 960
901 RBDLKHHPCLVFERLPABKRYDIQLAVQTLKTYIALGYIISLDKPARIRNVLPE 960
900 RBDYRHHPCLTHPFELPAABKRYDQLAVQTLKTYIALGYIISLDKPARIRNVLPE 959
961 PMQSNKYRPADLISAVTLTPKDELVDQLAENTHLMARERIOQGMWYGLNEDSDMR 1020
961 PMQSNKYRPADLISAVTLTPKDELVDQLAENTHLMARERIOQGMWYGLNEDSDMR 1020
960 PMQSNKYRPADLISAVTLTPKDELVDQLAENTHLMARERIOQGMWYGLNEDSDMR 1019
1021 SPHLVYPRVDAIKKANBDTSRTYRLLVYGYMLDPTGROHEALLLEASKOKQADR 1080
1021 SPHLVYPRVDAIKKANBDTSRTYRLLVYGYMLDPTGROHEALLLEASKOKQADR 1080
1020 SPHLVYPRVDAIKKANBDTSRTYRLLVYGYMLDPTGROHEALLLEASKOKQADR 1079
1081 TYRAEKTYAVSSGKYFFEBEILTAGPMRVGMADMAPGMLGODENSVAFDGYNEKY 1140
1081 TYRAEKTYAVSSGKYFFEBEILTAGPMRVGMADMAPGMLGODENSVAFDGYNEKY 1140
1080 TYRAEKTYAVSSGKYFFEBEILTAGPMRVGMADMAPGMLGODENSVAFDGYNEKY 1139
1141 SNTSFGKQAVGDVGVFIDLIDTISFSLNGELLMALDAGETTFADV--QGDNFVPA 1198
1141 SNTSFGKQAVGDVGVFIDLIDTISFSLNGELLMALDAGETTFADV--QGDNFVPA 1198
1140 SNTSFGKQAVGDVGVFIDLIDTISFSLNGELLMALDAGETTFADV--QGDNFVPA 1199
1199 CILGNGQKRLVYGGDVNTLKTFTTCGLQEGYBPCVNNRRRVTHMYTDOQIPENTDM 1258
1199 CILGNGQKRLVYGGDVNTLKTFTTCGLQEGYBPCVNNRRRVTHMYTDOQIPENTDM 1258
1200 CILGNGQKRLVYGGDVNTLKTFTTCGLQEGYBPCVNNRRRVTHMYTDOQIPENTDM 1259
1259 IDTRIDVTRI PAGSDTPCLIKISHTFETMEANNEFLTSLPVI CHNEFIDEAKVARE 1318
1259 IDTRIDVTRI PAGSDTPCLIKISHTFETMEANNEFLTSLPVI CHNEFIDEAKVARE 1318
1260 PDCKRIDVTRI PAGSDTPCLIKISHTFETMEANNEFLTSLPVI CHNEFIDEAKVARE 1319
1260 PDCKRIDVTRI PAGSDTPCLIKISHTFETMEANNEFLTSLPVI CHNEFIDEAKVARE 1319
1319 VEIKORQOILMKEA--VEAQ-----PAHIDQIMRSGFTNIDIKGLHYE--DNQBELPSSGM 1371
1319 VEIKORQOILMKEA--VEAQ-----PAHIDQIMRSGFTNIDIKGLHYE--DNQBELPSSGM 1371
1320 DEIKRQVRLMREBAEIAQMOVQTAHMDHMLKGGFNNDIKGLIRNFBHADAEADHM 1379
1320 DEIKRQVRLMREBAEIAQMOVQTAHMDHMLKGGFNNDIKGLIRNFBHADAEADHM 1379

Matches 2376, Conservative 272, Mismatches 314, Indels 67, Gaps 21;

1 MAEAGSAGBODVSELTEDMDVCLSTAGSERVCLAAFGNRRHGLNADKNIPDL 60
 1 MAEABEG -SEODVSTLTEDMDVCLSTAGSERVCLAAFGNRRHGLNADKNIPDL 59
 61 GGCVPVIEGALSVRALQELVTAAGSEFGKGTSGHRTLLYGNAILLRHNSDMYLA 120
 60 GGCVPVIEGALSVRALQELVTAAGSEFGKGTSGHRTLLYGNAILLRHNSDMYLA 119
 121 SSSODPLADPVGICQHSOGSACWTHLPASKORSSEBKRVGDDLLVSAATERVYHTTK 180
 120 SSSNDQLSFPVGLQHSOGSACWTHLPASKORSSEBKRVGDDLLVSAATERVYHTTK 179
 181 EMBVSIVNASPHYTHSVOPYGTGISMKRVGVYFGDVLRFPHGDECLTISTYTKG 240
 180 EMBQSIVNASPHYTHSVOPYGTGISMKRVGVYFGDVLRFPHGDECLTISTYTKG 239
 241 GGNIVVYEGGSVNASQARSIMRLRLARTKAGGFNNYHMRIRHITTGRTLVGNDONEL 300
 240 GGNIVVYEGGSVNASQARSIMRLRLARTKAGGFNNYHMRIRHITTGRTLVGNDONEL 299
 301 LVSRBATTAASCACLRQEKDDOKVLEKDLVIGAPITKYGDSTVYVQHSBTGLMST 360
 300 LVYKEBASIAITTFCLRQEKDDOKVLEKDLVIGAPITKYGDSTVYVQHSBTGLMST 359
 361 KSYETKGGKGVKVEKQALIHBEKGMDGLDFRSQSEBSRTARVIRKSSLTPTKFIN 420
 360 KSYETKGGKGVKVEKQALIHBEKGMDGLDFRSQSEBSRTARVIRKSSLTPTKFIN 419
 421 ETLQENRRHSMPASVNLGEMVCLBDLINYPAQPDMEHEBKONKPRALRRQDLFOE 480
 420 ETLQENRRHSMPASVNLGEMVCLBDLINYPAQPDMEHEBKONKPRALRRQDLFOE 479
 481 EGTLLILBAIDKINVTSGGFLAGLADGSGSGBMISGTYOULLAIIKKNHNCQA 540
 480 EGTLLILBAIDKINVTSGGFLAGLADGSGSGBMISGTYOULLAIIKKNHNCQA 539
 541 PANSNRLNMLFSLRGSQASGEGTGM.DYLHCVALIDSEBALNMRDEHIKVIISLEKHG 600
 540 PANSNRLNMLFSLRGSQASGEGTGM.DYLHCVALIDSEBALNMRDEHIKVIISLEKHG 599
 601 DPEVLDVLCGLCVGNVAVRSGQNNICDYLPGKNLLQTLVDVHVSVAENIPFVRVSG 660
 600 DPEVLDVLCGLCVGNVAVRSGQNNICDYLPGKNLLQTLVDVHVSVAENIPFVRVSG 659
 661 SAVTRKMYEVTMDIIEKTTMMPHLRIGMANTTGVYPPGSEKKGNGVGDLYSYGF 720
 660 SAVTRKMYEVTMDIIEKTTMMPHLRIGMANTTGVYPPGSEKKGNGVGDLYSYGF 719
 721 DCAVILMSGKRTVNNTHABEPIYIRKGDVGCALDLVPIINFMFGVNVYTSFTNPNLE 780
 720 DCAVILMSGKRTVNNTHABEPIYIRKGDVGCALDLVPIINFMFGVNVYTSFTNPNLE 779
 781 GMEFPYISGSSKLSGFLGSGHRLRYAPBEGSYPLVBSILPQOLISLEPCFYFGLSTK 840
 780 GMEFPYISGSSKLSGFLGSGHRLRYAPBEGSYPLVBSILPQOLISLEPCFYFGLSTK 839
 841 RALAGPPLVODDAPVPTPVDTLQITLPTVBOIRDKLAENIHEMANMKIEAGMYGDO 900
 840 RALAGPPLVODDAPVPTPVDTLQITLPTVBOIRDKLAENIHEMANMKIEAGMYGDO 899
 901 RBDLHICPLVPEBLRPAEKRYDOLANQTLKTLAAGUYISLQKPPAIRNVVLPNE 960
 900 RBDLHICPLVPEBLRPAEKRYDOLANQTLKTLAAGUYISLQKPPAIRNVVLPNE 959
 961 PFMOGNGYKAPPLDSLAVTLTPKMDBLVDOLAEKTNLMARERIQQGWTYGLNEDSDMR 1020
 960 PFMOGNGYKAPPLDSLAVTLTPKMDBLVDOLAEKTNLMARERIQQGWTYGLNEDSDMR 1019
 1021 SPHLVYPRKDDAIKKANRDTASBETVTLVYGMULDPTGEOHEALLBASQOKADR 1080
 1020 SPHLVYPRKDDAIKKANRDTASBETVTLVYGMULDPTGEOHEALLBASQOKADR 1079

1081 TYRAEKNTAVSSGKMYFEFEIITAGPMRVGMAHADMAPGMLGQDENSVAFDYNEKY 1140
 1080 TYRVERNTAVTSGKMYFEFEVLTSGPMRVGMARADCYPGAMLSBETSWAFGHNTKOH 1139
 1141 SGTBSFGQMAVGVVGFLLIDKTISSPLNGELLMALGERTPAV--QGDVFAVA 1198
 1140 ASIHBFVGRVARGDVTGCFIDVKEQTISPLNGELLMALGERTPAVAVTAVGCVFA 1199
 1199 CTGVGQKARLTYGQDVNTLKTFTTCGLQEGEYPCVNNKRDVHTVTKQDPIFENTDM 1258
 1200 CTGVGQKARLTYGQDVNTLKTFTTCGLQEGEYPCVNNKRDVHTVTKQDPIFENTDM 1259
 1259 IDTRIDVTRIPAGSDTPCLAKI SHNTFKTEKAMEFLALSLPVI GHNFPIDEAKARRN 1318
 1260 PCORIDVTRIPGADTPCLAKI SHNTFKTEKAMEFLALSLPVTGMEGFI SPOKARRRN 1319
 1319 VBIKROQILMKBA -VEAQM-----PAHIDQIMRSFTMWDIKGLHYE -DNGEELPSSGK 1371
 1320 DEIKNQYRLMEBAEALIAQOMOVOTQAAMHDHMLKGGFNNDIKGLTRNFBDAHADAEM 1379
 1372 KDLPSRPPKGSMTGRTVITQVNNILQPGVNGHRTSBAEMAKYDLGAQGLTPDDCKK 1431
 1380 MGEPMRPPKGSMTGRTVITQVNNILQPGVNGHRTSBAEMAKYDLGAQGLTPDDCKK 1430
 1432 RGRSPKPPKRSKGSBDRKSRKSTPDPFSDTEVSPPRGARRPQIKVSGAQRNG 1491
 1431 RGRSPKPPKRSKGSBDRKSRKSTPDPFSDTEVSPPRGARRPQIKVSGAQRNG 1488
 1492 MNAPEKRTVYSGVGLNATPQDRKQNTTSLAOSATETVGNELFDEBCLKLINEYF 1551
 1489 ASIPSPV-----POGPKQSGSMLGQAPVETSDEMFDAECLKLINEYF 1534
 1552 GVRIYPGDPTVYIGMTTOYHLSKDPNOSKVTSYVITDDYRVVENVNRQSCMY 1611
 1535 GVRIYPGDPTVYIGMTTOYHLSKDPNOSKVTSYVITDDYRVVENVNRQSCMY 1594
 1612 RADELTYNEVMAEATKAGASQGMETIGSVDSVTSVSPTGSGKQTSFKTKMBETKLPAL 1671
 1595 RADELTYNEVMAEATKAGASQGMETIGSVDSVTSVSPTGSGKQTSFKTKMBETKLPAL 1654
 1672 FVRAISKEILOTIELGHSATSLPSAAVLTSDKHTVTPQPPRLKVOCLKPHQARVPNOS 1731
 1655 FVRAISKEILOTIELGHSATSLPSAAVLTSDKHTVTPQPPRLKVOCLKPHQARVPNOS 1714
 1732 LOVHALKSDIGMSMLCEDAVSMLALHTPEBDRCTDIIEPTMDGLSFHSHTLTLYAA 1791
 1715 LOVHALKSDIGMSMLCEDAVSMLALHTPEBDRCTDIIEPTMDGLSFHSHTLTLYAA 1774
 1775 LCVQSNYRAAHLCTVPOKOLLYAISOYMSGPTLQGFYDILLALHLSHATMEACRY 1851
 1852 BPAVPLGPEIKALYEBPDMGHSLSLQTESVBPQMKMTDI-----AESITB 1897
 1835 EYTPPGABEIKELYSDEMGHSLSLQTESVBPQMKMTDI-----AESITB 1894
 1898 ISNLSYPRYELVAREFVNOALLAEVETNOYHRDVGSGSNELFLPLIKIVRLILLYG 1957
 1895 IDOLYPRYELVAREFVNOALLAEVETNOYHRDVGSGSNELFLPLIKIVRLILLYG 1954
 1958 MRDEVEKLLIMTNPETWPSFPGKSGDEHKKGLIMKRAEAKQOMCYLLQHTANDIOLR 2017
 1955 LTBEDVQRLVMDPEPTNOAPREBKDHKKGLIMKRAEAKQOMCYLLQHTANDIOLR 2014
 2018 HRVBAIIAPAHDFVGLDQTDOLRRYTEIKOSDLSAAVAAKTRBEPCCPBBQNALISRK 2077
 2015 HRVBAIIAPAHDFVGLDQTDOLRRYTEIKOSDLSAAVAAKTRBEPCCPBBQNALISRK 2074
 2078 HLEEDKENCPCGEELIAAMNEFHTLMAVSLAHALQEBDAENQ--PEAKPAPGKLYN 2136
 2075 NLEPDQDNCTGCLBLRGLRGLDHDLMQKVSANLQEBDAENQ--PEAKPAPGKLYN 2134

Qy	2137	IINIVKELBEEBAKLEEBPRKTPREKPKULIQTIVMAESSQJETPLQVNMPSLVRO	2196
Db	2135	FINIVKELEBGEKPEEBEKPTPEEBFKVYIKITIVSAESSQJENPLQVNMPSLLIRO	2194
Qy	2197	YDVAEGLIRALEKTYVINAKTKLDVAEWMVGISQIRALLPVMOSQOEBELARKKLMJLVN	2256
Db	2195	YDTVGEVLVRALEKTYVINTPARODVAEMWGLSQIRALLPVMOSQOEBELARKKLMJLVN	2254
Qy	2257	NHTPFQHPDLIRVLRVHENVMAVMNNTLGRBAQASDAQPSOPVAE--DSKEKOTJHEM	2314
Db	2255	NATPFQHPDLIRILRVHENVMAVMNNTLGRBAQASDAQ--PQOSEVABGAPSEKOTJHEM	2313
Qy	2315	VVACCRFLCYEPCRGROKQKAMFPHFDPLNNSNTLLSRBELRSTPLDVAYSSLMENTE	2374
Db	2314	VVACCRFLCYEPCRGROKQKAMFHFDFLLDNANLILRPSLRSTPLDVAYSSLMENTE	2373
Qy	2375	LALALREHYLEKIAVYLSRCSQOSNSELYVEKGYPLDGMDFVEGGRYDPLFLFCVMWNGES	2434
Db	2374	LALALREHYLEKIAVYLSRCSQOSNSELYVEKGYPLDGMDFVEGGRYDPLFLFCVMWNGES	2433
Qy	2435	VEENANLIVIRLLIRREPECLGPAIRGEGGLKAIYDANKMSERJADRKRLREMEQBDV-	2493
Db	2434	VEENANLIVIRLLIRREPECLGPAIRGEGGLFPAIYEANRMSERJSDRCXQOD--BAGETIA	2492
Qy	2494	--NBSHPLPSEDEDEDYIDTGAALINFCITVDLIGRCAPAGYIALGKNESLPARAILR	2551
Db	2493	GLNFPHPLPBBEBEDYIDTGAALINFCITVDLILGRCAPASVIEGKNESLPARAILR	2552
Qy	2552	SLVPLEDDQGYLSRFLTNPNPAGBERRKSPMSGLIRGHQOSGLFLERYGIEHQELF	2611
Db	2553	SLVPLEDDQGYLSLFTTILSQTPAGBERRKSPMSGLIRPNKQOSVTLPLERYGIEHADLP	2612
Qy	2612	YKLBEBAPLPLRAATMLDRNDGCSBDMALSMNRYIGNSILPLIRKHAYPEANENYASL	2671
Db	2613	YRLBEDAPLPLRATITLIDKSDGSBDMALMNNYIGNSILPLIRKSKFYNEANENYASL	2672
Qy	2672	LDATLHTYTRYLSKRNMLTKGOREAVSDFLVALTSAMQPSMLKILRLKLYDVSKLSEYTT	2731
Db	2673	LDATLHTYTRYLSKRNMLTKGOREAVSDFLVALTISQMPAMLKILRLKLYDVSKLSEYTT	2732
Qy	2732	VALLLTLTHYRCAKRYGSTGAGGAPGASDEBKRLLTMMLFSNIPOSLSKMOVEPLBFG	2791
Db	2733	VALLLTLTHYRCAKRYGST--QGQSGSYGASSDEBKRLLTMLFSNIPDLSMDVDPBLBFG	2791
Qy	2792	KALPCLIAIGCALPPDYSLSKNYDDEFYKGEQOAGLDLNPDPYDQPIINTSSVALNNDLANT	2851
Db	2792	KALPCLIAIGCALPPDYSLSKNTDEDDYGRGMGAP--DQPYQWNPPLDITNNVHLDDNDLNS	2849
Qy	2852	IVQKFSBHYHDAMASRKILENGWYVYGEGBMSDQKTHPRIKPYNMINDYERKRYKEPVNEST	2911
Db	2850	LVQKFSBHYHDAMASRRLEGWYTGDIRSDDRKHPRLKPYNMLSEYERERYDPAVECL	2909
Qy	2912	KALLAIGSVSHSVDLPSNNRSRMRQOSKSGGAPPEI--VTDSATPFDVNNPHPVDMTNL	2969
Db	2910	KGLLAIGVTHSEVEVALNHRGSTRQSK-----PQINEFQKSGSPFNYPHPVDMSNL	2964
Qy	2970	TLISREQMMAERLADNAHDIWAKKKEEL	2998
Db	2965	TLISREQMMAERLADNSHDIWAKKKEEL	2993
RESULT 10			
US-10-668-767-10			
: Sequence 10, Application US/10668767			
: Publication NO. US20040171114A1			
: GENERAL INFORMATION:			
: APPLICANT: Caspar, Timothy			
: APPLICANT: Cordova, Daniel			
: APPLICANT: Gutierrez, Steven			
: APPLICANT: Rauch, James			
: APPLICANT: Smith, Rejane			
: APPLICANT: Tao, Yung			
: APPLICANT: Wu, Lihong			

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; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: SeqIntn version 3.1
; SEQ ID NO 10
; LENGTH: 5109
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-668-767-10

```

Query Match 79.1%; Score 12460.5; DB 4; Length 5109;

Matches 2371; Conservative 273; Mismatches 316; Indels 53; Gaps 20;

OV 1 MAEAEAGGASEODDVSELTPTEDMVCISCTATGERVCIAEGEGNRHCFLBNITADKNIPDL 60

1 МАББС - СЕОДНИКЕР БЕДНАТИ СЧТАТЕСВУК 1 АБЕБЕДНИКЕР ЕВУТ АБЕДНИКЕР ЕО

1. The first step in the process is to identify the problem or issue that needs to be addressed. This involves gathering information and understanding the context of the problem.

01 00 C V F V I E B A L S V K A U G E L V I A M S E I G N I G S G N K I L U I G N A I L U R I L H S D M I L A C L S I 120

Db 60 SQCVFVIEQALSVRAQDELVTAGSETGKGTSGHRTLLYGNALLRRHNSDMYLACTST 119

121 SSSQDKLAFDVGLOQHSGEACWTLHPASKQRSEGEKVRVGDDLILSVATERYLHTTK 180

Db 120 SSSNDKLSFDVGLQEHSGGEACWTVHPASKQRSEGEKVRVGDGLPVSVATERYLHTTK 179

QY 181 ENEVSIVNASFHTHMSVQPYGTGISRMKYVGVFGGDLRFHGGDECLTIPSTWTKDG 240

db 180 ENEOSIYNASFEHTHTWSPDYGTGTSRPMKVGVVEGDIY.BFEHGGDECT.TIPSTWGPRA 239

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LD 240 GUN V I I E G S V M A Q A R S U M R U B E L A R I A M A G G F I N M I H P M R I K H I I T I G R I E G V N D S N E L I 299

301 LVSRREATTASCAFCRLRQEKDDOKVLEDKDLEVI GAPIIKYGDSTVIVQHSETGLWSY 360

Db 300 LVKKEBASIAITTFCLRQEKDEKVLIEDKDLLEVIGSPIIKYGDITVIVQHCEISLWLSY 359

QY 361 KSYETKKGVKVEKQAILHEEGKMDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420

Db 360 KSYETKKKGVGKVEEKQAILHEEGKMDCLDFSRSEQEEESKTARVIRKCSLFTQFITAL 419

421 FTI.QENRHSMEFASVNI.GEMMCT.EDI.TNYEAPDEDMEEKONKFRAT.BNRONT.EOF 480

[illegible][illegible]

481 BGLUNDLLEAIDKINVISQFLAGFLAGDESGQSWEMISGLIQLLAAI IKGNHINCAQ 540

D6 480 EGVNLILLEAIDKVNITSQGFLASFLAGDETGQSWDLISTYLYQLLAIIKGNHTNCAQ 539

QY 541 FANSNRLNWLFSRLGSQASGEGTGM LDV LHCVLIDSP EALNM RDEHIKVIISLLEKHGR 600

Db 540 FANSNRINWLF SRLGSQASSEGGM L D V L H C V L I D S P E A L N M R D E H I K V I S L L E K H G R 599

601 DPKVL D V L C S L C V G N G V A V R S S O N N I C D Y L L P G K N L L O T A L V D H V S S V R P N I F V G R V E G 660

500 DPKYI.DYI.CSI.CYGNQVAVPSSONNICDEILPKQNTILOTIYDHAISTPNTFVGRVYDG 659

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DB 660 SSMYQKWFEEVIMDHLEQILHMPHLRLGMANISGIVPEGGKKMGNGVGDDLYSFGF /19

721 DGAYLMSGGRKTPVNRTHAEEPIRKGDVIGCALDLTPINEMENGVRVTGSFTNMLE 780

Db 720 DGAFLWTGGRKTLVDALPEEPFIRKGDVIGVAIDLSVPIITFTFNGVKVRGSRFDNLD 779

781 GMFPVISCSSKLSRFLGGEHGRRLRYAAPEGYSPLVESLLPQILSLEPCFFYFGNLSK 840

Db 780 GHEFFPMWSSCKSCRFEGGDHGRLEKFAPMGFMALVQCIMPFQQLSLDPCFYFGLAK 839
Qy 841 BALAGPELVODDPAFVPTVDTLQITLPTVBEQIRKLAENHEMMAMKIEGMMYGDQ 900
Db 840 NYLAGMWLLIEDPAFVPKVDITGVTLPSVVDQIKKEGLAENHEMMALNKIEGMSWGEH 899
Qy 901 REDLHRIHCLVPEPELPAEKRYDQLAQVTKTILALGYISLDKPPAIRANVLPNE 960
Db 900 RODYHRIHCLTHPELPAEKRYDQNLAVTKTILISLGYITMDKPPAIRPVLPLNE 959
Qy 961 PPMQNGYKAPLIDLSAVTLTPRMBLVDQLAENTNLWABERIOGQWYGLNEDSDMR 1020
Db 960 IFMGNGYKAPLIDLSAVTLTPKLELVDQLAENTNLWABERIOGQWYGLNEDSENRH 1019
Qy 1021 SPHLVYPRYVDAIKKANBDTASEYRITLLVYGVMDLPRPGEHELLLEASQKQADR 1080
Db 1020 SPHLVYPRYVDAIKKANBDTASEYRITLLVYGVMDLPRPGEHELLLEASQKQADR 1079
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Db 1080 TYRABKQYAVSGKMYFEFELTAGPMRVGMADHAPGMWLGODENSMFADGYNESKY 1139
Qy 1141 SGNTSFGKQWAGDVVGFELDKTISFSLNGELMLDALGSETTPADV--OGDNFVPA 1198
Db 1140 AGSIBHFYRVEAGDVIGCFIDVKEQITISFSLNGELMLDALGSETTPADVAGVGFVPA 1199
Qy 1199 CTLGVOQKARLTGGOVNTLKYTTGGLDQGYRPFCCNMGRDVTHTYTDQPIFENTDEM 1258
Db 1200 CTLGVOQKARLTGGOVNTLKYTTGGLDQGYRPFCCNMGRDVTHTYTDQPIFENTDEM 1259
Qy 1259 IDRIIVTRIPAGSDTPPCIKISHNTFETMEKANWEFLRLSPVICINERPIDABAKARR 1318
Db 1260 PGRIDVTHIPGALDTPPHLKISHNTFETMEKANWEFLRLSPVICINERPIDABAKARR 1319
Qy 1319 VEIKROQILMKEA-VEAQW----PAHIDQINRSGFTNDIKGLHYE--DNOBELSSKX 1371
Db 1320 DEIKRQYLMREABEIAAQWQVTOQAHDHMLKGFNNNDIKGLRNPBEHADAEDH 1379
Qy 1372 KALPSRPRKGSRTGVTIONYNNLORGVNGHRSISEMAKYLQAGSLTPDDKOK 1431
Db 1380 MGPBNRPPKRGSLTRNIT---FETDMSALDEMQRSTS---VLMNGLGEBEMDKK-K 1430
Qy 1432 RGRSPKPRKSGESDRKSKRKTPOPSDTEVSPERGARPNPQIKVSOANQYNG 1491
Db 1431 RGRSPKPRKSGESDRKSKRKTPOPSDTEVSPERGARPNPQIKVSOANQYNG 1488
Qy 1492 MNARPERTNLGSGOVGNMATPTQDRKOMTSTYLAOSATETVGNBIFDAECLLINEBPY 1551
Db 1489 ABIPBPV-----PQGRKQLSGSNLGGQPVETSGDEMFAECLLINEBPY 1534
Qy 1552 GVARITYGODPTHYIGVTTQYHLHSKDPNOSKYVTSVYITDDYDRVAVENNRQSCIN 1611
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Db 1595 RADELNWMAEATAGASQGMFISGVDSVSTGSGXDTSPFKMPEPTKLPAL 1654
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Db 1655 FVEATSEKILQIELGHSATSLPLSAAVLPTSDKHVLPQPPRLKVOCLEKFMQARVPN 1714
Qy 1732 LOYHALKLSDIRGWSMLCEBDAVSMALHIFEBDRCIDLEPIMDKLSSHSTLTLYAA 1791
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Qy 1792 LCVQSYRAAHALCTHVQKQLLYATOSQVMSGLPGFYDLITALHLSHAATMEACK 1851
Db 1775 LCVQSYRAAHALCTHVQKQLLYATOSQVMSGLPGFYDLITALHLSHAATMEACK 1834
Qy 1852 BFVYLPGBELKALYEBPDMGHSLSRSLQTESVVRPQMKOTDIABSITISNLVSPYPLPVA 1911
Db 1911 BFVYLPGBELKALYEBPDMGHSLSRSLQTESVVRPQMKOTDIABSITISNLVSPYPLPVA 1911

Db 1835 EYITPGLABIKELYSDEENQHSLSRVTESVRPQUMTEIBEPIDQLYSKPEPLEV 1894
Qy 1912 REFVQALABAVETNOVNRDIPVGSNENLFLPLKLVNRLLVGMWREDEVEKLIIMTN 1971
Db 1895 RQFVEMALDQAVINOVNRDIPGVTNENLFLPLKLVNRLLVGMWREDEVEKLIIMTN 1954
Qy 1972 PETWDSFDEKGEDEHKKGLIMKMAEAKLQWQCYLLQHLNDIQLRHRVEALIIAFADPV 2031
Db 1955 PETWDSFDEKGEDEHKKGLIMKMAEAKLQWQCYLLQHLNDIQLRHRVEALIIAFADPV 2014
Qy 2032 GDLQDTQLRKYRTEIKSDLPASVAAKTBEPFCRPREQONALLSPHLSBEDKQNPCE 2091
Db 2015 GDLQDTQLRKYRTEIKSDLPASVAAKTBEPFCRPREQONALLSPHLSBEDKQNPCE 2074
Qy 2092 ELIARNEPHDTLMAHVSILHALOEPPAENQ--PEAKPGAFLKYNITVXELFEBA 2150
Db 2075 ELIARNEPHDTLMAHVSILHALOEPPAENQ--PEAKPGAFLKYNITVXELFEBA 2134
Qy 2151 IBERPKTPEBEKRYLQITIVNMAESQIETPKLVRENFSLVRODYAVGELIRALEKT 2210
Db 2135 IBERPKTPEBEKRYLQITIVNMAESQIETPKLVRENFSLVRODYAVGELIRALEKT 2194
Qy 2211 YVINAATKLDVAMWYGLSQRALLFPVQMSQEBEELMRKTKLVNNTFPQHPDLIRV 2270
Db 2195 YVINAATKLDVAMWYGLSQRALLFPVQMSQEBEELMRKTKLVNNTFPQHPDLIRV 2254
Qy 2271 RVHENVMAVMMNTIGRBAQSDAPSSQPVAE--DSKEDTSHENVAVCCRFLCYFCRT 2328
Db 2255 RVHENVMAVMMNTIGRBAQSDAPSSQPVAE--DSKEDTSHENVAVCCRFLCYFCRT 2313
Qy 2329 GRQNKAMFDHPDFFLENSNILLRSPSLRSGTPLDVAVSLMENTELALAREHYLEKIA 2388
Db 2314 GRQNKAMFDHPDFFLENSNILLRSPSLRSGTPLDVAVSLMENTELALAREHYLEKIA 2373
Qy 2389 VYLSRCGLQSNSELYEKGYPDLGMDPEGBRYDLPLFCVWNGSSVEBENANVITLLR 2448
Db 2374 VYLSRCGLQSNSELYEKGYPDLGMDPEGBRYDLPLFCVWNGSSVEBENANVITLLR 2433
Qy 2449 RPECGLPARGSEBGLKALIVANKSERIADBRKLRBMOBGDV---NPSHPLPSDEO 2505
Db 2434 RPECGLPARGSEBGLKALIVANKSERIADBRKLRBMOBGDV---NPSHPLPSDEO 2492
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Db 2493 EBYIIDGAAILNFCYLVDLGRCAPDAGVIALGKNESTRARALRSVLPLBLOGLVSL 2552
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Db 2553 RPTLNNPAAGBERPKSDMPSEGLIPGHKQSVGLEFERYVIGLEQELFYKLIBEAPFDLPA 2612
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Db 2673 RMLTKGQRAVSDPLVALTSAPQSMILKLRKLTVDVSKLSEYTVVALRLTLHYERCA 2732
Qy 2746 KYTGSTAGQGAFAASDEBKLTMLFENIPDSLSKMDYEBELFGKALPCLAIACALP 2805
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Qy 2806 PYSLSKMDYEBELFGKALPCLAIACALP--DOPOYMNPLDTNNVHLNDLNSLVQFESHYDANA 2865
Db 2792 PYSLSKMDYEBELFGKALPCLAIACALP--DOPOYMNPLDTNNVHLNDLNSLVQFESHYDANA 2849
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Db 2850 SRKIEGMYVGEQMSQKTHPRILKPYNNMLNDYEKERYKPYVESIKALIAIGMSVESH 2909
Qy 2926 VDIPSNNRSGMRQSSGGRPBEIVTDSATPPDYNHPVDMVNTLTSREKQNMABRLADN 2985
Db 2910 VDIPSNNRSGMRQSSGGRPBEIVTDSATPPDYNHPVDMVNTLTSREKQNMABRLADN 2962

1590 VIITDDYDVVENNVNOSCYMVRADLTYNEVMAATAKAGASQGMFIGSVDTSTGVSFT 1649
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 1650 CGGKOTSPFKKPEPEFKLPALFVETATSKILQIETGRSATSLPLSAVLPTSDKAVITQ 1709
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 1710 PPRLVVOCLKPHQMARVNPNSIQVHALKSDIRGMSMICEBVSMTALHIPEDDCIDI 1769
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 1770 LEPIDMKLLSFHSHTLTLYAALCYOSNRAAHLCTHYDQKOLLYAISOYMSGELRQ 1829
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 1890 DIAESTELSNLYSPYPLEVAREFVMAALAEVETNOVHNRDPVGSNENLFLPLIKY 1949
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 2010 HUNDIOLRHRVEALIFAHDPVGDLOTDLRRTETIKOSDLPASAVAKTREFRCPBRQ 2069
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 2070 NMAILSKLIEBDEKNCQGEELIARMEFHTLMAHYSIALQRPDAE-----NOE 2123
 2063 NMAILGPKLLDSDDKNCCLIGDELREBMEFNKMKOLLVALLQSEBDDKLDNNINR 2122
 2124 PEAKPAGFKLYNIITVKELEBEAKAIEBPCKTPEEKRYKLYITIVMAEBSQIETP 2183
 2123 -----QIKQFNFPIAIVD-EANENGLENHEKIEBEIFRKLITTIYSMAETQIETP 2176
 2184 KLVREMFSLVRQYDAVGBELRALBKTYYINAKTKLDVAMVGLSQRALLFVQMSQEB 2243
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 2244 BELMRKMLKLVNNHTFPOHPDLIRVLARHENVMAVMNTLGRRAQOQSSQPV-A 2302
 2237 BELMRKMLKLVNNHTFPOHPDLIRVLARHENVMAVMNTLGRRAQOQSSQPV-A 2294
 2303 BPS---KSKDTSHEWVACCRFLCYFCRTGRONOKAMPDHPFLLENSNIIILSRPLSG 2358
 2295 QGGEIVPKKEDTSHENVVACCRFLCYFCRTGRONOKAMPDHPFLLENSNIIILSRPLSG 2354
 2359 STPLDVAVSLMENTELALAREHYLEKIAVYLSRGLQSNSEILVEKGYPDLCMDPVEG 2418
 2355 STPLDVAVSLMENTELALAREHYLEKIAVYLSRGLQSNSEILVEKGYPDLCMDPVEG 2414
 2419 RYLDPLRFCTWVNGSVSEEVANVITRLIRREPCLOPALRGSEGLKAIIVANKSERI 2478
 2415 RYLDPLRFCTWVNGSVSEEVANVITRLIRREPCLOPALRGSEGLKAIIVANKSERI 2474
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 2475 ADRBRK-LREMBQGDVNFSPHCPESDEDEDYDTGAALNFYCTVLVDLGRCAPDAGVIA 2534
 2538 LGNBSBLARAILRSIPLVEDLQGVLSLRETLNPPAAGERPKSDMPSGILPCHKOSVGI 2597
 2535 LGNBSBLARAILRSIPLVEDLQGVLSLRETLNPPAAGERPKSDMPSGILPCHKOSVGI 2594
 2598 FLERVYGIETQELFYLLLEBAFLPOLRAATMLDRNCGESDMLSMRRTYIGNSIILPLIK 2657
 2595 FLERVYGIETQELFYLLLEBAFLPOLRAATMLDRNCGESDMLSMRRTYIGNSIILPLIK 2654
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Db 2655 HSKFYSESNDVNLDTATHTVYRLSKNRMLTKGQREAVSDPLVALTSAMQSMULTKLIR 2714
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 Db 2715 KLVVDSKLSXYTVALRLTLHYERCAKYGSTAGAGQAFGASDPEERLTMPLPSNIF 2773
 QY 2778 DLSKMDYEPFLFGKALPCLIAIGCALPPDYSLSKNYDDEPYG-KEQAAGLDLNPQYDQ 2836
 Db 2774 DLSKMDYEPFLFGKALPCLIAIGCALPPDYSLSKNYDDEPYG-KEQAAGLDLNPQYDQ 2832
 QY 2837 PINTSSVALNDLNTIVQFSEHYHDAMASRKIENGWYVYEGMSQKTHPLKPYNTLN 2896
 Db 2833 PINTSSVALNDLNTIVQFSEHYHDAMASRKIENGWYVYEGMSQKTHPLKPYNTLN 2892
 QY 2897 DYKERYKEPVRESKALLAIGMSVHSEVDIPSNRRSMBRQSKGCRPPLVDSATP 2956
 Db 2893 DYKERYKEPVRESKALLAIGMSVHSEVDIPSNRRSMBRQSKGCRPPLVDSATP 2944
 QY 2957 PDYHPVDMNTLTLSEBQNMALERLADNAHDIWAKKKEBELV 2999
 Db 2945 PDYHPVDMNTLTLSEBQNMALERLADNAHDIWAKKKEBELV 2987

RESULT 12
 US-11-097-143-22563 con. of 091614,150, filing date: 07/11/2000.
 ; Sequence 22563, Application us/11097143
 ; Publication No. US20050208558A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Venter, J. Craig
 ; APPLICANT: et al.
 ; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
 ; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
 ; TITLE OF INVENTION: DROSOPHILA GENES.
 ; FILE REFERENCE: CL000728
 ; CURRENT APPLICATION NUMBER: US/11/097,143
 ; CURRENT FILING DATE: 2005-04-04
 ; PRIOR APPLICATION NUMBER: 60/157,832
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: 60/160,191
 ; PRIOR FILING DATE: 1999-10-19
 ; PRIOR APPLICATION NUMBER: 60/161,932
 ; PRIOR FILING DATE: 1999-10-28
 ; PRIOR APPLICATION NUMBER: 60/164,769
 ; PRIOR FILING DATE: 1999-11-12
 ; PRIOR APPLICATION NUMBER: 60/173,383
 ; PRIOR FILING DATE: 1999-12-28
 ; PRIOR APPLICATION NUMBER: 60/175,693
 ; PRIOR FILING DATE: 2000-01-12
 ; PRIOR APPLICATION NUMBER: 60/184,831
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: 60/191,637
 ; PRIOR FILING DATE: 2000-03-23
 ; NUMBER OF SEQ ID NOS: 43008
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 22563
 ; LENGTH: 5107
 ; TYPE: PRT
 ; ORGANISM: DROSOPHILA
 ; US-11-097-143-22563

Query Match 78.6%; Score 12384; DB 6; Length 5107;
 Best Local Similarity 78.3%; Pred. No. 0;
 Matches 2356; Conservative 272; Mismatches 314; Indels 66; Gaps 20;
 QY 22 MYCLSTATGGRVCAABSGFGRNHCFLNFIADKNIPDPDISQCVFVIEQALSVRALQELVT 81
 Db 1 MYCLSTATGGRVCAABSGFGRNHCFLNFIADKNIPDPDISQCVFVIEQALSVRALQELVT 60
 QY 82 AAGSETGKGTGSGHRTLLYGNAIILRLHNSDWTYLAQLSTSSSQDCKAPVVGQOHSQGA 141
 Db 61 AAGSETGKGTGSGHRTLLYGNAIILRLHNSDWTYLAQLSTSSSQDCKAPVVGQOHSQGA 120


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Db      2256  AVMAMNTLGRRAQAQSDA-PTQSEVAGADSKKEDTSHENVVACREPLCYFCRTGRQNOKA 2314
Qy      2336  MEDHDFLENSNIILSRPLSGSTPLDVAYSISMENTELALAREHYLEKIAVYLSRGC 2395
Db      2315  MEDHDFLENDNANILARPSLKGSTPLDVAYSISMENTELALAREHYLEKIAVYLSRGC 2374
Qy      2396  LQNSSELVEKGYFDLQMDPVEGERYLDPLRFCVMVNGESVEENANIVIRLLIRPECLAP 2455
Db      2375  LQNSSELVEKGYFDLQMDPVEGERYLDPLRFCVMVNGESVEENANIVIRLLIRPECLAP 2434
Qy      2456  ARGBEELGLKALVDANKSERIADRKAREMEQEDV--NPSHLPSDEDEDTIDG 2512
Db      2435  ARGBEELGLKALVDANKSERIADRKAREMEQEDV--NPSHLPSDEDEDTIDG 2493
Qy      2513  AAILNFTCTVLDLGRCAPDAGVIALGKESLARAAILSLVLEBDLQVLSLFTLNMP 2572
Db      2499  AAILNFTCTVLDLGRCAPDAGVIALGKESLARAAILSLVLEBDLQVLSLFTLNMP 2553
Qy      2573  AAGBERPKSDMPSGLIPGHKQSVGLPLERVYGIETQELPYKLEBAFLPDLRAATMDRN 2632
Db      2554  AAGBERPKSDMPSGLIPGHKQSVGLPLERVYGIETQELPYKLEBAFLPDLRAATMDRN 2613
Qy      2633  DCGESDMALSKNRYIGNSILPLILKAYTYNEAENYASLLDATLHTVYLSKRMKLTQKQ 2692
Db      2614  DGSBSDMALAMRYIGNSILPLILKAYTYNEAENYASLLDATLHTVYLSKRMKLTQKQ 2673
Qy      2693  RBAVSDPLVALTSAMQPSMLKLRLKLTVDVSKLSYTTVALRLTLHYERCAKXYGSGTQ 2752
Db      2674  RBAVSDPLVALTSAMQPSMLKLRLKLTVDVSKLSYTTVALRLTLHYERCAKXYGSGTQ 2732
Qy      2753  AQOGAFGASDESDEKRLTMMFLPSNIPDLSKMDYEPFLPGALPCLLAIICALPPDYSLK 2812
Db      2733  AQOGAFGASDESDEKRLTMMFLPSNIPDLSKMDYEPFLPGALPCLLAIICALPPDYSLK 2792
Qy      2813  NYDEFEYGEQAAGLDLNFQYDPOPIINTSSVALNDLNTTVQKSHYHDAMASKIENG 2872
Db      2793  NYDEFEYGEQAAGLDLNFQYDPOPIINTSSVALNDLNTTVQKSHYHDAMASKIENG 2850
Qy      2873  WYEGESMSQKTHPRLKPYNMINDYEXERKYPVEESLKALLATQMSVESHVDIPSN 2932
Db      2851  WYEGESMSQKTHPRLKPYNMINDYEXERKYPVEESLKALLATQMSVESHVDIPSN 2910
Qy      2933  RSMERQSGSGRPERI--VTDSATPFDPYVPHFVDNTLTLSEKQMMARLADNADIM 2990
Db      2911  RSMERQSGSGRPERI--VTDSATPFDPYVPHFVDNTLTLSEKQMMARLADNADIM 2865
Qy      2991  AKKKKEEL 2998
Db      2966  AKKKKEEL 2973

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RESULT 13
US-10-668-767-125
/ Sequence 125, Application US/10668767
/ Publication No. US2004017114A1
/ GENERAL INFORMATION:
/ APPLICANT: Casper, Timothy
/ APPLICANT: Cordova, Daniel
/ APPLICANT: Guttridge, Steven
/ APPLICANT: Rauh, James
/ APPLICANT: Smith, Rejane
/ APPLICANT: Tao, Yong
/ APPLICANT: Wu, LiHong
/ TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
/ FILE REFERENCE: B1533 US NA
/ CURRENT APPLICATION NUMBER: US/10/668,767
/ PRIOR FILING DATE: 2003-09-23
/ PRIOR APPLICATION NUMBER: 60/412,795
/ PRIOR FILING DATE: 2002-09-23
/ PRIOR APPLICATION NUMBER: 60/427,324
/ PRIOR FILING DATE: 2002-11-18
/ NUMBER OF SEQ ID NOS: 149
/ SOFTWARE: Patentin version 3.1

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/ SEQ ID NO 125
/ LENGTH: 5112
/ TYPE: PRF
/ ORGANISM: Drosophila melanogaster
/ FEATURE:
/ OTHER INFORMATION: gi 2160477
US-10-668-767-125

Query Match      78.4%; Score 12354; DB 4; Length 5112;
Best local similarity 78.2%; Pred. No. 0;
Matches 2359; Conservative 265; Mismatches 337; Indels 54; Gaps 21;

Qy      1  MABEAGSAGSODVDFLRTEDVCLSGATGSRVCLAAFGNRRCHLENADKNIPDL 60
Db      1  MABEAGS-SEODVDFLRTEDVCLSGATGSRVCLAAFGNRRCHLENADKNIPDL 59
Qy      61  SOCVPIEBALVRLAQELVTAAGSTGSGHRTLLYGNAIILRHNSDMYLACLST 120
Db      60  SOCVPIEBALVRLAQELVTAAGSTGSGHRTLLYGNAIILRHNSDMYLACLST 119
Qy      121  SSSODKLAPDVLQOHSQGEACMWTLPASKORSEGEKRVGDLLIVSATERYHTTK 180
Db      120  SSSNDKLSPDVLQOHSQGEACMWTLPASKORSEGEKRVGDLLIVSATERYHTTK 179
Qy      181  ENEVSIIVNASFVYTHMSVQPYGTGISRMKCYGVFEGDYLPFHGDECLTIPSTYTKG 240
Db      180  ENEVSIIVNASFVYTHMSVQPYGTGISRMKCYGVFEGDYLPFHGDECLTIPSTYTKG 239
Qy      241  GQNIYVYEGGSVMSQARSIMRLRLARTKAGFIMYTHMRRLHTTGKRYLVNDQNELY 300
Db      240  GQNIYVYEGGSVMSQARSIMRLRLARTKAGFIMYTHMRRLHTTGKRYLVNDQNELY 299
Qy      301  LYSREBETASACAFCLROBKDOKOYLEDKDEVIAPFIKYGDSVVIQHSSTGLMLSY 360
Db      300  LYSREBETASACAFCLROBKDOKOYLEDKDEVIAPFIKYGDSVVIQHSSTGLMLSY 358
Qy      361  KSYETKKGKGVYBEKQALIHBEKMGDGLDPSRQSEBSRTARVIRKSSLPFKENG 420
Db      359  KSYETKKGKGVYBEKQALIHBEKMGDGLDPSRQSEBSRTARVIRKSSLPFKENG 418
Qy      421  ETLQENRRHSMFPASVNLCEMVCLEDLINYAOPDEMEHEKQKFPALNRRDLPOE 480
Db      419  ETLQENRRHSMFPASVNLCEMVCLEDLINYAOPDEMEHEKQKFPALNRRDLPOE 478
Qy      481  EGLNLTLEAIKINIVTSQGLAGLADSGQSSEMTSGLYOULAAIYKGNHTNCAQ 540
Db      479  EGLNLTLEAIKINIVTSQGLAGLADSGQSSEMTSGLYOULAAIYKGNHTNCAQ 538
Qy      541  PANSNRLNMLPRLSQASGEGTGMDLVLAHCVLIDSPALNMRRDEHIVIIISLEKGR 600
Db      539  PANSNRLNMLPRLSQASGEGTGMDLVLAHCVLIDSPALNMRRDEHIVIIISLEKGR 598
Qy      601  DEKVIDVCLSLCVGNGAVRSSQNNICDYLPLFGKNLLQTLALVDHYSSVREPIFVGRVGG 660
Db      599  DEKVIDVCLSLCVGNGAVRSSQNNICDYLPLFGKNLLQTLALVDHYSSVREPIFVGRVGG 658
Qy      661  SAVYRKVYEVYTMDEHEKTHMMPHLRIGMATTTGVVPYRGGEKMGKGVGDDLYSYXG 720
Db      659  SAVYRKVYEVYTMDEHEKTHMMPHLRIGMATTTGVVPYRGGEKMGKGVGDDLYSYXG 718
Qy      721  DGAYLMSGGRKTPVNRTHABEPYIRKGVYIGCALDLTVPIINFMENGAVTSSFTNFNLE 780
Db      719  DGAYLMSGGRKTPVNRTHABEPYIRKGVYIGCALDLTVPIINFMENGAVTSSFTNFNLE 778
Qy      781  GMPFVYISCSSTLSCRFLLGSHGRLYVAPRGYSPVLESLLPQOILSEPCFYRGNLSK 840
Db      779  GMPFVYISCSSTLSCRFLLGSHGRLYVAPRGYSPVLESLLPQOILSEPCFYRGNLSK 838
Qy      841  RALAGPVLVODDTAPVPPVDTLQITLPPYVQIDBKLAENIHEMMAMKIEAGMMYGLQ 900
Db      839  RALAGPVLVODDTAPVPPVDTLQITLPPYVQIDBKLAENIHEMMAMKIEAGMMYGLQ 898
Qy      901  REDLHKIHPLVFPFRLPPAEKRYDIOQLAVQTLKTLALGYVVISLDPKPARIRNVL PNE 960

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Db      899 RODYRIRHCLTHPELCPAERKYDQLAVOITLKTIIISLGYITMDKPARIRPVLEPBE 958
Qy      964 PEMQSGYAPAPLDLSAVTLTPKMDLVDQLAENTHNLWABERIQQGWTYGLNEDSDMKR 1020
Db      959 IMQSGNGYAPAPLDLSAVTLTPKLEBLVQDLAENTHNLWABERIQQGWTYGLNEDSENIR 1018
Qy      1021 SBLHVPYPRVDDAIKKANRDTASETVRTLLVYGVMLDPTGEOHEALLIENASKOKQADFR 1080
Db      1019 SBLHVPYAKVDBAIKKANRDTASETSANAPGLRI CLGSSDGRNNGTSGRGTTPOVRIRIP 1078
Qy      1081 TYRAENYAVSSGKMYFEFEILLAGBMYRGMAHADAPGMMLGODNSNAPFGYNEEKY 1140
Db      1079 TYRVERNVAVTSGKMYFEFEVLTSGPMRGMAADCPGAMLGSEDTSAFQSHNEEKY 1138
Qy      1141 SGNTESPGKQMAVDGVVGFLLIDIKTISFSLNGELMLDALGSETTFADV--QGNFVPA 1198
Db      1139 GGVSESPGQCGPBGDI VGVFLDADHTISFSLNGELMLDALGSETTFADVTAEGVGFVA 1198
Qy      1199 CTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNNKRDVTWYTKQPIFENTDEM 1258
Db      1199 CTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNNKRPVTHWYTKQPIFENTDEM 1258
Qy      1259 ITRRIDVTRIPAGSDPRLCKISHTFETMEKANMEFLRLSLPYCHNFIDBAEKARW 1318
Db      1259 PCORIDVTRIPGADTPRLCKISHTFETMEKANMEFLRLSLPYTCGSEFISQEKARW 1318
Qy      1319 VEIKRQOILMKEA--VEAQM-----PAHIDQIMRSGFTMNDIKGLHYE--DNOBELPSSKM 1371
Db      1319 DEIKRQYLYMREAEIYLAQMOMQOTOAAHNDHMLKGFNNNDIKGLTRNDEHADAEADIM 1378
Qy      1372 KRLPSRPRKSGMTRGVTTQNTNNILOPGVNGMHRSTSEAWAKYDLAGQSLTPDDKOK 1431
Db      1379 MEGPNRPKSGSLTRNIT--FETDWSALDEWQSTST-----VLDMMGLGSEMDKK-K 1429
Qy      1432 RGRSPRPFKRSKRGESDPAKRSKTPRPSPSTBVSPPRGARPRPOKVGQANRNG 1491
Db      1430 RGRSPRPFKRSKRGESDPAKRSKTPRPSPSTBVSPPRGARPRPOKVGQANRNG 1491
Qy      1492 KMARPERNTLYGSGVGLNATPTQDRKONTSTLAOSATEVGNELFDAECLKLINEFY 1551
Db      1488 AELIPSPV-----POGPKOUGSNTLQGPVETSGDBHFDLCKLINEFY 1533
Qy      1552 GVRILYPGODPTHYIGMVTTOYHLNSKDPNQSRYTKSVIITDDYDRVENVNROSQYV 1611
Db      1534 GVRILYPGODPTHYIGMVTTOYHLNSKDPNQSRYTKSVIITDDYDRVENVNROSQYV 1593
Qy      1612 RADELYNEVMAETAKGASQGMFICGSVPTSGSVSFTCEGKOTSKFKMEBETKLPRI 1671
Db      1594 RADELYNEVMAETAKGASQGMFICGSVPTSGSVSFTCEGKOTSKFKMEBETKLPRI 1653
Qy      1672 FVEATSKETILOTELGRASLPLSAVANLPTSDKHVLPFPPRLKYQCLKPHOMARVPNS 1731
Db      1654 FVEATSKETILOTELGRASLPLSAVANLPTSDKHVLPFPPRLKYQCLKPHOMARVPNS 1713
Qy      1732 LQVHMLKLSDIGMSMLCEDAVSMLAHLPEEDRCIDILEPIEMDKLSFHSHTLTLVA 1791
Db      1714 LQVHMLKLSDIGMSMLCEDAVSMLAHLPEEDRCIDILEPIEMDKLSFHSHTLTLVA 1773
Qy      1792 LCYQSNYRAAHLCTHVQKOLLYAIQSOYMSGRLAQGYDILLALHLSHATWMAKCN 1851
Db      1774 LCYQSNYRAAHLCTHVQKOLLYAIQSOYMSGRLAQGYDILLALHLSHATWMAKCN 1833
Qy      1852 EFVYIPLGRELKALYEBDMGHSRLSLOTESVVRPQMGTDIASGITELISMLYSPPLLEVA 1911
Db      1834 EFVYIPLGRELKALYEBDMGHSRLSLOTESVVRPQMGTDIASGITELISMLYSPPLLEVA 1893
Qy      1912 REFVQALAEAVETNOVHRDIPVGSNENLFLPLIKLVDRLLVGMARDEVEKLLIMTN 1971
Db      1894 RQVMEALDVAIEINVHRDIPGWTNENLFLPLIKLVDRLLVGLTLDEBDVQRLVMD 1953
Qy      1972 PETWDBSPKSGDERKGLILMKMAEGAKLQMCYLLQHLNDIQLHRYEALIAFADRV 2031

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Db      1954 PETWDBSPKSGDERKGLILMKMAEGAKLQMCYLLQHLNDIQLHRYEALIAFADRV 2013
Qy      2032 GDLQTDRLRYATEIKQSDLPESAIAKKTREPRCPREOMNAILSPKHLSEEDKENCPCGE 2091
Db      2014 GDLQTDRLRYATEIKQSDLPESAIAKKTREPRCPREOMNAILSPKHLSEEDKENCPCGE 2073
Qy      2092 ELIAMNEFHDTLMAHSLHLOEPDABENGE--PAKGAPOKLYNIINTVLEBEAKA 2150
Db      2074 ELIAMNEFHDTLMAHSLHLOEPDABENGE--PAKGAPOKLYNIINTVLEBEAKA 2133
Qy      2151 IEEPRKTPPEEKFRKYLITQTYNMAESQIETPKLVREMFSLVHQYAVGELIPALEKT 2210
Db      2134 VBEPRKTPPEEKFRKYLITQTYNMAESQIETPKLVREMFSLVHQYAVGELIPALEKT 2193
Qy      2211 VYINAKTLDVAEMVNGSLQIRALLPVQMSQEBEELMKRLKLVNNHTFQHPDLIRVL 2270
Db      2194 VYINAKTLDVAEMVNGSLQIRALLPVQMSQEBEELMKRLKLVNNHTFQHPDLIRVL 2253
Qy      2271 RYHENVVAVMNTTLGRRAQAGSDAOPSSQPVAE--DSKXKOTSHENVVACCRFLCYFCRT 2328
Db      2254 RYHENVVAVMNTTLGRRAQAGSDAOPSSQPVAE--DSKXKOTSHENVVACCRFLCYFCRT 2312
Qy      2329 GRONOKAMFDPDFLENSNITLSRPSLRGSTPLDVAYSLSMENTELALAREHYLEKIA 2388
Db      2313 GRONOKAMFDPDFLENSNITLSRPSLRGSTPLDVAYSLSMENTELALAREHYLEKIA 2372
Qy      2389 VYLSRQGLQNSNELVEKGYPDLGMDPVEGERYLDLRFQVWNGESVEBENAVIIRLLIR 2448
Db      2373 VYLSRQGLQNSNELVEKGYPDLGMDPVEGERYLDLRFQVWNGESVEBENAVIIRLLIR 2432
Qy      2449 RPECGLPALRGGBELKAIYDANKMSERIRADRRLREMOEGDV--NFSHPLPESDD 2505
Db      2433 RPECGLPALRGGBELKAIYDANKMSERIRADRRLREMOEGDV--NFSHPLPESDD 2491
Qy      2506 EDYIDTGAAILNFCTLYDLGRCAPDGVILAGKNEISLRARAIIRSLVPLEDLQGVSL 2565
Db      2492 EDYIDTGAAILNFCTLYDLGRCAPDGVILAGKNEISLRARAIIRSLVPLEDLQGVSL 2551
Qy      2566 RFTLNNPAAGBEPRKSDMPGSLIPGHKQSVGLFELRYVYGIETQELPYKLLBEAPLPDLRA 2625
Db      2552 RFTLNNPAAGBEPRKSDMPGSLIPGHKQSVGLFELRYVYVGIETQELPYKLLBEAPLPDLRA 2611
Qy      2626 ATMLDRNGCESDMLASNRRTYIGNSILPLILGHAFYNEAEVYASLLDATTHTVRLSN 2685
Db      2612 ATMLDRNGCESDMLASNRRTYIGNSILPLILGHAFYNEAEVYASLLDATTHTVRLSN 2671
Qy      2686 RMLTKGOREAVSDPLVALTSAMQPSMLKLRKLTVDYSKLSBYTTVALRLTLHYERCA 2745
Db      2672 RMLTKGOREAVSDPLVALTSAMQPSMLKLRKLTVDYSKLSBYTTVALRLTLHYERCA 2731
Qy      2746 KYTGSTGAGQAGFASDBEKKLTMLLPFSNIFDSLSKNDYBEELFGKALPCLIAIGCALP 2805
Db      2732 KYTGSTGAGQAGFASDBEKKLTMLLPFSNIFDSLSKNDYBEELFGKALPCLIAIGCALP 2790
Qy      2806 PYSLSKNTYDEFFYKEQAAGLDNPQYDPOPIINTSSVALNNDLNTIYQKSEBHTDANA 2865
Db      2791 PYSLSKNTYDEFFYKEQAAGLDNPQYDPOPIINTSSVALNNDLNTIYQKSEBHTDANA 2848
Qy      2866 SRKINGWYVYCGMSQKTHPRLLKPYMMLNDYEXERYKBPVRESIKALALIGMSVHSE 2925
Db      2849 SRKINGWYVYCGMSQKTHPRLLKPYMMLNDYEXERYKBPVRESIKALALIGMSVHSE 2908
Qy      2926 VDIPSNNNSMNRQSKSGGRPPEI--VTDSATPFPYNPAPVDMTULTSREMNQNAERLA 2983
Db      2909 VDIPSNNNSMNRQSKSGGRPPEI--VTDSATPFPYNPAPVDMTULTSREMNQNAERLA 2963
Qy      2984 DNADHIIWAKKKEEL 2998
Db      2964 ENSHDIWAKKKEEL 2978

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RESULT 14
US-10-668-767-56

```
/ Sequence 56, Application US/10668767
/ Publication No. US2004017114A1
/ GENERAL INFORMATION:
/ APPLICANT: Caspar, Timothy
/ APPLICANT: Cordova, Daniel
/ APPLICANT: Gutteridge, Steven
/ APPLICANT: Rauh, James
/ APPLICANT: Smith, Rejane
/ APPLICANT: Tao, Yong
/ APPLICANT: Wu, Jihong
/ TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
/ FILE REFERENCE: BB1533 US NA
/ CURRENT APPLICATION NUMBER: US/10/668,767
/ PRIOR FILING DATE: 2003-09-23
/ PRIOR APPLICATION NUMBER: 60/412,795
/ PRIOR FILING DATE: 2002-09-23
/ PRIOR APPLICATION NUMBER: 60/427,324
/ PRIOR FILING DATE: 2002-11-18
/ NUMBER OF SEQ ID NOS: 149
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 56
/ LENGTH: 5126
/ TYPE: PRT
/ ORGANISM: Drosophila melanogaster
/ US-10-668-767-56

Query Match      78.3%; Score 12338; DB 4; Length 5126;
Best Local Similarity 77.9%; Pred. No. 0;
Matches 2359; Conservative 266; Mismatches 336; Indels 68; Gaps 22;

Cy 1 MAABAGASBDDVDFLRTEDMVLCTATGERVCLAAEGFNHCELENADKNIPDL 60
Db 1 MAABEGG-SBEDDVSFLRTEDMTVLSTATGERVCLAAEGFNHCELENADKNIPDL 59
Cy 61 SQCFVIBQALSVBALDELVTAGSEGTGSGHRTILYGNAILRHNSDMTACLST 120
Db 60 SQCFVIEQALSVBALDELVTAGSEGTGSGHRTILYGNAILRHNSDMTACLST 119
Cy 121 SSSGDKLAFVVGLOOHGGEACMWTLPASKORSEGEVVRGDDLIVSVATERYHTTK 180
Db 120 SSSNDKLSFDVGOEHGGEACMWTLPASKORSEGEVVRGDDLIVSVATERYHTTK 179
Cy 181 ENESYIVNASFHTVMSVQPYGTGTSRMKVYGVYFGDVLAFPHGDBECLTIPSTWTKD 240
Db 180 ENESYIVNASFHTVMSVQPYGTGTSRMKVYGVYFGDVLAFPHGDBECLTIPSTWTKD 239
Cy 241 GONIVYEGGSVMSQASLWMLBELARTKMGAFINWYHMKIRHITTTGRYLVNDQNELY 300
Db 240 GONIVIEGGVYMAQASLWMLBELARTKMGAFINWYHMKIRHITTTGRYLVNDQNELY 299
Cy 301 LVSRBEATYASCACLRQEKDQKQVLEKDLVETGAPITKYGSTVYVHSEGTMLSY 360
Db 300 LVSRBEASIAATTTFSW-OEKDDEKQVLEKDLVETGAPITKYGSTVYVHSEGTMLSY 358
Cy 361 KSYTKKKKGVKVEKQALIEBGMDDGLDFSRQSEESRTAIVIRKCSLFTFKINGL 420
Db 359 KSYTKKKKGVKVEKQALIEBGMDDGLDFSRQSEESRTAIVIRKCSLFTFKINGL 418
Cy 421 ETLQENRRHSMFPASVNLGEMVCLBDLINTPAQPDDEMEHEKQNRKALRNODLEOE 480
Db 419 ETLQSNRRHSIFPKQVNLNEMVCLBDLINTPAQPDDEMEHEKQNRKALRNODLEOE 478
Cy 481 EGIINLLIEATDKINVTISQGLAGFLAGDSGSGEMISGYLYQLAAIKGNHTNCAQ 540
Db 479 EGIINLLIEATDKINVTISQGLAGFLAGDSGSGEMISGYLYQLAAIKGNHTNCAQ 538
Cy 541 PANSRRLWMLPSRLGSOASGEGTGLDVHLCVLISSPALNMDEHAKVIIISLEKGR 600
Db 539 PANSRRLWMLPSRLGSOASGEGTGLDVHLCVLISSPALNMDEHAKVIIISLEKGR 598
Cy 601 DPKVLDVLCSLCVNGVAVRSSONNICDYLLPGKULLLQTLVDRVSSVPRNIPVGRVGG 660
Db 599 DPKVLDVLCSLCVNGVAVRSSONNICDYLLPGKULLLQTLVDRVSSVPRNIPVGRVGG 658
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Cy 661 SAVYRKRYEEVTNDHIEKTTMMPHLRIGNATTTGVYPIPGGEGKNGGVGDLYSYGR 720
Db 659 SSMYOKMYEEVTNDHIEKTTMMPHLRIGNATTTGVYPIPGGEGKNGGVGDLYSYGR 718
Cy 721 DGAYLMSGKRTVNRTHAEPIYIRKGDVGCALDLTPRIINFMNGVRTVTSPTNPNLE 780
Db 719 DGAYLMSGKRTVNRTHAEPIYIRKGDVGCALDLTPRIINFMNGVRTVTSPTNPNLE 778
Cy 781 GMFFPVVYSSKSLSCRFILGEGHRLRYAPAEQSPVLESILPQOILSEPCFYGNLSTK 840
Db 779 GMFFPVVYSSKSLSCRFILGEGHRLRYAPAEQSPVLESILPQOILSEPCFYGNLSTK 838
Cy 841 RALAGPELVDDTAFAVPTPVDTLOITLPTVYEQIRDKLAENIHEMAMNKIEAGMYGQD 900
Db 839 NVLAGPELVDDTAFAVPTPVDTLOITLPTVYEQIRDKLAENIHEMAMNKIEAGMYGQD 898
Cy 901 REDLAKTHPCLVPERLPPAEKRYDQAVQTLKTIALLGYIISLDEKPARINVRLEPNE 960
Db 899 RDDYHRHPCLVPERLPPAEKRYDQAVQTLKTIALLGYIISLDEKPARINVRLEPNE 958
Cy 961 PFMOSNGYKRPAPDLISAVTLTPKMDLVDQLAENTHLMARERIOQGMWYGLNEDSPMR 1020
Db 959 IFMOSNGYKRPAPDLISAVTLTPKMDLVDQLAENTHLMARERIOQGMWYGLNEDSPMR 1018
Cy 1021 SPHLVYPRKYDDAIKKANRDTASBTVRTLLVYGYMLDPYGEQHEALLASRQKQADFR 1080
Db 1019 SPHLVYPRKYDDAIKKANRDTASBTVRTLLVYGYMLDPYGEQHEALLASRQKQADFR 1078
Cy 1081 TYRAEKYAVSGKMYEPEBITLAGPMRVMAHADMAPGMMLQODENSNAFDGNEKYV 1140
Db 1079 TYRAEKYAVSGKMYEPEBITLAGPMRVMAHADMAPGMMLQODENSNAFDGNEKYV 1138
Cy 1141 SGMTESEFKQWAVGDVGVFLDIDKTIISFLNGELMDLAGEETTPADV--QGDNVPVA 1198
Db 1139 SGMTESEFKQWAVGDVGVFLDIDKTIISFLNGELMDLAGEETTPADV--QGDNVPVA 1196
Cy 1199 CTGAGVQKARLYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKQOPIFENTDM 1258
Db 1197 CTGAGVQKARLYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKQOPIFENTDM 1256
Cy 1259 IDTRIDYTRIAGSDTPPCIKISHTNFTMEKANWELRLSLPTCHNEPIDEKARRW 1318
Db 1257 IDTRIDYTRIAGSDTPPCIKISHTNFTMEKANWELRLSLPTCHNEPIDEKARRW 1316
Cy 1319 VEIKDROQILMKKA-VAQW-----PAHQIOWMSGFTMDIKGLHYE-DNQEGLPSSKM 1371
Db 1317 VEIKDROQILMKKA-VAQW-----PAHQIOWMSGFTMDIKGLHYE-DNQEGLPSSKM 1369
Cy 1372 KRLSPRPKSGMSRTGVTIQYNNILOQVYNGMHRSTSEAMAKYDLAGOGLTPDDKDK 1431
Db 1370 KRLSPRPKSGMSRTGVTIQYNNILOQVYNGMHRSTSEAMAKYDLAGOGLTPDDKDK 1429
Cy 1432 RGRSPFKFRRKSGSSDRKSRKSTPDPSPDTEVSBERGARRNPQIVKQANQRYNG 1491
Db 1430 RGRSPFKFRRKSGSSDRKSRKSTPDPSPDTEVSBERGARRNPQIVKQANQRYNG 1489
Cy 1492 MNARPSTNLVGSQVGLMAATPTQDRKQMTSTLAQATETVNGEIDAECLKILNXYFY 1551
Db 1490 MNARPSTNLVGSQVGLMAATPTQDRKQMTSTLAQATETVNGEIDAECLKILNXYFY 1549
Cy 1552 GVRILYPGODPTHVYIGWTTQYHLHSKQFQNSKTKYSVITDDYDVEVENVNSQSCMY 1611
Db 1550 GVRILYPGODPTHVYIGWTTQYHLHSKQFQNSKTKYSVITDDYDVEVENVNSQSCMY 1609
Cy 1612 RADELVYNEVAEATAKASQGMFTGSGVDSTSGSVSTCEGKQTSYFKPKNEPFTKLPPAI 1671
Db 1610 RADELVYNEVAEATAKASQGMFTGSGVDSTSGSVSTCEGKQTSYFKPKNEPFTKLPPAI 1669
Cy 1672 PVEATSKETIOLIEGRATSLPLSAAVLTPNSDKVITQOFPRLKLVQCLKPHQWARPVNS 1731
Db 1670 PVEATSKETIOLIEGRATSLPLSAAVLTPNSDKVITQOFPRLKLVQCLKPHQWARPVNS 1729
```


QY 1732 LQVHALKLSIDIRGSMUCEDAVSMALHIPEEDRCIDILIEPINDKLSFHSHTLTYYAA 1791
 DB 1714 LQVHALKLSIDIRGSMUCEDPVSMTALHIPEEDRCIDILIEPINDKLSFHSHTLTYYAA 1773
 QY 1792 LCVSNYRAAHALCTHYDOKOLLAIOSOVMSGPRGOFYDLIALHLESATMEACN 1851
 DB 1774 LCVSNYRAAHALCOHPOKOLLAISSEYMSGPRGOFYDLIALHLESATMEACN 1833
 QY 1852 EPVPLIGPELKALEYEPDMGHSLSLQTESVRPQMKNTDI-----AESITE 1897
 DB 1834 EYIPLIGPELKALEYEDEMGSLSLSLQTESVRPQMKNTDI-----AESITE 1893
 QY 1898 ISNYSYPPLEVAAREPYMOMALAEVETNOYHNDPVGGSNENPLPLIKLVDRLLVGM 1957
 DB 1894 IDOLYSBPFLPVLRQFVMEALKDAVEINQVHNDPIGWTNENPLPLIKLVDRLLVGM 1953
 QY 1958 MRDEDVKELIMTPEFTMDSPDKGKDEHRKGLHMKMAAGALQMCYLLQHLNDIOLR 2017
 DB 1954 LTDEDOVRLVMDPEFTMDQAFEREGKDEHRKGLHMKMAAGALQMCYLLHLYDTOLR 2013
 QY 2018 HRVBAIIAFADPVGDLQDOLRREYTEIKOSDLPSSAAKTRERCPREOMNALISFK 2077
 DB 2014 HRVBAIIAFSHDFGDLQDOLRREYTEIKOSDLPSSAAKTRERCPREOMNALISFK 2073
 QY 2078 HLEBEDKENCPCGEBELARANEFTDTLMAVSLHALQEPDAENQ-PEAKPGAFCULN 2136
 DB 2074 NLEBDDDNCTCGELRGLDFDSDLMOKVSLNALQEPDVEGTAIEVYKGPITKYN 2133
 QY 2137 IINTVKELEBEAKAIEBPCKTPEKPKRYLQITIVMAESQIETKLVREMSLLVRQ 2196
 DB 2134 PITVKELEBEKPEVEBEKKTPEBEVRKVLKITYVAESQIENKPLVREMSLLVRQ 2193
 QY 2197 YDAVGBELIRALEKTYVINAKTKLDVAEMVYGLSGIRALLPVQMSQEBELMRKMLV 2256
 DB 2194 YDTVGBELVRLALEKTYVINTRABDVAAEMVYGLSGIRALLPVQMSQEBELMRKMLV 2253
 QY 2257 NHTFPQBPDLIRVLVHENVAVMANTLGRRAQOASDAQOSSQOPVAE--DSKEKDISHEM 2314
 DB 2254 NATFPQBPDLIRVLVHENVAVMANTLGRRAQOASDAQOSSQOPVAE--DSKEKDISHEM 2312
 QY 2315 VVACCRFLCYFCRTGRONOKAMPDHPFLLENSNIIILSRPSLGSPTLDVAVSLMNTTE 2374
 DB 2313 VVACCRFLCYFCRTGRONOKAMPDHPFLLENSNIIILSRPSLGSPTLDVAVSLMNTTE 2372
 QY 2375 LALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLCMDPEVEGERYDLPLFCVWNGES 2434
 DB 2373 LALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLCMDPEVEGERYDLPLFCVWNGES 2432
 QY 2435 VERNANIVITLLRRPPECLOPALRGESEGLKALVANKKSERIADRRKLRMEQSGDV- 2493
 DB 2433 VERNANIVITLLRRPPECLOPALRGESEGLKALVANKKSERIADRRKLRMEQSGDV- 2491
 QY 2494 --NFSHPLPESDEDEYIDTGAAILNFCYTLVLDLGRCAPDAGVIALGKKESSIRARAILR 2551
 DB 2492 GINFTHPLRGEDEDEYIDTGAAILNFCYTLVLDLGRCAPDAGVIALGKKESSIRARAILR 2551
 QY 2552 SLVPLEDLQGVLSLRLTNNPAAGERPKSDMPSGLPGHKOSVGLFLERVYGIETQELP 2611
 DB 2552 SLVPLEDLQGVLSLRLTNNPAAGERPKSDMPSGLPGHKOSVGLFLERVYGIETQELP 2611
 QY 2612 YKLEBAEFLPDLOAATMLDNDGCESPMALSNRYIGNSLPLILIKAYIYNEAENYASL 2671
 DB 2612 YKLEBAEFLPDLOAATMLDNDGCESPMALSNRYIGNSLPLILIKAYIYNEAENYASL 2671
 QY 2672 LDATLTHVYLSKRMULTKGRBAVSDPLVALTSAOMPMLKLRLTJYDVSKSEYTT 2731
 DB 2672 LDATLTHVYLSKRMULTKGRBAVSDPLVALTSAOMPMLKLRLTJYDVSKSEYTT 2731
 QY 2732 VALRLTLHYERCATKYGSGTGAQGAFGASDESEKLTMLFSGNIPDSIKMDYEBELFG 2791
 DB 2732 VALRLTLHYERCATKYGSGTGAQGAFGASDESEKLTMLFSGNIPDSIKMDYEBELFG 2790
 QY 2792 KALPCLIAIGCALPPDYISLSKNTDDEFFYGEQAAGLDNPQYDPQPIINTSSVALNDLNT 2851

DB 2791 KALPCLIAIGCALPPDYISLSKNTDDEFFYGEQAAGLDNPQYDPQPIINTSSVALNDLNT 2848
 QY 2852 IYQFSEHYHDANASRKLXENGVYGEBSQSOQTHPRLKRYNMINDYEXERYEPVRESL 2911
 DB 2849 IYQFSEHYHDANASRKLXENGVYGEBSQSOQTHPRLKRYNMINDYEXERYEPVRESL 2908
 QY 2912 KALLAIGMSVSEHSEVDIPSNRRSMRQSKSGRPREI--VTDSATPPDYVPHFVDMTNL 2969
 DB 2909 KALLAIGMTVEHSEVEVPLNHRGSTRQSK-----PQINFQNGSPFNTPHPVDMTNL 2963
 QY 2970 TISREMNMAERLADNADHIMAKKKEEL 2998
 DB 2964 TISREMNMAERLADNADHIMAKKKEEL 2992
 RESULT 15
 US-10-668-767-124
 ; Sequence 124, Application US/10668767
 ; Publication No. US2004017114A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Caspar, Timothy
 ; APPLICANT: Cordova, Daniel
 ; APPLICANT: Guttridge, Steven
 ; APPLICANT: Rauh, James
 ; APPLICANT: Smith, Rejane
 ; APPLICANT: Tao, Yong
 ; APPLICANT: Wu, Lihong
 ; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
 ; FILE REFERENCE: B1533 US NA
 ; CURRENT APPLICATION NUMBER: US/10/668,767
 ; CURRENT FILING DATE: 2003-09-23
 ; PRIOR APPLICATION NUMBER: 60/412,795
 ; PRIOR FILING DATE: 2002-09-23
 ; PRIOR APPLICATION NUMBER: 60/427,324
 ; PRIOR FILING DATE: 2002-11-18
 ; NUMBER OF SEQ ID NOS: 149
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 124
 ; LENGTH: 5126
 ; TYPE: PRP
 ; ORGANISM: Drosophila melanogaster
 ; FEATURE:
 ; OTHER INFORMATION: g1 2160476
 US-10-668-767-124
 Query Match 78.3%; Score 12338; DB 4; Length 5126;
 Best Local Similarity 77.9%; Pred. No. 0;
 Matches 2359; Conservative 266; Mismatches 336; Indels 68; Gaps 22;
 QY 1 MAEABGASBODDVSFLRTEDMVCLSCTATGERVCLAAFGNRCFLXNIADKNI.PPDL 60
 DB 1 MAEABG-SEODDVSFLRTEDMVTLSCTATGERVCLAAFGNRCFLXNIADKNI.PPDL 59
 QY 61 SOCVPYIEQALSVRALQELVYTAAGSETGKGTSGRHTLLYGNAILLRLHNSDMYLA 120
 DB 60 SOCVPYIEQALSVRALQELVYTAAGSETGKGTSGRHTLLYGNAILLRLHNSDMYLA 119
 QY 121 SSSODLADPDVGIQHSQSEBACMWTLPASKQSEBEXRVGDDLLVSVATERYLAHTK 180
 DB 120 SSSNDLADPDVGIQHSQSEBACMWTLPASKQSEBEXRVGDDLLVSVATERYLAHTK 179
 QY 181 ENEVSIVNASFHTYHNSVOPYGTGTSRMKYVGVYFGADVLPFRHGDECLTIPSTWKDG 240
 DB 180 ENEQSIVNASFHTYHNSVOPYGTGTSRMKYVGVYFGADVLPFRHGDECLTIPSTWKDG 239
 QY 241 GQNTIVYEGSVNSQARSIMRLBELARTKXAGFINNYHPMRIRHITTYGAYGVNDONELY 300
 DB 240 GQNTIVYEGSVNSQARSIMRLBELARTKXAGFINNYHPMRIRHITTYGAYGVNDONELY 299
 QY 301 LYSREANTTASACFLARQKQKQKQVLEBKQLELVIGAPPIIKYGDSYVIYQHSRTGLMLST 360
 DB 300 LYSREANTTATTFSW-QEKDDEKVLBDKDLVIGSPPIIKYGDTYIVQHCETSLMLST 358

QY 361 KSYETKKGVKYEKQAILHEBGRKMDGLDFSRQSEESRTARVIRKCSLFTKPIINGL 420
 DB 359 KSYETKKGVKYEKQAILHEBGRKMDCLDFSRQSEESRTARVIRKCSLFTKPIITAL 418
 QY 421 ETLQENRRHMFASVNLGEMVNCLEDLINYPADPDEMEHEKONFRALRRQDLFOE 480
 DB 419 ETLQENRRHMFASVNLGEMVNCLEDLINYPADPDEMEHEKONFRALRRQDLFOE 478
 QY 481 EGTLLNLEAIIDKINVTSGQPLAGLADGESQSWEMISGYLXOLLAITIKGHTNCAQ 540
 DB 479 EGTLLNLEAIIDKINVTSGQPLAGLADGESQSWEMISGYLXOLLAITIKGHTNCAQ 538
 QY 541 FANSNRLNMLFSLRGSQASGEQTMLDVLCVILDSDEALNMRDEHIKYILSLERKGR 600
 DB 539 FANSNRLNMLFSLRGSQASGEQTMLDVLCVILDSDEALNMRDEHIKYILSLERKGR 598
 QY 601 DPKVLVLCGLCVNGVAVR58QNNICDYLPGKNLLQTLVVDHVASVRPNIFVGRVGE 660
 DB 599 DPKVLVLCGLCVNGVAVR58QNNICDYLPGKNLLQTLVVDHVASVRPNIFVGRVGE 658
 QY 661 SAYVRKKYREVTMDHIEKTHMPLRIGMANVTGYVPYRGGGKMGNGVGDLYSGF 720
 DB 659 SAYVRKKYREVTMDHIEKTHMPLRIGMANVTGYVPYRGGGKMGNGVGDLYSGF 718
 QY 721 DGAYLWGGKRTPVNRTHAEBPYIRKGDVIGCALDLTVPIINFMFNGVATGSPFTNLE 780
 DB 719 DGAYLWGGKRTPVNRTHAEBPYIRKGDVIGCALDLTVPIINFMFNGVATGSPFTNLE 778
 QY 781 GMPFPVISCSSKLSGREFLAGEHGRRLYAPBEGYSPVBSLPOQILSLBPCYFQNLISK 840
 DB 779 GMPFPVISCSSKLSGREFLAGEHGRRLYAPBEGYSPVBSLPOQILSLBPCYFQNLISK 838
 QY 841 RALAGPVLVDDDTAFVPTPVDTLOITLPTVBOQRDLCAENIHEMAMNKTIEAGMYGDO 900
 DB 839 RALAGPVLVDDDTAFVPTPVDTLOITLPTVBOQRDLCAENIHEMAMNKTIEAGMYGDO 898
 QY 901 RBDLHKHPCLVPERLPBAEKRYDIOAVOTLKITIALGYISLDPKPARIRVRPNL 960
 DB 899 RBDLHKHPCLVPERLPBAEKRYDIOAVOTLKITIALGYISLDPKPARIRVRPNL 958
 QY 961 PFMQNGYKAPRDLSDAVTLTPKMDLVLDLAENTHNLMAERIQQGWTYGLNEDSMHR 1020
 DB 959 PFMQNGYKAPRDLSDAVTLTPKMDLVLDLAENTHNLMAERIQQGWTYGLNEDSMHR 1018
 QY 1021 SPHLVPYAKYDEAIKKANRDTASSTVTLVYGMIDPPYGEQBALLLEASQKODFR 1080
 DB 1019 SPHLVPYAKYDEAIKKANRDTASSTVTLVYGMIDPPYGEQBALLLEASQKODFR 1078
 QY 1081 TYRABKRYAVSSGKMYEPFELLTAGPMRVGMADHADAQMMGLGODENSMAPDGYNEEKY 1140
 DB 1079 TYRABKRYAVSSGKMYEPFELLTAGPMRVGMADHADAQMMGLGODENSMAPDGYNEEKY 1138
 QY 1141 SGNTSEFGKQMAVGVDFDLIDKTISSFLNGELMDALGSETTPADY--OGDNFVPA 1198
 DB 1139 SGNTSEFGKQMAVGVDFDLIDKTISSFLNGELMDALGSETTPADY--OGDNFVPA 1198
 QY 1199 CTIGVGOKARLTYGQDVNTLKYFTTGGLOGYEBPCVNMKRDVTHMYTKOPIFENTDM 1258
 DB 1199 CTIGVGOKARLTYGQDVNTLKYFTTGGLOGYEBPCVNMKRDVTHMYTKOPIFENTDM 1258
 QY 1259 IDRIIDVTRIPASDTPPCIKISHTNFTMEKAMWELRLSLPVCNNEFIDEAKRWR 1318
 DB 1259 IDRIIDVTRIPASDTPPCIKISHTNFTMEKAMWELRLSLPVCNNEFIDEAKRWR 1318
 QY 1319 VEIKRQOILMKEA-VEAOM-----PAHIDQIMSGFTMDIKGLAYE-DNOBELPSSKM 1371
 DB 1319 VEIKRQOILMKEA-VEAOM-----PAHIDQIMSGFTMDIKGLAYE-DNOBELPSSKM 1371
 QY 1372 KRLPSRPRKGSMTRGVITYONTYNTLPQOVNGMHRSTSEBAMKYDUGAOGILTPDDKDK 1431
 DB 1372 KRLPSRPRKGSMTRGVITYONTYNTLPQOVNGMHRSTSEBAMKYDUGAOGILTPDDKDK 1431
 QY 1431 MRGPNRPRKGSILTRNIT---FETDMGSAALDEMORST---VLDWNGLEBEMDKK-K 1429

QY 1432 RGSPPKPFKSGESSDRKSRKSTPDPFSDTEVSPERGARPNPQIKVSOANDRNG 1491
 DB 1430 RGSPPKPFKSGESSDRKSRKSTPDPFSDTEVSPERGARPNPQIKVSOANDRNG 1487
 QY 1492 MARRPSTNLYGQVGLNATTPQDRKOMTSTLAGSATTEVNEIFDACCILINEXFY 1551
 DB 1488 MARRPSTNLYGQVGLNATTPQDRKOMTSTLAGSATTEVNEIFDACCILINEXFY 1551
 QY 1552 GVALIPEQDPTHYIGVNTTYHHLHSDPFQNSKYTKSSVITTDYDREVENVARQSCYV 1611
 DB 1534 GVALIPEQDPTHYIGVNTTYHHLHSDPFQNSKYTKSSVITTDYDREVENVARQSCYV 1593
 QY 1612 RADELINERVAABATANGASQGMFICGSVDSTSGVSFTCEKQDSTFKXKEPETKLPAL 1671
 DB 1594 RADELINERVAABATANGASQGMFICGSVDSTSGVSFTCEKQDSTFKXKEPETKLPAL 1653
 QY 1672 FVEATSKETIQLIGSATSPLSAVLPISDGHVLPQPPRLKVQCLAKHONARVPNOS 1731
 DB 1654 FVEATSKETIQLIGSATSPLSAVLPISDGHVLPQPPRLKVQCLAKHONARVPNOS 1713
 QY 1732 LOYHALKLSDIRGSMUCEDAVSMALHIEEDRCIDIEPIEMDKLLSPHSHTLTLYAA 1791
 DB 1714 LOYHALKLSDIRGSMUCEDAVSMALHIEEDRCIDIEPIEMDKLLSPHSHTLTLYAA 1773
 QY 1792 LCTQSNYRAAHALCTHVQKQLYALQSOYMSGRLRGFYDLLIALHLSHATTEACXN 1851
 DB 1774 LCTQSNYRAAHALCTHVQKQLYALQSOYMSGRLRGFYDLLIALHLSHATTEACXN 1833
 QY 1852 EYIPIGPELKLAYEEDPMKHSRLSTQESVVRQMKTDI-----ABSITE 1897
 DB 1834 EYIPIGPELKLAYEEDPMKHSRLSTQESVVRQMKTDI-----ABSITE 1893
 QY 1898 ISNLYSPYPLVAREPVMQALABAVETQVNHKRDIPGSGENMLPLILGLVDRLLLYGM 1957
 DB 1894 ISNLYSPYPLVAREPVMQALABAVETQVNHKRDIPGSGENMLPLILGLVDRLLLYGM 1953
 QY 1958 MRDEDEKLIINTNPETWDPFKDEKDEHKKGLHMKABAGAKQMCYLLQHLNDIQLR 2017
 DB 1954 MRDEDEKLIINTNPETWDPFKDEKDEHKKGLHMKABAGAKQMCYLLQHLNDIQLR 2013
 QY 2018 HRYEBAIIAFANDVGVGLQDQLRRTYRKSDPSAVAAKTBEPFRCPREBQNALISFK 2077
 DB 2014 HRYEBAIIAFANDVGVGLQDQLRRTYRKSDPSAVAAKTBEPFRCPREBQNALISFK 2073
 QY 2078 HLEEBDKENCPGEBELIARNEFHDTLMAVSLHALOEPPAENOS--PEAKPGAQGL 2136
 DB 2074 HLEEBDKENCPGEBELIARNEFHDTLMAVSLHALOEPPAENOS--PEAKPGAQGL 2133
 QY 2137 IINTVKELEBEAKAIEBPCKTPEBKRYKVLQTIIVMAEESQIETPKLVRENFSLVRO 2196
 DB 2134 IINTVKELEBEAKAIEBPCKTPEBKRYKVLQTIIVMAEESQIETPKLVRENFSLVRO 2193
 QY 2197 YDAVBELIRALEKTYVINAKTKLDVABMVVGLSOLPALLPVONSQEBEELMRTKL 2256
 DB 2194 YDAVBELIRALEKTYVINAKTKLDVABMVVGLSOLPALLPVONSQEBEELMRTKL 2253
 QY 2257 NHTFPQHPDLIRLRYAHENNAVMNTLGRRAAQAQSDAQSSQPVAE--DSKEKDSHEM 2314
 DB 2254 NHTFPQHPDLIRLRYAHENNAVMNTLGRRAAQAQSDAQSSQPVAE--DSKEKDSHEM 2312
 QY 2315 VVACRFLCYFCRTGRONKAMFDFPLENSNILLSPSLGSTPLDVAYSLEMLNTE 2374
 DB 2313 VVACRFLCYFCRTGRONKAMFDFPLENSNILLSPSLGSTPLDVAYSLEMLNTE 2372
 QY 2375 LALALREHYLEKIAVILSRGLOSSELVKGYPDLGMDPVEGERYLDLRFYVWNGS 2434
 DB 2373 LALALREHYLEKIAVILSRGLOSSELVKGYPDLGMDPVEGERYLDLRFYVWNGS 2432
 QY 2435 VVENANLVIRLLLRREBCCGALRGEGBGLKLIYDANKSERIADRRKLRBEMOGDV- 2493
 DB 2433 VVENANLVIRLLLRREBCCGALRGEGBGLKLIYDANKSERIADRRKLRBEMOGDV- 2491
 QY 2494 --NFSPHLPRESDEDEYIDTGAAILNFYCTLVLDLGRCAPDAGVIALGKNESILRABAILR 2551

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Db      2492  GUNFTPLPGEDEDEYIDTGAALNFTCLVDLRCAPDASVIEQKNESLRARSLR 2551
Qy      2552  SLVPLEDLQGVLSIRFTLNNPAGBERPKSDMPGSLPGHKQSVGFLEERVYGIETQBLE 2611
Db      2552  SLVPLEDLQGVLSLKTSLSTAGBEKPKSDMPGSLPNNKOSIVLFLERVYGIENQDLF 2611
Qy      2612  YKLEBAFLPDJLRAATMLDRNDGCSDMALSMNRVYIGNSILPLLIGHAYFYNEAENYASL 2671
Db      2612  YRLLEDAPLPDLRTATITLSDGSESDMALMNRVYIGNSILPLLIGHSKFYNEAENYASL 2671
Qy      2672  LDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPSMLLKLRLTYDVSKLSEYTT 2731
Db      2672  LDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPMALLKLRLTYDVSKLSEYTT 2731
Qy      2732  VALRLTLHYERCAKYYGSTGAGQAFGASSDEKRLTWMLFSNIFPSLSKMDYEPFLPG 2791
Db      2732  VALRLTLHFDRCAKYYGST-QQGSYGAASSDEKRLTWMLFSNIFPSLSNMDYDPFLPG 2790
Qy      2792  KALPCLIAIGCALPPDYSLSKNYDDEFYGEQAAGDLNPOXDPOPIINTSSVALNNDLNT 2851
Db      2791  KALPCLIAIGCALPPDYSLSKNTDEDDYGRQMGAP--DQQYWNPIIDTNVHLNDLNS 2848
Qy      2852  IVQKSEHHDAMASRKIEGMYIGSGWSDOKTHPRLKPYNMLANDYEKERYKEPYRESL 2911
Db      2849  LVQKFESEHYHDAMASRRLEGGWYGDIRSDNDRKHPRLKPYNMLSEYERBRYPDPVRECL 2908
Qy      2912  KALLAIGMSVEHSEVDIPSNRRSSMRQSKSGGRPPEI--VTDSATPFVDNPHPVDMTNL 2969
Db      2909  KGLLAIGWTVHSEVEVPLNHRGSTRQSK----PQINEFQNEGSPFNYNPHFVDMSNL 2963
Qy      2970  TLSREMNMAERLADNADIMAKKKEEL 2998
Db      2964  TLSREMNMAERLAEASHDIMAKKKEEL 2992
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Search completed: April 14, 2006, 01:48:46
Job time : 307 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 14, 2006, 01:28:43 ; Search time 417 Seconds

(without alignments)
5075.743 Million cell updates/sec

Title: US-10-668-767-128_COPY_1_3000

Perfect score: 15748
Sequence: 1 MAEAGGASQDVDFLRT.....RLADNADHDWAKKKEELVT 3000

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12581	79.9	5105	Q7PMK5_ANOGA	Q7PMK5 anopheles g
2	12518	79.5	5105	Q7PJ09_ANOGA	Q7PJ09 anopheles g
3	12473.5	79.2	5127	RY44_DROME	Q24488 drosophila
4	7214	45.8	5071	P91905_CABEL	P91905 caenorhabdi
5	7078.5	44.9	5207	Q60WP5_CABER	Q60WP5 caenorhabdi
6	6986.5	44.4	5317	Q8TA74_HEMPU	Q8TA74 hemiteutro
7	6828	43.4	5107	Q94279_CABEL	Q94279 caenorhabdi
8	6778	43.0	4968	Q29621_RABIT	Q29621 oryctolagus
9	6770.5	43.0	4968	RYR2_RABIT	Q29657 oryctolagus
10	6769	43.0	4967	RYR2_HUMAN	Q22736 homo sapien
11	6769	43.0	4967	Q546N8_HUMAN	Q546N8 homo sapien
12	6758	42.9	4967	Q9ERN6_MOUSE	Q9ERN6 mus musculu
13	6566.5	41.7	4965	Q5VMP1_HUMAN	Q5VMP1 homo sapien
14	6534.5	41.5	5037	Q29104_PIG	Q29104 sus scrofa
15	6453.5	41.0	5035	RYR1_PIG	P16960 sus scrofa
16	6452.5	41.0	5035	Q29105_PIG	Q29105 sus scrofa
17	6452.5	41.0	5035	Q80X16_MOUSE	Q80X16 mus musculu
18	6449.5	40.9	4859	Q95201_MUSVI	Q95201 muscivora
19	6445.5	40.9	5035	Q29104_PIG	Q29104 sus scrofa
20	6443	40.9	5038	RYR1_HUMAN	P11817 homo sapien
21	6439	40.9	5037	RYR1_RABIT	P11776 oryctolagus
22	6438.5	40.9	4859	Q7M2F9_GCANR	Q7M2F9 muscivora
23	6434.5	40.9	4870	RYR3_HUMAN	Q15433 homo sapien
24	6422	40.8	4869	Q90985_CHICK	Q90985 gallus galli
25	6415	40.7	4868	Q91319_RANCA	Q91319 rana catesb
26	6413	40.7	4872	Q91319_RABIT	Q91319 oryctolagus
27	6275	39.8	5081	Q13054_MAKRI	Q13054 makaria nig
28	6169.5	39.2	4864	Q5RQ04_BRABE	Q5RQ04 brachydario
29	6146	39.0	3398	Q4RL00_TETNG	Q4RL00 tetraodon n
30	5964	37.9	4910	Q4SFN5_TETNG	Q4SFN5 tetraodon n
31	5555.5	35.3	4833	Q4RNG0_TETNG	Q4RNG0 tetraodon n

32	4937	31.4	4251	Q4RFS4_TETNG	Q4RFS4 tetraodon n
33	4854	30.8	3383	Q4S750_TETNG	Q4S750 tetraodon n
34	2998.5	19.0	1138	P79271_PIG	P79271 sus scrofa
35	2800.5	17.8	1020	Q80Z25_MOUSE	Q80Z25 mus musculu
36	1805	11.5	1135	Q4TSB8_TETNG	Q4TSB8 tetraodon n
37	1564.5	9.9	357	Q951G7_CANPA	Q951G7 canis fam1
38	1495	9.5	671	Q951G6_CANPA	Q951G6 canis fam1
39	1379.5	8.8	2583	Q4S752_TETNG	Q4S752 tetraodon n
40	1318.5	8.4	753	Q4T4U8_TETNG	Q4T4U8 tetraodon n
41	1062.5	6.7	487	Q4SYB3_TETNG	Q4SYB3 tetraodon n
42	1035	6.6	379	Q991P9_MOUSE	Q991P9 mus musculu
43	772	4.9	329	Q4R606_MACPA	Q4R606 macaca fasc
44	603	3.8	239	Q6UC92_MEICA	Q6UC92 meleagris g
45	553.5	3.5	497	Q4T7D1_TETNG	Q4T7D1 tetraodon n

ALIGNMENTS

RESULT 1
Q7PMK5_ANOGA PRELIMINARY; PRT; 5105 AA.
ID Q7PMK5_ANOGA
AC Q7PMK5;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000019607.
GN ORFNames=ENSANGS00000017118;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=160454;
RN [1]
RP NCBIOTIDB SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NCBIOTIDB SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
DR EMBL; AAB01008979; EAA13701.3; -; Genomic DNA.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005622; F:calcium channel activity; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005819; F:ryanodine-sensitive calcium-release channel. . .; IEA.
DR GO; GO:0006814; P:calcium ion homeostasis; IEA.
DR GO; GO:0006816; P:calcium ion transport; IEA.
DR GO; GO:0006812; P:calcium transport; IEA.
DR InterPro; IPR000699; Ca-rel_channel.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR003608; MIR.
DR InterPro; IPR003103; Ryanodine_recept.
DR InterPro; IPR001215; Ryanodine_recept.
DR InterPro; IPR009460; Ryanodine_recept.
DR InterPro; IPR003877; SPRY_receptor.
DR Pfam; PF02815; MIR_1.
DR Pfam; PF06459; RR_TM4-6; 1.
DR Pfam; PF01365; RyR_4.
DR Pfam; PF02026; RyR_4.
DR Pfam; PF00622; SPRY_3.
DR PRINTS; PR00795; RYANODINER.
DR ProDom; PD000012; EF-hand; 1.

DR SMART; SM00472; MIR; 4.
DR SMART; SM00449; SPRY; 3.
DR PROSITE; PSS0919; MIR; 5.
SEQUENCE 5105 AA; 577467 MW; 2168209E723AD77A CRC64;

Query Match 79.9%; Score 12501; DB 2; Length 5105;
Best Local Similarity 79.2%; Preal. No. 0;
Matches 2400; Conservative 251; Mismatches 293; Indels 88; Gaps 24;

QY 1 MAAEAGSAGSODVVSFLRTEDMYCLSTATGERVCLAAEGFNRCFLTNIADKNIPDL 60
DB 1 MAAEAGS-SEODVVSFLRTEDMYCLSTATGERVCLAAEGFNRCFLTNIADKNIPDL 59
QY 61 SGCYFVIEQALSVRALQELVTAAGSETGKTGSGHRTLLYGNAILLRLHNSDYLACT 120
DB 60 SGCYFVIEQALSVRALQELVTAAGSETGKTGSGHRTLLYGNAILLRLHNSDYLACT 119
QY 121 SSSODKLAFLVGLQOHSQGAQWMTLHAPASKORSEGGKAVGDDLLIVSATERYLTTK 180
DB 120 SSSNDKLSFVGLQOHSQGAQWMTLHAPASKORSEGGKAVGDDLLIVSATERYLTTK 179
QY 181 ENEVSIVNASPHYTHMSVPGTGI SHMKYGVVFGDVLRFPHGDECLTIPSTWKD 240
DB 180 ENDLSTVNASPHYTHMSVPGTGISMKYGVVFGDVLRFPHGDECLTIPSTWSDS 239
QY 241 GQNIIVYEGGSVMSQASRLRLRLIARTKMAGFIMNTHPMRIRHITTTGRYLGVNDQNELY 300
DB 240 GQNIIVYEGGSVMSQASRLRLRLIARTKMAGFIMNTHPMRIRHITTTGRYLGVNDQNELY 299
QY 301 LVREBEATTSCAPCLARQEKDQKQVLEDEDLVIGAPRIIKYGDSTVYVHSTGMLMST 360
DB 300 LMSRDQATTISQTAFLVRLKEDDKVLEDEDLVIGAPRIIKYGDSTVYVHSTGMLMST 359
QY 361 KSJETKKKGKGVKAEKQKAILHEEGKMDGDLFSGRQEEBRTARVIRKCSLTFKPIGL 420
DB 360 KSJETKKKGKGVKAEKQKAILHEEGKMDGDLFSGRQEEBRTARVIRKCSLTFKPIGL 419
QY 421 ETLQENRRHSMFPASVNLGEMVCLBDLLINYPAPDEMEHEKONKFRALRRRDLFOE 480
DB 420 ETLQENRRHSMFPASVNLGEMVCLBDLLINYPAPDEMEHEKONKFRALRRRDLFOE 479
QY 481 EGLNLILLEADIKINVTTSQGLAGPLAGDSGQSWEMISGYLYOLLAATIKENHNCQ 540
DB 480 EGLNLILLEADIKINVTTSQGLAGPLAGDSGQSWEMISGYLYOLLAATIKENHNCQ 539
QY 541 FANSNRLNMLFSLRGSQASGEQGLDVLHCVLIDSPBALMMRDEHIKIVISLEKGG 600
DB 540 FANSNRLNMLFSLRGSQASGEQGLDVLHCVLIDSPBALMMRDEHIKIVISLEKGG 599
QY 601 DPKYLDVLCSLCVGNQVAVASSQNNICDYLPGKNILLQTLAVDVHSSVAPNI FVGRVSG 660
DB 600 DPKYLDVLCSLCVGNQVAVASSQNNICDYLPGKNILLQTLAVDVHSSVAPNI FVGRVSG 659
QY 661 SAYRRKVPYEVMTDHI EKTTHMMPHLRIGWANTGVVYRGGEGKKGAGVGDLYSYGR 720
DB 660 SAYRRKVPYEVMTDHI EKTTHMMPHLRIGWANTGVVYRGGEGKKGAGVGDLYSYGR 719
QY 721 DGAYLVSGGRKTPVNRTHAEPRYIRKGDVIGCALDVLPIINFMFGVNRVYSGFTFNLE 780
DB 720 DGAYLVSGGRKTPVNRTHAEPRYIRKGDVIGCALDVLPIINFMFGVNRVYSGFTFNLE 779
QY 781 GMFPVIVSCSSKLSGPFLLGEGHRLRYAAPGYSPLVESLAPQIILSLPCEYFQNLK 840
DB 780 GMFPVIVSCSSKLSGPFLLGEGHRLRYAAPGYSPLVESLAPQIILSLPCEYFQNLK 839
QY 841 BALAGRPYVODDPAFVPTVDTLOITLPTVVEQIRDKLAENIHMAANKIEGMMYQGD 900
DB 840 NYLAGPWLVEDDSAFVPKPVDTSIVTLPSSEVERIKKLAENIHMAANKIEGMMYQGD 899
QY 901 REDLHKIHPCLVPEERLPPAEKRYDQLAVQTLKTIILAGYVSLDKPPAIRANVLPNE 960
DB 900 RDDVYIHPCLVPEERLPPAEKRYDQLAVQTLKTIILAGYVSLDKPPAIRANVLPNE 959

QY 961 PFMQSNQYRAPIDLSAVTLTPRMDLVQDLAENTNLNARERIQQGWTYGLNEDSMKR 1020
DB 960 PYMQNGYRAPIDLSAAVLTTPRMEELVQDLAENTNLNAKERIQGWTYGLNEDSENLR 1019
QY 1021 SPHLVYPPKVDADIKKANDTASETVRTLIVGYCMLDPPRGCHALLLEASQKODAFR 1080
DB 1020 SPHLVYSPKVDKIKKANDTASETVRTLIVGYCMLDPPRGCHALLLEASQKODAFR 1079
QY 1081 TYBAEKRYAVSSGKWTFFEEIILLAGPMRVGMADNAPGMMLGQDENSWAFDGYNEKUY 1140
DB 1080 TYRVEKTYAVTSGKWTFFEEFVLJAGPMRVGMADNAPGMMLGSDASNAFDGYNEKUS 1139
QY 1141 SGNTEBFGQMAVDVGVFLDIDKTIISPLNGELMDALGSETTPADV--GQNFVP 1197
DB 1140 GGATESFGQMAVGDVGVFLDIDHTISPLNGELMDALGSETTPADVNAVDGVGVFP 1199
QY 1198 ACTLGVQKARLTYGGDVNTLAKFTTCGLOBGEPVCMMKBDVTHMYTKDQIPENTRE 1257
DB 1200 ACTLIGQKARVYGGDVNSLKMFTTCGLOBGEPVCMMKBPVTHMYTKDQIPENTRE 1259
QY 1258 MIDTRIDVTRIPAGSDTPCLKISHNTFETMEKAMNPLRLSPVICHNEFLDEAKAAR 1317
DB 1260 IPECKIDVTRIPGADTPPCMKISHNTFETMEKAMNPLRLSPVICHNEFLDEAKAAR 1319
QY 1318 WVEIKDRQOILMKEAVEAPAHIDQIMSGFTMNDIKGLATBEDNOBELPSSNM---KR 1373
DB 1320 WVEIKDRQOILMKEAVEAPAHIDQIMSGFTMNDIKGLATBEDNOBELPSSNM---KR 1378
QY 1374 LBSRPGRKSMTRGVTLQVYNNLQPG-QVNGHNRSSSEAMKY-DLGAQGLTPDDKXK 1431
DB 1379 LBSRPGRKSGLS-----PGEIRING--EATSDSELNYSNLEAG-GDDRK-K 1422
QY 1432 RGRSPKFPFRSRKGSSEBDAKSRKSKTPDPFDETEVSFERGARPPQIKVQSANQRYNG 1491
DB 1423 RGRSPKFPFRSRKGSSEBDAKSRKSKTPDPFDETEVSFERGARPPQIKVQSANQRYNG 1491
QY 1492 KNABPRTNLVYSQVGLNATPTODRKQNTSTLAQASATYVGNELFDEACLYINERY 1551
DB 1464 QATRMSSNDLRA-----QAPLTPERKGM-----GSPQVSEFGNEYYDADCLRLINEYF 1512
QY 1552 GVRIVPGDPTHYVIGMTVTOVHNSKDFNOSKVTSSVITDDVDRVVENNRQSCYAV 1611
DB 1513 GVRIVPGDPTHYVIGMTVTOVHNSKDFNOSKVTSSVITDDVDRVVENNRQSCYAV 1611
QY 1612 RADELTYNEVMAEATKAGASQGMFICGSYDTSIGSVFTCEGDKTSFKFPMZEPKLPFPI 1671
DB 1573 RADELTYNEVMAEATKAGASQGMFICGSYDTSIGSVFTCEGDKTSFKFPMZEPKLPFPI 1671
QY 1672 FYEATSKELIQLBELGRATSPLSAVLTPTSDGAVIPOPFPRLKVOCLKPHOMARVPNOS 1731
DB 1633 FYEATSKELIQLBELGRATSPLSAVLTPTSDGAVIPOPFPRLKVOCLKPHOMARVPNOS 1731
QY 1732 LOVHALKSIDIGMSWLCSDAVSMALNTPBEDRCIDLEPIEMDGLSFGHSHTLLLYAA 1791
DB 1693 LOVHALKSIDIGMSWLCSDAVSMALNTPBEDRCIDLEPIEMDGLSFGHSHTLLLYAA 1791
QY 1792 LCVQSNYRAAHLCTHVQKQKLLVYAIQSQYMSGRLRQGFYDLIALHLSHATTMEACKN 1851
DB 1753 LCVQSNYRAAHLCTHVQKQKLLVYAIQSQYMSGRLRQGFYDLIALHLSHATTMEACKN 1851
QY 1852 EFVILPGLPELKYEBPDMGHSLSLQTESVPRQMKTDIA-----E 1893
DB 1813 EFVILPGLPELKYEBPDMGHSLSLQTESVPRQMKTDIA-----E 1893
QY 1894 SITETSNLYSPFPLVAREFPMQALAEVETNOVHNRPVPGSNNENLPLIKLVDRLL 1953
DB 1873 SITETSNLYSPFPLVAREFPMQALAEVETNOVHNRPVPGSNNENLPLIKLVDRLL 1953
QY 1954 LVGMARDEDEVEKLLIMTNPETVDPFDEKSGDHEKRGKLLHMKAGAKLQMCYLLQHLND 2013
DB 1933 LVGVITNEVEKLLIMTNPETVDPFDEKSGDHEKRGKLLHMKAGAKLQMCYLLQHLND 2013
QY 2014 IQLRRHVEALIAFAHDFVGDLQTDQLRRYTEIKQSDLPBAVAAKTREFRCPPREQMAI 2073

QY 241 GONI VVEGGS VMSOARSLMRLIARTKMA GPFINTWPMRIRHITTTGRYLGVANDONELY 300
DB 240 GONI VVEGGS VMSOARSLMRLIARTKMA GPFINTWPMRIRHITTTGRYLGVANDONELY 299
QY 301 LVREBEATTSACA PCJROEKODKOVLEDLEJIGA PIIKYGDSVTIYVHSESTGLMSTY 360
DB 300 LMSRDOATTSIQTAFVLEKEDOKVLEDDOLETIGAPIIKYGDSTVIMQVYESGLMSTY 359
QY 361 KSYETKKKGKGVKYEKOAILHEBGMKMDGLDFSRQSEBSRTARVIRKCSLFTFKINGL 420
DB 360 KSYETKKKGKGVKYEKOAILHEBGMKMDGLDFSRQSEBSRTARVIRKCSLFTFKINGL 419
QY 421 ETLQENRRHSMPFASVNLGEMVNCLEDLINYPAOPDEDMHEEKONKFRALRRQDLFOE 480
DB 420 ETLQENRRHSIPLQTVNLGEMVNCLEDLINYPAOPDEDMHEEKONKFRALRRQDLFOE 479
QY 481 EGLNLILLEADIKINVTSGGFLAGLADSGSGSWMISGYIYOLLAALIKNNHTNCAQ 540
DB 480 EGLNLILLEADIKINVTSGGFLASDPSGSGSWMISGYIYOLLAALIKNNHTNCAQ 539
QY 541 FANSNRLNMLFSRLGSGASGEQGLMDVLCVLDSPBALNMRDEHIKVIISLLEKGR 600
DB 540 FANSNRLNMLFSRLGSGASGEQGLMDVLCVLDSPBALNMRDEHIKVIISLLEKGR 599
QY 601 DPEVLDVLCGLCVNGVAVNRSSQNNICDYLLPGKNLLQTLVYDVHVSVRNIFVGRVGG 660
DB 600 DPEVLDVLCGLCVNGVAVNRSSQNNICDYLLPGKNLLQTLVYDVHVSVRNIFVGRVGG 659
QY 661 SAYARKMYFEVNTMDHI EKTTHMMPHLRIGMANTGVVYVPGGEEKGNGVGGDLSYGP 720
DB 660 SAYARKMYFEVNTMDHI EKTTHMMPHLRIGMANTGVVYVPGGEEKGNGVGGDLSYGP 719
QY 721 DGAYLMSGGRKTEVNTTHABEPIYIRKGDVIGCALDLTPRIINFMENGVRVTSQFTFNILE 780
DB 720 DGAYLMSGGRKTEVNTTHABEPIYIRKGDVIGCALDLTPRIINFMENGVRVTSQFTFNILE 779
QY 781 GMEFPVYISGSSKLSGCRPLLGEBGRRLRYAAPBGYSPLVBSLRLQOILISLEPCFYFGANLST 840
DB 780 GMEFPVYISGSSKLSGCRPLLGEBGRRLRYAAPBGYSPLVBSLRLQOILISLEPCFYFGANLST 839
QY 841 BALAGRPVODDPAFVPTPDTLOITLPTVYEOIRPKLANIHEMAMNKIEGMMYAGQ 900
DB 840 BALAGRPVODDPAFVPTPDTLOITLPTVYEOIRPKLANIHEMAMNKIEGMMYAGQ 899
QY 901 REDLHKIHPCLVPERLPRAEKRYDQLAVQTLKTIILAGYIISLDPKPARIRNVLJNE 960
DB 900 REDLHKIHPCLVPERLPRAEKRYDQLAVQTLKTIILAGYIISLDPKPARIRNVLJNE 959
QY 961 PFMQNGYKRPALDLSAVTLTPKMDBLVDQLAENTNLMARERIIOGWTYGLNEDSDMR 1020
DB 960 PFMQNGYKRPALDLSAVTLTPKMDBLVDQLAENTNLMARERIIOGWTYGLNEDSDMR 1019
QY 1021 SPHLVYPRKYDDAIKKANRDTABEYVRLIVYGYMDLDPYGEHEALLLEASQOKQADR 1080
DB 1020 SPHLVYPRKYDDAIKKANRDTABEYVRLIVYGYMDLDPYGEHEALLLEASQOKQADR 1079
QY 1081 TYRAEKVAVYSGSKTYFEFEIITLAPGPMRVGMAMADMAPGMMLGODENSNAFDGYNEKY 1140
DB 1080 TYRAEKVAVYSGSKTYFEFEIITLAPGPMRVGMAMADMAPGMMLGODENSNAFDGYNEKY 1139
QY 1141 SGNTESFGKQMAVGVAVGLDLIDKTIISLNGELIMDALGGETTADY--QSDNFPV 1197
DB 1140 SGNTESFGKQMAVGVAVGLDLIDKTIISLNGELIMDALGGETTADY--QSDNFPV 1199
QY 1198 ACTLIGVQKARLYYGDVNTLKYFTTCGOEGYEPRCVANMKRVNTYMTYDQOIFENTDE 1257
DB 1200 ACTLIGVQKARLYYGDVNTLKYFTTCGOEGYEPRCVANMKRVNTYMTYDQOIFENTDE 1259
QY 1258 MIDTRIDVTRIPASGDTPLCKTSHNTFETMEXKANEFLRLSLPVI CHNFIIDEAKARR 1317
DB 1260 MIDTRIDVTRIPASGDTPLCKTSHNTFETMEXKANEFLRLSLPVI CHNFIIDEAKARR 1319

QY 1318 WVEIKROQIIMKEAVEAOQMPAHIDQIMSGFTMNDIKGLHYEDNOBELPSSKM---KR 1373
DB 1320 WVEIKROQIIMKEAVEAOQMPAHIDQIMSGFTMNDIKGLHYEDNOBELPSSKM---KR 1378
QY 1374 LPSRPRKSGMTRGVITQVNNLQPG-OVNGMRSTSEAMACY-DLGAQGLPDDKDK 1431
DB 1379 LPSRPRKSGMTRGVITQVNNLQPG-OVNGMRSTSEAMACY-DLGAQGLPDDKDK 1422
QY 1432 RGRSPKFRSRRKSGSSDRASKRSKTPDPFSDTEVS PERGARPPNPOIKVSGANORYNG 1491
DB 1423 RGRSPKFRSRRKSGSSDRASKRSKTPDPFSDTEVS PERGARPPNPOIKVSGANORYNG 1463
QY 1492 MNARPSRTULYSGVGLNATPTPODRKQNTSTLQASATETVONEIPLDECLKLINEFY 1551
DB 1464 MNARPSRTULYSGVGLNATPTPODRKQNTSTLQASATETVONEIPLDECLKLINEFY 1512
QY 1552 GVRITYPGODPTHYIGMTVTOYHLKSDNOSKVTSYVITTDVYRVYENVRQSCYV 1611
DB 1513 GVRITYPGODPTHYIGMTVTOYHLKSDNOSKVTSYVITTDVYRVYENVRQSCYV 1572
QY 1612 RADELVNEVMAEATAKAGSQGMEFGCSVDTSIGSVFTEBGKDTSPFKVMEPETKLPAL 1671
DB 1573 RADELVNEVMAEATAKAGSQGMEFGCSVDTSIGSVFTEBGKDTSPFKVMEPETKLPAL 1632
QY 1672 FVEATSKETIOTELGHSATSPLSAVLPSTDKNVLPQPPRLKVOCCLKPHQARVPOS 1731
DB 1633 FVEATSKETIOTELGHSATSPLSAVLPSTDKNVLPQPPRLKVOCCLKPHQARVPOS 1692
QY 1732 LOVHALKSDIRGMSLCEDAVSMLAHLIPEEDRCIDILEPIEMDKLSHSHITLTYLA 1791
DB 1693 LOVHALKSDIRGMSLCEDAVSMLAHLIPEEDRCIDILEPIEMDKLSHSHITLTYLA 1752
QY 1792 LCYQSNYRAAHALCTHVODKOLLYAIQSGYMSGPLRQGFYDULLIALHLSHATTMBAQON 1851
DB 1753 LCYQSNYRAAHALCTHVODKOLLYAIQSGYMSGPLRQGFYDULLIALHLSHATTMBAQON 1812
QY 1852 EPIYIPGPELKALEYEPDMGHSLSIQTESVPRQKMTTOLA-----E 1893
DB 1813 EPIYIPGPELKALEYEPDMGHSLSIQTESVPRQKMTTOLA-----E 1872
QY 1894 STETISNLSPYPPLEAVAREFWMQALABAVENOVNRRPVGSGSNLFLPLIKYDRLL 1953
DB 1873 STETISNLSPYPPLEAVAREFWMQALABAVENOVNRRPVGSGSNLFLPLIKYDRLL 1932
QY 1954 LVGMKDEBDEKLLIMTNPETMDPSEFKEGKEHRKGLIMKQABGAKLQMCYLLOHND 2013
DB 1933 LVGMKDEBDEKLLIMTNPETMDPSEFKEGKEHRKGLIMKQABGAKLQMCYLLOHND 1992
QY 2014 IOLRRVBAIIAPANDFVGDLOTDOIRRYTEIKOSDLPBAVAAKKTREPRCPREBOMAI 2073
DB 1993 IOLRRVBAIIAPANDFVGDLOTDOIRRYTEIKOSDLPBAVAAKKTREPRCPREBOMAI 2052
QY 2074 LSPKHLSEEDKENCPCGEELIARMBNEFHTLMAHYSIHALOBDAAE-NOBPRAKGANG 2132
DB 2053 LSPKHLSEEDKENCPCGEELIARMBNEFHTLMAHYSIHALOBDAAE-NOBPRAKGANG 2112
QY 2133 KLYNLIINTVKELEBEAKAIEBPKKTPBEKFRKVLQITIVNNAEBSQIETPKLVREMFSL 2192
DB 2113 KLYNLIINTVKELEBEAKAIEBPKKTPBEKFRKVLQITIVNNAEBSQIETPKLVREMFSL 2172
QY 2193 LVROVDANGELIYALAKTYVYNAKTKLDVAEMVGLSQTIRALLPVOMSGOBBELKRLIM 2252
DB 2173 LVROVDANGELIYALAKTYVYNAKTKLDVAEMVGLSQTIRALLPVOMSGOBBELKRLIM 2232
QY 2253 KLVNHTPFQHPDILRYLVREHENVAVMMNTTGRAPAOQSDPOPSQPAVABDS--REKOT 2310
DB 2233 KLVNHTPFQHPDILRYLVREHENVAVMMNTTGRAPAOQSDPOPSQPAVABDS--REKOT 2291
QY 2311 SHEMVACCRFLCYFCRTGRQONQKAMFDFDLELNSNITLSRPSLRGSTPLDVAVASLM 2370
DB 2292 SHEMVACCRFLCYFCRTGRQONQKAMFDFDLELNSNITLSRPSLRGSTPLDVAVASLM 2351
QY 2371 ENTBELALRBYHLEKIAVYLSRCGLQSNLSBLVEKGYPDGLGMDPVEGGRYLDLFLPCVAV 2430

Db 2352 ENTLMALALREHYLTKIAIYLSRCGLQSNSESLIERGYDLPVGEERYLDFIRFCVWV 2411
 Qy 2431 NGSSVERNANLVRLIRREPCGPNALRGEGELKAIYVANKMSEIABRRLREMOE 2490
 Db 2412 NGSSVERNANLVRLIRREPCGPNALRGEGELKAIYVANKMSEIABRRLREMOE 2470
 Qy 2491 GDV---NFSHPLEPSEDEDEYIDTGAAILNPFYCTVYLLRCAPDAGVIALGKNESLAR 2547
 Db 2471 GTTGTALNFSHPLEPSEDEDEYIDTGAAILNPFYCTVYLLRCAPDAGVIALGKNESLAR 2530
 Qy 2548 AILRSVLPLEDLOGVLSLRFPLNNPAGBERRPKSDMSGIIPGHKQSVGLPLERVYGIET 2607
 Db 2531 AILRSVLPLEDLOGVLSLRFPLNNPAGBERRPKSDMSGIIPGHKQSVGLPLERVYGIET 2590
 Qy 2608 QELFYKLEBAFPLPDLRAATMLDRNOCESDMALSMRRTYIGNSLPLILIKATPYNAEN 2667
 Db 2591 QELFYKLEBAFPLPDLRAATMLDRNOCESDMALSMRRTYIGNSLPLILIKATPYNAEN 2650
 Qy 2668 YASLLDATTHTVYRLSKGRMLTKGQRAVSDPLVALSAMOPSMILKILKRLTYDVSKLS 2727
 Db 2651 YASLLDATTHTVYRLSKGRMLTKGQRAVSDPLVALSAMOPSMILKILKRLTYDVSKLS 2710
 Qy 2728 EYTTVALRLTLHYERCATYGYGTAGCGA-FGASDEBKRLTMMPLFSNIPDSLSKNDYE 2786
 Db 2711 EYTTVALRLTLHYERCATYGYGTAGCGA-FGASDEBKRLTMMPLFSNIPDSLSKNDYE 2770
 Qy 2787 PELFGKALPCLIALIGCALPPDYSLSKRYDDEFFYKEQADLNPQYDPOPIINTSVYALN 2846
 Db 2771 PELFGKALPCLIALIGCALPPDYSLSKRYDDEFFYKEQADLNPQYDPOPIINTSVYALN 2829
 Qy 2847 NDINTYVOKSEHHDMAARKIENGWYVGBGMSDOKTHPRLEKPYMLNDYKERYKPEP 2906
 Db 2830 NDINTYVOKSEHHDMAARKIENGWYVGBGMSDOKTHPRLEKPYMLNDYKERYKPEP 2889
 Qy 2907 VRSLKALALIGSVSEHSEVDIPENNRSMSRKOSKSGRPEIYTDATPFDYVPHFVDM 2966
 Db 2890 VRSLKALALIGSVSEHSEVDIPENNRSMSRKOSKSGRPEIYTDATPFDYVPHFVDM 2946
 Qy 2967 TNLTLISREOMMAERLADNADHDIWAKKKEBEL 2998
 Db 2947 TNLTLISREOMMAERLADNADHDIWAKKKEBEL 2978
 RESULT 3
 RY44_DROME STANDARD; PRT; 5127 AA.
 AC Q24438; Q24321; Q24499; Q24500; Q24501; Q8MKS3; Q8MKS4; Q8MKS5;
 AC Q9V4Y7;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ryanodine receptor 44F.
 GN Name=RYA-r44F; Synonym=dry; RYR; ORFNames=CG10844;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxId=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (ISOFORMS A; B; C AND D), FUNCTION, TISSUE
 RP SPECIFICITY, AND DEVELOPMENTAL STAGE.
 RX MEDLINE=94102409; PubMed=8276118; DOI=10.1016/0014-5793(94)80634-9;
 RX Takehima H., Nishii M., Iwabe N., Miyata T., Hoshiyama T., Maehai I.,
 RA Hoshiyama T.,
 RT Isolation and characterization of a gene for a ryanodine
 RT receptor/calcium release channel in Drosophila melanogaster.";
 RL FEBS Lett. 337:81-87(1994).
 RN [2]
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.B., Richard S., Ashburner M., Henderson S.N.,
 RA Sutton G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chame M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Agbayani A., An H.-O., Andrews-Pfannkoch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolhakov S.,
 RA Borkov D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
 RA Burkova K., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fowler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Jengam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kammei B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Matrei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Munz D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheefer F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Stryer S., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Sylvestre R., Tector C., Turner B., Venter B., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasekar D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RA The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [3]
 RP GENOME REANNOTATION, AND ALTERNATIVE SPLICING.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Miera S., Crosby W.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.B.,
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE OF 4619-5127, DEVELOPMENTAL STAGE, AND TISSUE
 RP SPECIFICITY.
 RX MEDLINE=93202018; PubMed=1338312;
 RA Hasan G., Roebash M.,
 RT "Drosophila homologs of two mammalian intracellular Ca(2+)-release
 RT channels: identification and expression patterns of the inositol
 RT 1,4,5-trisphosphate and the ryanodine receptor genes.";
 RL Development 116:967-975(1992).
 RN [5]
 RP FUNCTION, AND TISSUE SPECIFICITY.
 RX MEDLINE=20283930; PubMed=10811919; DOI=10.1073/pnas.110145997;
 RA Sullivan K.M.C., Scott K., Zuker C.S., Rubin G.M.,
 RT "The ryanodine receptor is essential for larval development in
 RT Drosophila melanogaster.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:5942-5947(2000).
 CC -1- FUNCTION: Communication between transverse tubules and
 CC sarcoplasmic reticulum. Contraction of muscle is triggered by
 CC release of calcium ions from SR following depolarization of T-
 CC tubules (By similarity).
 CC -1- FUNCTION: Intracellular calcium channel that is required for
 CC proper muscle function during embryonic development and may be

essential for excitation-contraction coupling in larval body wall muscles.
CC -1- SUBUNIT: Homotetramer (Potential).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=A;
CC IsoId=Q24498-2; Sequence=Displayed;
CC Name=B;
CC IsoId=Q24498-3; Sequence=VSP_050196;
CC Name=C;
CC IsoId=Q24498-4; Sequence=VSP_050195;
CC Name=D;
CC IsoId=Q24498-5; Sequence=VSP_050195, VSP_050196;
CC -1- TISSUE SPECIFICITY: During embryonic stages 9-10, expression is seen in mesoderm of all segments in progenitors of the cephalic and somatic muscles. Adults exhibit high expression in tubular 'jump' muscles of thorax and leg, and lower expression in the brain, ventral ganglion, head muscles and prothoracic muscles.
CC -1- DEVELOPMENTAL STAGE: Abundant in 6-12 hours embryos, reduced expression in second and third instar larval stages and adults.
CC -1- MISCELLANEOUS: The calcium release channel is modulated by calcium ions, magnesium ions, ATP and calmodulin (By similarity).
CC -1- MISCELLANEOUS: The calcium release channel activity resides in the C-terminal region while the remaining part of the protein constitutes the 'foot' structure spanning the junctional gap between the SR and the T-tubule. It is possible that the foot structure interacts with the cytoplasmic region of the dihydropyridine receptor (By similarity).
CC -1- MISCELLANEOUS: Ryanodine is an alkaloid that binds to the Ca-release channel in junctional SR and modulates its activity (By similarity).
CC -1- SIMILARITY: Belongs to the ryanodine receptor family.
CC -1- SIMILARITY: Contains 5 MIR domains.
CC -1- SIMILARITY: Contains 3 SPRY domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC -----
CC EMBL, D17389; BAA04212.1; -; Genomic DNA.
CC EMBL, D17389; BAA41469.1; -; Genomic DNA.
CC EMBL, D17389; BAA41470.1; -; Genomic DNA.
CC EMBL, D17389; BAA41471.1; -; Genomic DNA.
CC EMBL, AE003835; AAF59036.2; -; Genomic DNA.
CC EMBL, AE003835; AAM71082.1; -; Genomic DNA.
CC EMBL, AE003835; AAM71083.1; -; Genomic DNA.
CC EMBL, AE003835; AAM71084.1; -; Genomic DNA.
CC EMBL, Z18536; CAW79221.1; -; mRNA.
CC EMBL, CG10844; Drosophila melanogaster.
CC FLYBase; FBgn0011286; Rya-r44F.
CC GO, GO:0016021; C:Integral to membrane; NMS.
CC GO, GO:0005219; F:Ryanodine-sensitive calcium-release channel. . .; TAS.
CC GO, GO:0006816; P:calcium ion transport; TAS.
CC GO, GO:0006936; P:muscle contraction; IMP.
CC InterPro; IPR001682; Ca-rel channel.
CC InterPro; IPR011992; Ca/Na pore.
CC InterPro; IPR002046; EF-hand type.
CC InterPro; IPR005821; Ion_trans.
CC InterPro; IPR003608; MIR.
CC InterPro; IPR003032; Ryanodine recept.
CC InterPro; IPR001215; Ryanodine receptor.
CC InterPro; IPR009460; Ryanrecept_TM4-6.
CC InterPro; IPR003877; SPRY_receptor.
CC PANTHER; PTHR13715:SF1; Ryanodn_receptor; 10.
CC Pfam; PF00520; Ion_trans; 1.
CC Pfam; PF02815; MIR; 1.
CC Pfam; PF06459; RR_TM4-6; 1.
CC Pfam; PF01365; RyDR_TPR; 2.
CC Pfam; PF02026; RyR; 4.

DR Pfam; PF00622; SPRY; 3.
DR PRINTS; PR00795; RYANODINER.
DR ProDom; PD000012; EF-hand; 1.
DR PROSITE; PS50919; MIR; 5.
KW Alternative splicing; Calcium; Calcium channel; Calcium transport; Developmental protein; Glycoprotein; Ion transport; Ionic channel; Phosphorylation; Receptor; Repeat; Transmembrane; Transport.
FT TOPO_DOM 1 3232
FT TRANSMEM 3233 3253 M' (Potential).
FT TRANSMEM 3301 3321 M' (Potential).
FT TRANSMEM 3376 3396 M1 (Potential).
FT TRANSMEM 3963 3983 M2 (Potential).
FT TRANSMEM 4452 4472 M3 (Potential).
FT TRANSMEM 4651 4671 M4 (Potential).
FT TRANSMEM 4683 4703 M5 (Potential).
FT TRANSMEM 4742 4762 M5 (Potential).
FT TRANSMEM 4885 4905 M5 (Potential).
FT TRANSMEM 4924 4944 M8 (Potential).
FT TRANSMEM 4963 4983 M9 (Potential).
FT TRANSMEM 5004 5024 M10 (Potential).
FT DOMAIN 94 148 MIR 1.
FT DOMAIN 155 200 MIR 2.
FT DOMAIN 210 264 MIR 3.
FT DOMAIN 270 328 MIR 4.
FT DOMAIN 336 394 MIR 5.
FT DOMAIN 663 802 SPRY 1.
FT REPEAT 845 956 1.

Query Match 79.2%; Score 12473.5; DB 1; Length 5127;
Best Local Similarity 78.4%; Pred. No. 0;
Matches 2376; Conservative 272; Mismatches 314; Indels 67; Gaps 21;

QY 1 MAEAGSAGBODVSVFLRTEDWVCLSGTATGERVCLAAFGNRCFLENADKNIPDL 60
1 MAEAGSAGBODVSVFLRTEDWVCLSGTATGERVCLAAFGNRCFLENADKNIPDL 59
DB 1 MAEAGSAGBODVSVFLRTEDWVCLSGTATGERVCLAAFGNRCFLENADKNIPDL 59
QY 61 SOCVPVIEQALSVRALQELVTAAGSTGKGSGHRTLLYGNAILLRHNSDMYLA 120
60 SOCVPVIEQALSVRALQELVTAAGSTGKGSGHRTLLYGNAILLRHNSDMYLA 119
DB 60 SOCVPVIEQALSVRALQELVTAAGSTGKGSGHRTLLYGNAILLRHNSDMYLA 119
QY 121 SSSODKLAFDPVGLQHSQSGBACWTLHPASKRSBEXRVGDDLIVSVATERYLHTTK 180
120 SSSODKLAFDPVGLQHSQSGBACWTLHPASKRSBEXRVGDDLIVSVATERYLHTTK 179
DB 120 SSSODKLAFDPVGLQHSQSGBACWTLHPASKRSBEXRVGDDLIVSVATERYLHTTK 179
QY 181 ENEVSIVNASFVTHMSVOPVGTGTSRMKYVGVYFVGADVLPFRHSGDECTIPSTW 240
180 ENEVSIVNASFVTHMSVOPVGTGTSRMKYVGVYFVGADVLPFRHSGDECTIPSTW 239
DB 180 ENEVSIVNASFVTHMSVOPVGTGTSRMKYVGVYFVGADVLPFRHSGDECTIPSTW 239
QY 241 GQNIIVYEGGSVNSQARSIMRLRLATKKAAGFINNYHPRIRHITTTGKLYGVNDONELY 300
240 GQNIIVYEGGSVNSQARSIMRLRLATKKAAGFINNYHPRIRHITTTGKLYGVNDONELY 299
DB 240 GQNIIVYEGGSVNSQARSIMRLRLATKKAAGFINNYHPRIRHITTTGKLYGVNDONELY 299
QY 301 LVSRREATPASCFCILROKDKOVLEBDKDLLEVIGAPILIKYGDSTVIYVHSTGLM 360
300 LVSRREATPASCFCILROKDKOVLEBDKDLLEVIGAPILIKYGDSTVIYVHSTGLM 359
DB 300 LVSRREATPASCFCILROKDKOVLEBDKDLLEVIGAPILIKYGDSTVIYVHSTGLM 359
QY 361 KSYETKKKGVKVEEKAALIEBEGKMDDELDFSRQSEBSRTARVIRKCSLTFKFINGL 420
360 KSYETKKKGVKVEEKAALIEBEGKMDDELDFSRQSEBSRTARVIRKCSLTFKFINGL 419
DB 360 KSYETKKKGVKVEEKAALIEBEGKMDDELDFSRQSEBSRTARVIRKCSLTFKFINGL 419
QY 421 ETLQENRRHSMPFASVNLCEMVCLEDLINYPADPEDEMBHEKONKPPALNRNOLP 480
420 ETLQENRRHSMPFASVNLCEMVCLEDLINYPADPEDEMBHEKONKPPALNRNOLP 479
DB 420 ETLQENRRHSMPFASVNLCEMVCLEDLINYPADPEDEMBHEKONKPPALNRNOLP 479
QY 481 EGIUNLILAIKINIVTSOGFLAGLADBSGQSEMISGVLYOLLAIIKGNHNCQ 540
480 EGIUNLILAIKINIVTSOGFLAGLADBSGQSEMISGVLYOLLAIIKGNHNCQ 539
DB 480 EGIUNLILAIKINIVTSOGFLAGLADBSGQSEMISGVLYOLLAIIKGNHNCQ 539
QY 541 PANSRNLNMLFSLRSGQASGEGTGMLDVLAHCVLIDSPBALNMRRDEHIIKVIISLEK 600
540 PANSRNLNMLFSLRSGQASGEGTGMLDVLAHCVLIDSPBALNMRRDEHIIKVIISLEK 599
DB 540 PANSRNLNMLFSLRSGQASGEGTGMLDVLAHCVLIDSPBALNMRRDEHIIKVIISLEK 599
QY 601 DPKVLIDVLCISLCVNGVAVRSSQNNICDYLPLFGKNILLQDTALVDHVSVPNI FVGR 660
600 DPKVLIDVLCISLCVNGVAVRSSQNNICDYLPLFGKNILLQDTALVDHVSVPNI FVGR 659

Db 600 DPKVLVDLCSLGVNGVAVSSQNNICDFLLPGKNTLLQTLVLDHVASIRPNIFVGRVDG 659
Qy 661 SAVYRKVFEYTMDDHIEKTHMMPHLRIGMANTGVVPRGGEGKGVGDGLXSYP 720
Db 660 SBNYQWYEVYTMDDHIEQTHMMPHLRIGMANTGVVPRGGEGKGVGDGLXSYP 719
Qy 721 DGAVLSGGRKTEPVNTHABEPIYRKGDVIGCALDITVPINFMFNGVRYTGSFTFNLE 780
Db 720 DGAFMTGGRKTLVNDALPEEPIRKGDVIGCALDITVPINFMFNGVRYTGSFTFNLE 779
Qy 781 GMEFPVISCSSKLSGCFLLGEGHGLRYAABEGYSPVLESLLPQOILSIEPCFYFGNLSK 840
Db 780 GMEFPVMSCKSLSCSFCGLGEGHGLRYAABEGYSPVLESLLPQOILSIEPCFYFGNLSK 839
Qy 841 PALAGRPVODDPAFVPTVDTLOITLPTVVEIOIRKLAENHEMAMKIEGMVYGDQ 900
Db 840 NYLAGPMLIEDDPAFVPKVDITGVTLPSVVDQIKELAEHHEMAMKIEGMVYGDQ 899
Qy 901 REDLHRIHCLVPERLPPAEKRYDQLAVQTLKTIILAGYISLDPKPARIRANVLEPN 960
Db 900 RDDYRIHCLVPERLPPAEKRYDQLAVQTLKTIILAGYISLDPKPARIRANVLEPN 959
Qy 961 PFMOSNGYKAPLDLSAVTLTPRMDLVDQLAENTHLMARERIQQGWTYGLNEDSDMR 1020
Db 960 IFMOSNGYKAPLDLSAVTLTPRMDLVDQLAENTHLMARERIQQGWTYGLNEDSDMR 1019
Qy 1021 SPHLVYPRYKDAIKKANPDTASEYVTLVYGMMDPRGEGHEALLBASQOKADR 1080
Db 1020 SPHLVYKADYDEAIKKANPDTASEYVTLVYGMMDPRGEGHEALLBASQOKADR 1079
Qy 1081 TYRABGNVAVSSGKWFEEFELTAGPMRVGMAMADAPGMALGODSNMFAFGYNEKY 1140
Db 1080 TYRVENAVVTSKMTFEEFELTAGPMRVGMAMADAPGMALGODSNMFAFGYNEKY 1139
Qy 1141 SGNTSEFGQMAVADVGVFLDIDKTIISFLNGELLMALGSETTFADY--OGDNFVPA 1198
Db 1140 ASGSIHFVRYEAGDVIGCFIDVKEQIISFLNGELLMALGSETTFADYTAGVGVPA 1199
Qy 1199 CTLVGQKARLYGQDVNTLKTYTGGLOEGYEPFCVNMKRDVTHYTKQPIFENTDEM 1258
Db 1200 CTLVGQKARLYGQDVNTLKTYTGGLOEGYEPFCVNMKRDVTHYTKQPIFENTDEM 1259
Qy 1259 IDPRIDVTRIPAGSDPRPCIKSHNTPETMEKAMWEIRLSLPIVCNBERPIDAEKAR 1318
Db 1260 IDPRIDVTRIPAGSDPRPCIKSHNTPETMEKAMWEIRLSLPIVCNBERPIDAEKAR 1319
Qy 1319 VEIKDROQILMKEA-VEAQM-----PAHIDQIRSGFTMNDIKGLHYE--DNOEELPSKY 1371
Db 1320 DEIKRQYRLMRBAEILAAQMOVTOQAAMHMDMLKGGNNMDIKGLTRNPEHADAEADHY 1379
Qy 1372 KRLPSRPRKSGMTRGVTTQNTNNOLOQOVNGHRSISEAKMAYDLAAGLTPDDKOK 1431
Db 1380 MRGPNRPRKGLTRNIT--FETDMAALDEMQRSTS-----VLDMNGIGSEMDKK-K 1430
Qy 1432 RGSPPKFRSRRKGSDBAKSRKSTPRPSPDTRVVSBERGARPRPQIKVSGANQRYNG 1491
Db 1431 RGSPPKFRSRRKGSDBAKSRKSTPRPSPDTRVVSBERGARPRPQIKVSGANQRYNG 1488
Qy 1492 MNARPERTNLVGSQVGLNMAATPQDRKQMTSTTLAOSATETVGNELIFDAECLKLINEFY 1551
Db 1489 AELPFPV-----FQGRKQSGSNLGOQPVETSGDEMFDAECLKLINEFY 1534
Qy 1552 GVARIVGQDPTHYIGAVTTQYHLKSDFNQSKVYSSVITTDYDRVENVNRQSCYV 1611
Db 1535 GVRIFGQDPTHYIGAVTTQYHLKSDFNQSKVYSSVITTDYDRVENVNRQSCYV 1594
Qy 1612 RABELNEMWAAETAKGASQGMPIGCVDTSTGSVSTCEGKQTSRFXKPEPTELAPAI 1671
Db 1595 RABELNEMWAAETAKGASQGMPIGCVDTSTGSVSTCEGKQTSRFXKPEPTELAPAI 1654
Qy 1672 FVEATSKELIQEILGSRATSLPLSAAVLPTSDKHVLEPQFPRLLKVOCLKPHQMARVPOS 1731
Db 1672 FVEATSKELIQEILGSRATSLPLSAAVLPTSDKHVLEPQFPRLLKVOCLKPHQMARVPOS 1731

Db 1655 FVEATSKELIQEILGSRPTTLPLSAAVLPTSDKHINPOSPEBKVKQCLRPHQMARVPOS 1714
Qy 1732 LOYHALKLSIDIRGMSMLCEDAVSMALAHIPEDRCIDIEPIEMDKLSFSHSHTLLTYAA 1791
Db 1715 LOYHALKLSIDIRGMSMLCEDAVSMALAHIPEDRCIDIEPIEMDKLSFSHSHTLLTYAA 1774
Qy 1792 LQYQSNYRAAHLCTHVDQKOLLVYAIQSQYMSGPRLOGFYDLLALHESHAATWEACKN 1851
Db 1775 LQYQSNYRAAHLCTHVDQKOLLVYAIQSQYMSGPRLOGFYDLLALHESHAATWEACKN 1834
Qy 1852 EYVPIGPELKLALYEPDMGHSLRSIQTESVPRQMMTDI-----AESIRE 1897
Db 1835 EYVPIGPELKLALYEPDMGHSLRSIQTESVPRQMMTDI-----AESIRE 1894
Qy 1898 ISNLVSPYPPLEVARFVQALAEAVETQVHNRDVGGSNENLFLPLIKLYDRLLVGM 1957
Db 1895 ISNLVSPYPPLEVARFVQALAEAVETQVHNRDVGGSNENLFLPLIKLYDRLLVGM 1954
Qy 1958 MDEDEYKLLIMTNPETWDPSPFDEKGEDEHRRKGLHMKRAEGAKLQMCYTLQHLNDIQLR 2017
Db 1955 MDEDEYKLLIMTNPETWDPSPFDEKGEDEHRRKGLHMKRAEGAKLQMCYTLQHLNDIQLR 2014
Qy 2018 HRYEALIAAPDVFGLQTDOLRYTEIQSDLPSSVAAKTREPCCPREQOMALLSKR 2077
Db 2015 HRYEALIAAPDVFGLQTDOLRYTEIQSDLPSSVAAKTREPCCPREQOMALLSKR 2074
Qy 2078 HLEEDKENCQGEELIAPNNEPHDTLMAVSLHMLQEBDAENGE--PEAKPGAFGLYN 2136
Db 2075 HLEEDKENCQGEELIAPNNEPHDTLMAVSLHMLQEBDAENGE--PEAKPGAFGLYN 2134
Qy 2137 INTVKELEEBEAKALBEPKKTPEEKFRKVLQTIIVMAEBSQIETPKLVREMFSLVNO 2196
Db 2135 INTVKELEEBEAKALBEPKKTPEEKFRKVLQTIIVMAEBSQIETPKLVREMFSLVNO 2194
Qy 2197 YDAVELIAPLEKTYIYNAKTKLDVAKWVGSQIPLALLPVQMSQEBELMRKMLKYN 2256
Db 2195 YDAVELIAPLEKTYIYNAKTKLDVAKWVGSQIPLALLPVQMSQEBELMRKMLKYN 2254
Qy 2257 NHTFQHPDLIRLRYHENVMAVMNNTLGRBAQAGSDAOPSPQVAB--DSKEKQTSHEM 2314
Db 2255 NHTFQHPDLIRLRYHENVMAVMNNTLGRBAQAGSDAOPSPQVAB--DSKEKQTSHEM 2313
Qy 2315 VVACRFLCYFCGTGQONKAMFHDHFDPLLENSNILLSPSRIGSTPLDVAYSSLMENTE 2374
Db 2314 VVACRFLCYFCGTGQONKAMFHDHFDPLLENSNILLSPSRIGSTPLDVAYSSLMENTE 2373
Qy 2375 LALAREHTLEKIAVTLISRCQIQSNSELYEKGYPDLGMDPVGBERYLDTLRFVWYNGS 2434
Db 2374 LALAREHTLEKIAVTLISRCQIQSNSELYEKGYPDLGMDPVGBERYLDTLRFVWYNGS 2433
Qy 2435 VEENANLVRLIRREBEGPALRGGBGLKAYIVDANKMSBRLIARRKLRMEBEGDV- 2493
Db 2434 VEENANLVRLIRREBEGPALRGGBGLKAYIVDANKMSBRLIARRKLRMEBEGDV- 2492
Qy 2494 --NFSHPLPESDEDEDYIDTGAAILNFYCTLYDLGRCAPDAGVILAGKNEISLRARAILR 2551
Db 2493 GANFTHPLPESDEDEDYIDTGAAILNFYCTLYDLGRCAPDAGVILAGKNEISLRARAILR 2552
Qy 2552 STVPLEDLQGVSLKFTLSQTPARGEERPKSDMPSGILLPNKKSIVLFLRVYVIGIEAQDIF 2612
Db 2553 STVPLEDLQGVSLKFTLSQTPARGEERPKSDMPSGILLPNKKSIVLFLRVYVIGIEAQDIF 2612
Qy 2612 YKLEBAFLPDLAAATMLDRNGCESDMALSMNRYIGNSILPLIIGAYFVNEAENYASI 2671
Db 2613 YKLEBAFLPDLAAATMLDRNGCESDMALSMNRYIGNSILPLIIGAYFVNEAENYASI 2672
Qy 2672 LDATLHTVRLISGRMLTKGOREAAVDFVALTSAMQPMMLKLEKLTVDSKLSSEYTT 2731
Db 2673 LDATLHTVRLISGRMLTKGOREAAVDFVALTSAMQPMMLKLEKLTVDSKLSSEYTT 2732
Qy 2732 VALRLTLHYERCARYGSGTAGQAGFAGASDEBEKLTMLPSNIFDSISKNDYEPBELG 2791
Db 2733 VALRLTLHYERCARYGSGTAGQAGFAGASDEBEKLTMLPSNIFDSISKNDYEPBELG 2791

Oy		2792	KALPCLIALGCALEPPYISLAKRYDDBEFYCKEQAADLDNPQYDPODPINTSSVALLANDJNT	2851
Dd		2792	KALPCLIALGCALEPPYISLAKRTKTDIDYGRQMGAP--DOPQYMFPNIDITNVHLDNLDLNS	2849
Oy		2852	IYQKSEHHDMASRKILENGWVGEGMSDSOKTTPRLKPYNMLNDYEKERIEKEPVREST.	2911
Dd		2850	IYQKSEHHDMASRKILRLEGWTTGYEDISDNDRKPRLPKPYIMLSFEYERRETRDYECFL	2909
Oy		2912	KALLAIGSVSEHSVDIPBNNSSMRROSKSGGRPPEI--VTDSATPPDYPNHPYDMTNL	2969
Dd		2910	KOLLIAIGTVSEHSEVEVALNHRCSTRRQSK-----PQINEFONEGSPPNNYPHPVDMSNL	2964
Oy		2970	TLSREMOMNAERLADNAHDIVAKKKCEEL	2998
Dd		2965	TLSREMOMNAERLAENSHDIVAKKKCEEL	2993
<hr/>				
RESULT 4				
ID	P91905_CAEEL	PRELIMINARY,	FRT;	5071 AA.
AC	P91905;			
DT	01-MAY-1997	(TREMBLrel. 03, Created)		
DT	01-MAY-1997	(TREMBLrel. 03, Last sequence update)		
DT	01-MAY-2004	(TREMBLrel. 26, Last annotation update)		
DE	Ryanodine receptor.			
GN	Name=ryr-1;			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;			
CC	Rhabditidae; Peloderinae; Caenorhabditis.			
OX	NCBI_TaxId=6239;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=BrStCol_N2;			
RX	MEDLINE=97280790; PubMed=9135117; DOI=10.1006/jmbi.1997.0910;			
RA	Sakabe Y., Ando H., Kagawa H.;			
RT	"An abnormal ketamine response in mutants defective in the ryanodine			
RL	receptor gene ryrr-1 (unc-68) of Caenorhabditis elegans.";			
EMBL	J.Mol.Biol. 267:849-864(1997).			
DB	EMBL; D45899; BAA08309.1; --; Genomtc_DNA.			
DR	HSP; P09860; IDTL.			
DR	GO; GO:0016021; C:integral to membrane; IEA.			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0005502; F:calcium channel activity; IEA.			
DR	GO; GO:0005509; F:calcium ion binding; IEA.			
DR	GO; GO:0016165; F:liron ion binding; IEA.			
DR	GO; GO:0004872; F:receptor activity; IEA.			
DR	GO; GO:0005219; F:ryanodine-sensitive calcium-release channel. . . ; IEA.			
DR	GO; GO:0006874; P:calcium ion homeostasis; IEA.			
DR	GO; GO:0006816; P:calcium ion transport; IEA.			
DR	GO; GO:0006816; P:cation transport; IEA.			
DR	GO; GO:0006118; P:electron transport; IEA.			
DR	InterPro; IPR001682; Ca/Na_pore.			
DR	InterPro; IPR002048; EF-hand.			
DR	InterPro; IPR005209; EGF-like.			
DR	InterPro; IPR002202; HMG-CoA_red.			
DR	InterPro; IPR005821; Ion_trans.			
DR	InterPro; IPR000907; Lipoxygenase.			
DR	InterPro; IPR003608; MIR.			
DR	InterPro; IPR001032; Ryanodine_recept..			
DR	InterPro; IPR001215; Ryanodn_recept.			
DR	InterPro; IPR009460; Ryanrecept_TM4-6.			
DR	InterPro; IPR003877; SPRY_receptor.			
DR	Pfam; PF00036; ehand; 2.			
DR	Pfam; PF00520; Ion_trans; 1.			
DR	Pfam; PF02815; MTR; 1.			
DR	Pfam; PRO6459; RR_TM4-6; 1.			
DR	Pfam; PF01365; KHDR_ITPR; 2.			
DR	Pfam; PF02026; RYR; 4.			
DR	Pfam; PF00622; SPRY; 3.			
DR	PRINTS; PR00795; RYANODINER.			

Query Match	Local Similarity	Score	DB 2	Length	5071
Best Match	47.2%	Pred. No. 0			
Matches 1462	Conservative 539	Mismatches 881	Indels 218	Gaps 51	
DB	SMART; SM00054; Eph; 2.				
DB	SMART; SM00472; MIR; 4.				
DB	SMART; SM00449; SPRY; 3.				
DB	PROSITE; PS00018; EF_HAND; UNKNOWN 2.				
DB	PROSITE; PS00186; EGF 2; UNKNOWN 1_				
DB	PROSITE; PS00066; HMG_COA_REDUCTASE_1; UNKNOWN_1.				
DB	PROSITE; PS00919; MIR; 5.				
KW	Receptor.				
SEQUENCE	5071 AA; 576357 MW; 145EF32288613324 CRC64;				
Query Match	45.8%	Score 7214	DB 2	Length 5071	
Best Local Similarity	47.2%	Pred. No. 0			
Matches 1462	Conservative 539	Mismatches 881	Indels 218	Gaps 51	
DB	SMART; SM00054; Eph; 2.				
DB	SMART; SM00472; MIR; 4.				
DB	SMART; SM00449; SPRY; 3.				
DB	PROSITE; PS00018; EF_HAND; UNKNOWN 2.				
DB	PROSITE; PS00186; EGF 2; UNKNOWN 1_				
DB	PROSITE; PS00066; HMG_COA_REDUCTASE_1; UNKNOWN_1.				
DB	PROSITE; PS00919; MIR; 5.				
KW	Receptor.				
SEQUENCE	5071 AA; 576357 MW; 145EF32288613324 CRC64;				

Db	1137	QG-AYTGGKXKIGDVVGCFLDLDNRITISLSNEELLDDPSGSEMAFDNVCGDGLVPAF	1195
Db	1200	TLVGQAKARLYTGGDVNTLKFTTCGLOAEYEPCCVAMKBDVTMTYTKODPIFENTDEMI	1259
Db	1196	TLGSGQGRNLNFGQGSLSKFFTCGLOEYEPCCVAMYTRMPPWPAKQLPREFDLSITLK	1255
Db	1260	DTRI-DVTRI-PASGDTPECLKISNHTET---MEKANWEFLRLSPVICHNEPIDEAEK	1314
Db	1256	SGSLIEVTRIPATGNSPPCLKILOKVITSEGGPEKKAMEYIRLSLTVKCNDFTVKKKDK	1315
Db	1315	---ARRVWEIDROQIILMKEAVEAMPHNDQIN-RSGFTTNDIKGLHYENOEELSPSK	1370
Db	1316	EAINRQLODYPRQSVASQIRACGIRPEFNDKXKGLPERS---WLSQDSHSSDDRN	1372
Db	1371	MKRLPSRPKRGKSTWGTGVIQNVNLTQGVNCHNSTSEAKMAKYDLGAQGLTRDDKDO	1430
Db	1373	RSRTTSKQP-----SISGDEPAPARRGLBELPHEERQIAEHNHR--DLDN	1415
Db	1431	KRGSRP-----FKCFRSKRGSSDPANSRK-----	1455
Db	1416	RHAEPKPKGILSRILRDSNSNTRKQDSRKHEDKAAALROMKSNRSRFDAGSLDTSTLPTG	1475
Db	1456	-----SKTRDPF-----SDP-EVSPERGARRPNQIVSQANGRYNEMNARPS	1497
Db	1476	QKDYLEBESBEDLPIWLYQDFHEBDVTASASEMPLSGRQLTIKKGYSV-KKKKXK-	1533
Db	1498	RTNLGSOVGNAMTPTQDRKOMTSTSLAQSATYEGNIEPDAECT---KLINIEFYGV	1553
Db	1534	-----ABIALKXMM---EREKKGSIITPMARQUDVLOE-GDARALVALMDKXDVEYLYGV	1582
Db	1554	RIYEGODPTHVYIGWTTQYHLSKDPNQSK-VTKSSVITTDYDVRVENVRNOSCYMR	1612
Db	1583	RIFPGQPTQYVWVGMVTTQYHYVWVHFQDGNVKKCFSEADHHGTTVDVSQONCYMVN	1642
Db	1613	ADELYNEVMAEATKAGSOGMFIQCSVDTSIGSVISFTCEGQDTSFVKEMBERTLPPAIF	1672
Db	1643	VSEILLEKTADVANKR--VSGTLIICIIDTISIGBLSFOVGTTDGVKTLERGAMLPPAFAF	1700
Db	1673	VEATSKETILOELGRSATSLPISAAYLPTSDKVTIPOPPEPKTKYQCKLPHOMAVRPNOST	1732
Db	1701	VTPATPDILOELGRIKTTPFLPSAAMPKSCSKSLVPPCPRLVITQOIESVYMAVAPMETL	1760
Db	1733	QVHALKSLDINGSMNLCEDAVSMILMNIPEEDRCIDILPEIEMDKLSFHSHTLYLYAAL	1792
Db	1761	RTTALPKLSVAGSVGLCNDPVRIMSVYIPKQDSIDILEMTEMDFLEFHNQTLNLYCKL	1820
Db	1793	CYQSNTRAAHALCTHVDOKQLLYAIQSGYMSGFLPQGFYDLLLYAHNESAHTTBAKSNR	1852
Db	1821	ASHGNHKAUHALCOHIDEDQIMVAKISHTYLSGPMRQGFHDLIIGHIMSHPAANSMAKE	1880
Db	1853	FVILFGLBELKALYEBRDMGHSRLSLQESVSRPCKMMDIASIWEISNLVSFPYRPLEVAR	1912
Db	1881	Y-----MAAEPRVKGHLSRE-----EEMKILRPSVDFFALK	1910
Db	1913	EYVNOALAEAVETAOVHNHRDVGGSNENLFLPLIKLVDRLLVGMEDDEVEKLLIMTNP	1972
Db	1911	KHWNESIQSAFHHAVMNCRDLIGDDNTHHEFLPLFPQQLLVGLINDEBELCGLRIIHR	1970
Db	1973	ETWDPSPDKSGKDEHRRKGLHMKRAEGAKLOMCTYLQHLANDIQLRHYEALIAANDFVG	2032
Db	1971	QAPBESY-KNGTTOQ--KGLTQLELAEPVKQLOVBIIDHLCIDIOLRHYRESLVAFTEGPGV	2027
Db	2033	DLQTDQRLRYTRIKOSDLSAIVAAKTRREPCPRREONNALLSPHLEEBEKE-----	2085
Db	2028	ELQSDQOCRWYIEIKQTDMPRABAACKTFFPCPRPEQCFRLMKCVKSEBRPEEMEDAD	2087
Db	2086	--NCPGCELLIARMEFHDITLMATVSLHALQEPDAAENQEP-----EAKDG--AFKG	2133
Db	2088	VDQCFPMASLQOQQRDFCELLVGKIG-----NAKGBESSDQALATJESSEGSVNDSPAR	2140
Db	2134	LYNIINTVKELEBEAKALIEBRPKCTPEEKFRKVLQITVNAAESQITFPGLVEMFSL	2193

Db	2141	I--VVKVPPELBEESGEMQ-----KKGNQNRREIIVTMLREMAQADFIESKOLIRSMFKL	2199
Qy	2194	VROVDANGELIRALEKTYIVINAKTKLDVAMWYGLSIRALLPYQNSQEESEELMRKLYK	2253
Db	2195	LRQYSGRIRERIDAMSQAUVFERMAADVTDFIVLLQIRRELTQVFENHTEALIKRGLMK	2254
Qy	2254	LNNHTFPOHQDILRLVLRVHENWVAVMNNTLGRRAQOASDAQSPQVADSDKERTSHE	2313
Db	2255	LMNRRIFPOHQDILRLSLVHENWVSIMNNTL--TAQQGVHEHGEDVEKAPFKDAS-E	2310
Qy	2314	MVVAACRPFICYFCRTGRONQKAMPDHPDFLENSNILLSRPSLRGSPFLDVAYSLMENT	2373
Db	2311	MVVAACRPFICYFCRTGRONQKAMPDHPDFLENSNILLSRPSLRGSPFLDVAYSLMENT	2370
Qy	2374	ELALALREHYLEKTAIVYLISRCGIQSNSELYEKGPDIQMDPVBERYLDPLRCPWYNGE	2433
Db	2371	ELALALKEEELDKAAVYVLISRCGIQSNSELYEKGPDIQMDPVBERYLDPLRCPWYNGE	2430
Qy	2434	SVEENANILVIRLIRREPCIGPRLRGSEGLYKIVANQMSSEIRADRRLREMEQGDV	2493
Db	2431	NVEENANILVIRLIRREPCIGPRLRGSEGLYKIVANQMSSEIRADRRLREMEQGDV	2479
Qy	2494	NFSHP-----LPESD-EDBEDYIDTGAALINFCTVLDLIGRCAPDAGVIALG	2539
Db	2490	NDSHPNMLTSGLGLENPTYPBSKEIEGSDYIDLGAATIDFISLVDLAKCAPDPMALQAG	2539
Qy	2540	KNESLRARAILRSLVPLEBILQGVLSLRPLNPPA-----	2574
Db	2540	KGDSLARAILRSLISHDIGQILALFPTIPNLAPSIKAVRRANAVQASHOKAVMAHT	2599
Qy	2575	-----GEE-2577	
Db	2600	FAMVASLASEVSNTRSQTFTSGANLARGLPCVEEYVSDSDSKSDYASVHTSBSGNEI	2659
Qy	2578	-RPSDMP-----GLPGHKQSGVGLERAYNG	2604
Db	2660	PAPSEKQKALQILNEKKTPIYQRRSSKRNPIDNTGRLPGLLPHNKGSVLEFLDNYG	2719
Qy	2605	IEIQLPYKLEBAFLPDLRAATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYYNE	2664
Db	2720	IDQDMLPHFLQGFPLDLRAATMMDSPRALIESDTALANRYLCNSVLPILLNHSHPFS	2779
Qy	2665	AENYASLIDATLHTVYLSKRMKTLTKQREAVSFLVALYSANQPSMLKLIRKLTVDVS	2724
Db	2780	AENHSALIDATLHTVYLRKNRKLSTLTKQORAVSFLVALITRELPGMWIKLKKVINDIL	2839
Qy	2725	KLSEYTT-VATRLTLTYERCAKYYGSGAQGAFGASDSEKRLTYMLFSNIPDSLSKM	2783
Db	2840	TMDNDNVLVPLRLTLTHYERCGKYYG---GNHYGASDEKRLSMULDALIDTIGSR	2895
Qy	2784	DYBEPLEFKALPCLIAIGCALPPDYSLSKNYDDEFYKEQAAGLDNPQYDPOEINTSV	2843
Db	2896	PYDPELEFKALPCLIAIGSALISPDYSLTSGLEDVYNNKKREBG-----AMIPRTDVSRC	2950
Qy	2844	ALANDLNTIYKSESHHDAMASKIENGWYGGGMSDQKTHRLRCPYMLNDYEXRY	2903
Db	2951	EINIDLEKMTLEFAEHFIDSWASRKLEKGNWAGELYSRANFTHRLRCPALDKOFESFY	3010
Qy	2994	KEPRESIKALLAIGWSEHSEYVIPSNNRSMRQSKSGRPREIYTDSATPE-DVNP	2962
Db	3011	KERGSECKALMA--WYSFPMVDRDANDRASAAR-----TLGTSISNAPK	3056
Qy	2963	PVDMTNLTLSREMOMARLADNADHDIWAKKCKEELVT	3000
Db	3057	PIDLSMTLEKDMVNAABKMAHSHLLWAKKVMNDLMT	3094
RESULT 6			
Q8TA74 HEMPU			
ID	Q8TA74 HEMPU	PRELIMINARY;	PRT; 5317 AA.
AC	01-JUN-2002	(TTEMBLrel. 21, Created)	
DT	01-JUN-2002	(TTEMBLrel. 21, Last sequence update)	

[illegible]

Qy	366	MDDGLDERSQOEBERTKRVIRKCSGLTKYKINGLIETTQENRRHSMFASVNLGSMVCL	445
Db	300	MDDCCTFFMALZBEERSKARVIRKCSVYANKPLKGI:IDAQLGANOISTDWTYDLNVLNKLX	359
Qy	446	EDLIYFAPQPEBDMHEEKONKFRALRRORDLPQEEGILNINLEAIDKINTVTSQGPAG	505
Db	360	EDLIYFAPQPEBDOFEKONHRLRBRODLPQEEGYLNMIDTIDFSGMBALPDRAG	419
Qy	506	PLAGDESGQSBEMISGYLYOLLAITIKGNHTNCAOPANSNRLNMLFSLGQASGEETGM	565
Db	420	-LIGETTHVKEQJSTLYLLVLAAMIKGNHTNCAQFASQRLDMTFGRLSNPOSAE--GI	476
Qy	566	LDVHLCVLDSPALNMNRDEHIKVIISLEKRGDPVYLDVLSLVCYNGAVAVSSONN	625
Db	477	LDVLCVLTSEBESALNMINEGHISVLSLEKRVGDPVYLDVLSLCEGNGAVASSOUL	536
Qy	626	ICDYLLPGKNLLQTLADVHVSVPENLFEVRVBSGSAVYRKRYPEVTMDHIEKTHMMPH	685
Db	537	ITQVLLPGKDLLOQSMRDHVSMMVPMVLGVBSAFLRKMYFEAVYEHIEHTMKQRPY	596
Qy	666	LRIGMANTGYVPYRPGGEKMGNGVGDLYSGYDGAYLMSGKAKTYVNRTHAEPYIR	745
Db	597	LRIGMANSVGRPEFGSGDKMGKCVGVDFFSYGDKGSMYFGGKSRRVG----HKLLE	651
Qy	746	KGDVYGCALDVTVPYINFMFNGVRVTSFTFNLEGMFFPYISCSKISCFRLGSEGR	805
Db	652	KGDVYGCSDITLPIRKFSVNGYTMSSGFKKFNIDGYFFPMLSIAKYSCTFLLGNGR	711
Qy	806	LRYAPBEGYSPVLESLLPQOLISLEPCFYFGNLSKRALAGPPLVODD-TAFVFPYVDTLQ	864
Db	712	LYRGPPTFSFVAVEAVNGS--LOITDCLSPFDLGNINFSGEOITFNNELEPITPIDVSA	769
Qy	865	ITLFPYVQIADKLAENHEMMANNKIBAGMYGQORBDLKIRPCLVPFELPABKRY	924
Db	770	TOLNHNATEMOKTAENHEIMARKIEBLSYGETNSETSRKPCILKFEYLPETBEKY	829
Qy	925	DIOLAVOTLKTIYALGYVYISDKKPPAIRNRYL-PNEBPMOSNGYKAPBLDSAVTLPK	983
Db	830	NILALATTKMTIBALGYHLITEDPPCRRLRAVRLGN--FOONGYKPPRLDHEIQLPAB	887
Qy	964	MDELVDOLAENTHNLMAERIQQGTYTLANE--DSDMHRSHLVYPRKYDAILKANDT	1044
Db	888	LOPLTEALARNTNIMAKEKIKRGTFELSHVAYATOKRSHLVYEVVDRIKQANES	947
Qy	1042	ASEVRYTLVYGYMDLPTGEOHEATLLEASOKOADPRTYRAEGNVAVSSGKWFEFEI	1102
Db	948	AAENIRLQJLGIFLEPPABH-HQVBAKEKELARAKDNRITRYABETIVAVCGKWFPEBI	1006
Qy	1102	LTAGBMRVGAHADNAPGMLGQDENSMAFDGYNEEKYSGNTBSPGOMAVGVYVYFL	1167
Db	1007	LTAGMKGMDIGSTPEIQLGADDRSAFPGYLGKRMHQG-AEYVGEKWKIGDVVGCFL	1065
Qy	1162	DLIDPITISFSLNGELLMALGSETTFAVYO-GDNVPVPACTGVGVGOKALTGYGODVNTKY	1222
Db	1066	DLANDRTISFSLNGELLDPSGSEMAFDVNVCGDGLVPMTYLSGQGRGLANTGQOONSILKE	1122
Qy	1221	FTTGLQGBGYRPPCVNMKRDVTHWYTKDQPIFENTDENIDTRI-DVTRI:PAQSDTPCLX	1279
Db	1126	FTTGLQGBGYRPPCVNMRYTRPMPWFQQLPFREDISTLKSGSILEVSRIPATNGSPCLX	1185
Qy	1280	ISHNTEF---MEKANEFLRLSPVCHNEPILBAEK---ARRWVXIKROOILMKEA	1333
Db	1186	ILQKVYTSSEGQSEBAKMEYIKLSIPVACNDTPVANKQKETTIRLOLOKYKPRSSQSVSQI	1245
Qy	1333	VEAQFPAHIDQIM-RSGFTMADIKGLIHEDYQOELPSSKMRQLPS---REPRKGSMTRG	1387
Db	1246	RAPGIPKPEFDNKKKGGFLRSMLSKXSHESDDDRSRSTNSKQPSVQSDERRA-----	1296
Qy	1388	VTIQNYNNLQPGQVNGMRSTSEABMAKYDLAGOGLRPDDCKDYKRGSPFFKFS---K	1443
Db	1299	-----VRSLSLELPEDEROILBDSMRDLNDR---HSSKPPKGGJLSTLRSSNTRK	1346

Qy 1444 RGE5SDRAKGR-----SKTPDPSPDTEVSPERGARRPNPKY 1482
 Db 1347 NFRSDBRKBEKAAQLRQMKANSRSDAGSLDSTLTGTQKDVLA55EMPLSGRGRLTI 1406
 Qy 1483 SOANORNGMANRPSRTNLVGSQVGLMAMPPTDRKQMTTSLAQSTETVNGEIPAE 1542
 Db 1407 KR8S-----IKKKKKKKAIEALBKREKKSIIIPMDQLVLLEG-----DANA 1452
 Qy 1543 L-----KLINEFYGVRIYPPGDPPTHVYIGWTTQYHLKSDPNOSK-VTKSSVITTDYD 1597
 Db 1453 LVHKKQVDEYYIGIRIFPGDPSQVWGVVTTQYHYNVNPDSQGRKRCSSEADHIG 1512
 Qy 1598 RVEYNVROSCTYVRADELVNEVBAATAGASQGMFSGSVDTSGSVFTCEGKDTSF 1657
 Db 1513 TTYDSVQSONCYMNVNSELATTPDVANTK--VSGTLIGCIIDHSIBELSPQVSGSTDTGI 1570
 Qy 1658 KPKMEPTKLPRAIPEATSKETIQTILSGSANSLPISAVALPSSDKVTPQPPRLKVQ 1717
 Db 1571 KFKLEPGAMLPFAAFVPTATETIQFELGRIKYTPPLSAMFKSCSKSLVFPCLTVB 1630
 Qy 1718 CLKPHQARVPNQSLOVHALKSDIRGMSMCSDAVMMLAHPEEDRCIDLEPIMDK 1777
 Db 1631 QISBVARVPNETLRTTALKLSEVRGMSVLCNDPVMISVYIPEKQSLDILMIMPD 1650
 Qy 1778 LLSFHSHTLTLYALCYOSNYRAHALCTHVQKQLYATOSQYMSGPLRGFYDLIAL 1837
 Db 1691 MLEHNRITLVLYCGLASHGNHKNVANTLCQHIDEDQIMYAIKSHNLSRPMQGFIDLIGL 1750
 Qy 1838 HLEBHAATMBACKNEFYIPLAPELKAL-YEBRDKGHSLSLQTESVVRPQMKTDIASIT 1896
 Db 1751 HLMSTHAAKNSMAKEVYIPLVPLQIQNVLDPR-----SESRYPQI-----TGESVS 1797
 Qy 1897 EISNLYS-----PYRPLEVABEPNQALAEAVETQVYHNRDPVGSNE 1939
 Db 1798 MLCQMA5EPVKQVSRDEMKLPPSVDFEALKGVNBSLQSAVHAAVMNCRDILIGDNT 1857
 Qy 1940 NLFLPLKLVRLLVGMMDREDEVEKLLIMTNPETWPSFDKEGDEHKKGLLMAKAE 1999
 Db 1858 NHPEPLKLPDQLAVIGLINDEXELRLHPOAPBENY--TGTTQKGLDLELAP 1914
 Qy 2000 AKLQMCYLLOHLNDIOLEHRYEALIAFANDFVGLQTDQLRYTEIKOSDIPSAVAAKT 2059
 Db 1915 VKIQV6ITLHLCIOQLRYRISLVAFTGEGVGLQSDQCKRYMEIKQTDWPAABA 1974
 Qy 2060 REPRCPREOMNALISFKHLEBDEK-----NCPGSELBARNNPHDTLMAVSL 2110
 Db 1975 KEPRCPREOMFRLMKVKEBRDPLMEBDADVDQCPMAEGLOQQLRDFCELLVKGIG- 2033
 Qy 2111 HALQEPDAAS-----NOBPEAKPGAFCGLYNIINTVKELEBEAKAIEBRPKTPEEKFRK 2165
 Db 2034 -NVKEGSDOQLALIEBEGSWD5FARI--VAVYPPVLEBGMQ-----KKGTFNRE 2086
 Qy 2166 VLICTIVNVAE5QIETPKLVREMF5LLVROYDVGELIRALEKTYVINAKTKLDVAMW 2225
 Db 2087 IIVTMLBMAQADFI5ESKSLIRNMFRLLRQYSGIREIRDMQ5TYVHEBNEKDVDFL 2146
 Qy 2226 VGL5QITALLPVOVQ5EBE5LARKLWKLVNNTFPQHPDLIRLVRCHENMAAMNTIG 2285
 Db 2147 VYLLQI0IELLVQ0EHTEBALIKRGLKGLMNNRIFFQHPDMLRLLSVHENW5IMAIL- 2205
 Qy 2286 RBAQAGDAQ5SPVADSKEKDT5HEMVVAC5RFLCYFCRTORONOKAMFHPDFLLE 2345
 Db 2206 --TNOQGTVEHGEDELKEKAPIKDAS--BMVVA5CRFLCYFCRTORONOKAMFHL5FLD 2262
 Qy 2346 NSNILLRSPSLR5TPLDVA5BSLMENTELALAREHYLEKIAVYLSRGLQ5NSLVEK 2405
 Db 2263 NATMLLARPSLR5GVPDLVA5SPDNNDELALAK5EELDKVAAYLSRCSGLQ5PSSEILTK 2322
 Qy 2406 GYPLGMDPVTEGERYLDLFR5CVWVNG5VE5ENANLVRLIRRP5CIGPLR5GB5EL 2465
 Db 2323 GYPIGMDPVTEGERYIDPLR5CVWVNG5VE5ENANLVRLIRRP5CIGVALLK5EG5OLF 2382
 Qy 2466 KAIYDANM5ERIADRRL5REMEQ5GVN5GHP-----LPE5D-EB5DYIDT 2511

Db 2383 SAEKAIALSEDI-----RLR-----ND5HPSLLSSGLG5NPYPSKAG5EDIDL 2431
 Qy 2512 GAALNPFCTLYDLR5CAPDAGVIALGK5ESRABAIIR5VLE5DLO5L5RFTLN 2571
 Db 2432 GAAITLDR5SYLVLAKCAPDPAIQA5K5DSL5RARI5NSL5L5DLO5L5RFTLN 2491
 Qy 2572 PAA-----GE5R5K5DM 2584
 Db 2492 LAA5P5I5AV5RANA5Q5SH5TQ5AVMA5HTPAMVASL55V5NT5R5Q5FT5G5TMLAK5GLP 2551
 Qy 2585 ----- 2584
 Db 2552 C5E5EVD5D5K5SD5YASVHT5F5SG5NEL5PAPKAEK5VDVLKLN5NKYPII5OR5SRFN 2611
 Qy 2585 -----SGLIRPHK5Q5VGL5PL5RYVY5IGT5O5LE5FYK5LEA5PL5DL5RAAT5ML5DRN5CE 2636
 Db 2612 PIDNTG5PL5GL5LPHK5Q5VLL5FLDRYV5GID5Q5DL5FV5L5Q5SL5PL5RAAT5ML5DRN5SPAL5E 2671
 Qy 2637 SDMA5MNR5YI5G5N5IL5PL5IKHAY5FYNEA5ENYASL5DATI5HTY5RL5SK5NML5TK5G5EAV 2696
 Db 2672 SDPLA5MNR5YI5G5N5IL5PL5IKHAY5FYNEA5ENYASL5DATI5HTY5RL5SK5NML5TK5G5EAV 2731
 Qy 2697 SDFV5AL5TSAM5Q5SM5L5K5L5R5K5L5TV5V5K5SE5TT-VAA5LL5TH5Y5R5CA5K5Y5G5TA5Q 2755
 Db 2732 SDFV5AL5TR5EL5PAM5MI5K5L5K5K5Y5T5D5L5T5M5M5V5L5PL5L5IT5HY5R5CK5Y5G5S-----G 2787
 Qy 2756 GAF5AS5DE5ER5K5L5TM5L5FSNIP5LSMD5Y5E5L5F5G5AL5P5L5A5IG5AL5P5D5Y5LS5KNYD 2815
 Db 2788 NH5GVAS5E5Q5K5R5L5SM5L5F5D5L5P5L5G5RP5D5P5L5F5G5AL5P5L5A5IG5AL5P5D5Y5L5T5G5L5E 2847
 Qy 2816 D5F5Y5G5K5Q5A5G5DL5DN5P5Q5D5P5Q5INT5S5VAL5ND5L5NTI5VQ5F5SH5Y5DAM5AR5KI5ENG5Y 2875
 Db 2848 D5V5R5K5R5E5B5G-----AM5IR5YD5V5R5C5E5IN5R5D5E5K5TEL5P5A5H5F5H5M5AR5K5L5E5K5MVH 2902
 Qy 2876 G5E5G5SD5Q5K5TH5P5L5K5P5Y5N5L5ND5Y5K5E5R5Y5K5E5P5V5E5SL5K5AL5AL5G5V5H5E5VDI5P5NNR5S 2935
 Db 2903 GDI5Y5RAN5P5H5P5L5K5P5AL5K5D5E5K5F5Y5K5E5C5E5CL5AL5MA--WNY5F5EM5D5R5D5AN5RAS 2960
 Qy 2936 M5R5Q5S5G5G5R5P5EL5VDSAT5P--DYN5P5D5M5NT5L5SR5M5Q5MA5E5L5N5AH5I5MA5KK 2994
 Db 2961 AAR-----TL5G5IS5IN5FAP5K5PID5L5SM5TL5K5M5VNA5R5A5H5SHL5I5MA5KV 3008
 Qy 2995 K5E5BL5VT 3000
 Db 3009 MNDLANT 3014

RESULT 8
 Q29621_RABIT
 ID Q29621_RABIT PRELIMINARY; PRT; 4968 AA.
 AC Q29621;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DB Cardiac ryanodine receptor.
 GN Name-BVR-2;
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
 OC Oryctolagus.
 OX NCBI_TaxId=9986;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=91032060; PubMed=2226801; DOI=10.1016/0014-5793(90)80399-4;
 RA Nakai J., Imagawa T., Hakamata Y., Shigekawa M., Takehana H., Numa S.;
 RT "Primary structure and functional expression from cDNA of the cardiac
 ryanodine receptor/calcium release channel.";
 RL FEBS Lett. 271:169-177(1990).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Heart;

RX MEDLINE-93147066; PubMed-1337083;
RA Imagawa T., Nakai J., Takeshima H., Nakasaki Y., Shigekawa M.;
RT "Expression of Ca(2+)-induced Ca2+ release channel activity from
cardiac ryanodine receptor cDNA in Chinese hamster ovary cells.";
RL J. Biochem. 112:508-513 (1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RA Nakai J.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Regulatory light chain of myosin. Does not bind calcium
(By similarity).
CC -1- SUBUNIT: Myosin is an hexamer of 2 heavy chains and 4 light chains
(By similarity).
CC -1- DOMAIN: Each of the four internal repeats contains five
hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
positively charged transmembrane segment (S4). S4 segments
probably represent the voltage-sensor and are characterized by a
series of positively charged amino acids at every third position
(By similarity).
CC EMBL; U50465; AAA93465.1; -; mRNA.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0016020; C: membrane; IEA.
DR GO; GO:0005262; F: calcium channel activity; IEA.
DR GO; GO:0005509; F: calcium ion binding; IEA.
DR GO; GO:0004972; F: receptor activity; IEA.
DR GO; GO:0005219; F: ryanodine-sensitive calcium-release channel. .; IEA.
DR GO; GO:0006874; P: calcium ion homeostasis; IEA.
DR GO; GO:0006816; P: calcium ion transport; IEA.
DR GO; GO:0006812; P: cation transport; IEA.
DR InterPro; IPR000699; Ca-rel_channel.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR011992; EF-hand_type.
DR InterPro; IPR002048; EF-hand_Ca_bd.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR003608; MIR.
DR InterPro; IPR003032; Ryanodine_recept.
DR InterPro; IPR001215; Ryanodine_receptor.
DR InterPro; IPR009460; Ryanodine_recept_TM4-6.
DR InterPro; IPR003877; SPRY_receptor.
DR Pfam; PF00036; efhand; 1. _receptor.
DR Pfam; PF00050; Ion_trans; 1.
DR Pfam; PF02815; MIR_1.
DR Pfam; PF06459; RR_TM4-6; 1.
DR Pfam; PF01365; RYR_IRPR; 2.
DR Pfam; PF02062; RYR; 4.
DR Pfam; PF00622; SPRY; 3.
DR PRINTS; PR00795; RYANODINER.
DR PRODOM; PD000012; EF-hand; 1.
DR SMART; SM00054; EFh; 2.
DR SMART; SM00472; MIR; 2.
DR SMART; SM00449; SPRY; 3.
DR PROSITE; PS00919; MIR; 5.
KW Ion transport; Ionic channel; Motor protein; Muscle protein; Myosin;
KW Receptor; Repeat; Transmembrane; Transport.
KW Sequence 4968 AA; 565086 MW; 04816A35D068852D CRC64;
SQ
Query Match 43.0%; Score 6778; DB 2; Length 4968;
Best local similarity 45.6%; Pred. No. 0;
Matches 1401; Conservative 530; Mismatches 851; Indels 290; Gaps 57;
QY 4 AEGGASQDDVSLRTEDVYGLSCTAT---GERVCLAAEGFGNRHCFLENTAD-KNIPP 58
DB 2 ADGGEGE-DEIGQLFRIDDEVVLQCTATIHKEQKLCIAAGFGNRLCFLESTNSGNVPP 60
QY 59 DLSQCFVLEQALSVNLAQELVTAASFGTKG-----TSGHRTILYGNAI 104
DB 61 DLSICFVLEQSLSVLAQELM-ANTVEKSEGVVDEKFKFMKTAQGGGHRTRLVGHAI 119
QY 105 LRLHLNSDWYLAQLSTS-SSQDLAFVYGLQHSQGEACMWTLPAPSKORSEGEKYVSD 163
DB 120 LRLHSTSGMYLCLCLSTSRSTDLAFVGLQEDVTGEACMWTLPAPSKORSEGEKYVSD 179

QY 164 DLLIVSVAERLYHTTKENEVSIVNASFHVTHNSVOPVGTGISMKXVGVYFGGDVLRFF 223
DB 180 DLLIVSSSRHYHLISYSGNSLHVDAFOQTLSVAPISGSSBAQ--GYLIGDVLRL 237
QY 224 HGG-DECLTPSWTDDGGGNTVYVEGSGVMSQASRLMLRLARTKAGFIMMYHMKI 262
DB 238 HGHMDECLTVPSGEHBEORRTVYEGGAVASVARSLSRLRTLRVAMSGSHIMGQFRL 297
QY 283 RHITGRTYLVNDQNELVYVSREATTAAACAFCLARQEKDOKOVLEDELEGVIGAPIRKY 342
DB 298 RHITGRTYLSIMEDKNLLMDKEKADVKSTAFPRSSKEKLDGVR-KVDDGKGTSEIKY 356
QY 343 GDSVTIVQSEGTGLMYSYSEYTKKGVGKEEKOAILHEEGMDDELDFRSQSEBSRT 402
DB 357 GDSICYQHVDYGLMLTYGSDVYKSVMGSIQRK-AIMHHEGHMDGLNLSRQSEBSRT 415
QY 403 ARVIRKSSLSFTKFTINGLTLOENRHSFPASVNL--GEMVCLDLINYPQPDME 460
DB 416 ARVIRSTVPLFNKFTGLDLSKKAVAS---SVDLPIBSVSLDLDLGYFHPDHELR 471
QY 461 HEEKKRPALRRQDLFOEGILNLLBAIDKINITYSQGFLAGFAGDSQSWEMIS 520
DB 472 HEKQKRLRLAKRQNLFOEBGMINLVLECIDRLHYSSAHPAD-VAGREAGSSKSL 530
QY 521 GYLYOLLAIIKGNHTNCAQFANSNRLNMLFSRLGSAQSGEGTMLDVHLVLDSEPAL 580
DB 531 NSLYELLAIIKGNRNCQAQFSGS--LDWLISRL--ERLEASGILLEVHLVAVESPEAL 586
QY 581 NMNRDHIIVYIISLEKHDRPRLVDVLSLCYGNQVANRSSQNNICDYLIPKKNLLQ 640
DB 587 NIKKEGHKISILSLDKHGRNHRVLDVLSLCYCHQAVARSNQHLLCDMLLPERDLLQ 646
QY 641 ALVDHVSVPNPIFVGRVSGSAVYRKMPFEVMTDHEK--TYHMPHLIRIGMANTGVYVP 699
DB 647 RLNVNHSNRPNIFLVGSSGSAQYKKMYELMWDHREPVTAETHLRIGMASTBEYSY 706
QY 700 PGGEKRWGNGVQDDLYSTGPDGAVYMSGGRKTPVNRTABEYIRKGDVIGCALDLYVP 759
DB 707 PGGEKRWGNGVQDDLYSTGPDGHLMSGCIARTVSSPN--QHLLRTDVIISCCLDLSAP 764
QY 760 IINFMNGVRLVGSFTFNELBGMFPFVISCSSKLSRFLGEBHGLRRAAPGYSPLVE 819
DB 765 SISFRINGQPVQGFENFNIDGLFFPVVFSAGIKRFLGLGHSFKLPPGVAPCYE 824
QY 820 SLTPQQLISLEPC--FYFGNLSKRALAGPLVQDDTAFVPTVDLTQTLPTVVEQIRDK 877
DB 825 AVLPRKELKLVHSRREKQERTTROLLGPTVSLTQAAPFIPVDISQIVLPHLEIRREK 884
QY 878 LAENIHMMAMNKIEAGMYGQREBDLHKIRCLVFEERLPPAEKRYDIQLAVQTLKTL 937
DB 885 LAENIHMMAMNKIEAGMYGQREBDLHKIRCLVFEERLPPAEKRYDIQLAVQTLKTL 944
QY 938 ALGYVYISLDKPPA--RIRVRVRLPNEFMQSNQYKAPLDLSAVTLTPKMDLVDOEAEMT 995
DB 945 ALGCHVGISDEHAEVEVKMKLPKN-YQLTSGYKAPMLDSTKLTSPQEAAMDKLAENA 1003
QY 996 NMLMARERIQQGMYTGLNEDSDMHSRPHLVPPKYVDAIKKANRDPASTVETILVYGYM 1055
DB 1004 HVMARADRIRGMYTGLIQDDVKNRBNRPLVPTLLDDRKSNKDSLRANVTLIGYGN 1063
QY 1056 LDPTGEQHEALLLEASQKQADFTTYRAEKYAVSSGMYFEBPILITAGPMEVGAHAD 1115
DB 1064 LEAP--DDHARAEVCSGTGERFPIFRAEKTYAVAGWYEPFEAVTSGDMRVGMSRG 1121
QY 1116 MAPGMILGDDNSMAFDGNEEKYVSGNTESGKQMAVDVYGVPLDLIDKTIISPLNER 1175
DB 1122 COPDELGSDEFAFADGFKAKRMHQN--EHYGRMQADVVGCVDNMEHTMMFTLNBE 1180
QY 1176 LLMDLAGESTPADVQ-GDNFVPACTLIGVQYARLTYYGQDVNTLLKFTTCGLQOEGYEP 1234
DB 1181 ILDDSGSLAPAKDIDVGDGFIPIVCSLGYAUGRANFGDVSITLKITTCGLQOEGYEP 1240
QY 1235 VNMKRDVTHMYTKQPIFENTDEMIDTRLIDVTRIPAGSDTPCLKISHTFTMEKANE 1294

Db 1241 VNTNRDITWMLSRKLPQFLQVPSNHB-HIEVTRIDGTIDSSPCIKYTKQKFSGS-QNSNTD 1298
 Qy 1295 --PLRSLPVCINEFIDEAKARRWWEIDRQOILMKEAVEAQMRAHIDQINRSGETNM 1352
 Db 1299 IMFYRLSMPIBCAEVF----- 1314
 Qy 1353 DIKGLHYBDNQBELPSSKMKRLPSRPKSGMTRGVITQYNNILQPGQVGMGRSTSEAR 1412
 Db 1315 -----SKTVFGLPGAGLP-----GPKNDLIDYDADSD 1342
 Qy 1413 MAKYDLGAQG-LTPDDKDKRGRSPFKPFRSKGESSDRKSKSKTPDDPSDTEVS PER 1471
 Db 1343 FEVLMTAGHGLVP-----DRVDKXETTKAEFN----- 1372
 Qy 1472 GAARPPQIVSQANQRYNQAMAPSRNTNLYGSOVLNMAVTPQDRKMTSTLAGSAT 1531
 Db 1373 --HKDYAOBKPSRLKRFLLRRTKP-----DYSTSHSARLTED 1408
 Qy 1532 TVGNBIFDAECLLINEFYGVRIYPGODPTHYIGVNTTQYHLHSDFNQSKYTSV 1591
 Db 1409 VLADDDDDFLMQTSTYTSVRIFFQGEPAVAVWGHTISDFHOYDTGFLDRVRYTVT 1468
 Qy 1592 ITDDYRVVENVAROSCYVVRADELYNEVAAEATAGASQGMFSGSVDTSGSVPTCE 1651
 Db 1469 LGDEKQKHESIIRSNCTWCA-----GESMSPGQGRN-NGGLBICGVVDAASGLITFIAN 1523
 Qy 1652 GKDTSPKPKNEPTKLPRAIFVEATSKELIQIBLGSATSLPISAANLTPSDKHVITQPP 1711
 Db 1524 GKELSTYYQVPESTKLPFAVFAQATSPNVVFOFELGRKKNVPLSAGLFKSEBKNKPVQCP 1583
 Qy 1712 PRLKVOCLKPMARVAVNOSLOVHALCLSDIRGSMSCEDAVSMALHIEBDRCIDLE 1771
 Db 1584 PRLHVPGLSHVLSRPNQFLKVDVSRISERQGLVCLDPLQFMSLHIEBNSVDILR 1643
 Qy 1772 PIEMDKLSFHSHTLTLYALCYOSNYRAAHALCTHDOXOLLYATOSQYMSGRLRGFY 1831
 Db 1644 LTEQBELKFNHTLRYSAVCAIGNRVAHALCSHDEPQLLYAENKTKMGLRFGY 1703
 Qy 1832 DLIALHLBSHAATTEACKNEFVILQPELKA--LYEPPMGSLSL-OTESVPRPMKA 1888
 Db 1704 DLIDILHSYATARLMMNNEFIVPMTEFTSKITLFPDENKKIKGLPDIIGLSTSLRPMQF 1763
 Qy 1889 TDIAESTTEISN--LYSPRPLEVABEFMQLABEVETNOVNRBPVGSNENLPL 1945
 Db 1764 S--SPSPVSIINNECYQSPSPPLDILAKTIQMLTEAVKESGLHARPVGITFEFLVPL 1821
 Qy 1946 IKLVDRLLLVGMARDEVEKLLIMTNPETV-----DPSFDK--EGKDEH 1987
 Db 1822 IKLPTLLINGIFRNEDELRIHILQILBPSVFKDAATPEEBGDTLEEBESVDTLKEGAGEB 1881
 Qy 1988 -----RKGLLHMKAEGAKLQMCYLQHLNDIQLRHREVAIIAHPVGDQLQTDQL 2039
 Db 1882 EAKMGKRPCKGLQMKLPBPVKLQMKLLQYLCCQYRHRIEALIVASDDFVALQDNQR 1941
 Qy 2040 RRTTEIRQS-DLBSAVAAKTRBRCPPRQOMAIISFKLIEEDKNCCEBELIARMN 2098
 Db 1942 FRNVEVQALNMSAALLTARKTKERPSPOBQINMLNPK---DDKSECEPBEIRQLL 1997
 Qy 2099 EPHDTLMAHYSLNALQEPDAENQBPRAKGAFGKLIINTVGLSEB--AKAIEBPP 2156
 Db 1998 DFHEDLMTNCGIBLDEBGSIDGNSDLTR---GRLSLVKTYLLKKQTEKRVESDSR 2053
 Qy 2157 KTPBEKFRKYLQITVMAEBSQIETPLVEMFSLVROYDAVGBELIRALEKTYVINAK 2216
 Db 2054 KS--STLQGLISETMVMAQSVIEDPELVAMFVLLHRYQDGIAGLVRALPKTYTINGV 2111
 Qy 2217 TKLDVAMWGLSITRALLPQWQSEBEBELMKRLMLVNNHTFPQRPDLIRLVAREN 2276
 Db 2112 SVBETITVLASLGIRSLSTRMKKEBKIKMIRGLGIIMNNKYVYQHNNLMRALGMBETV 2171
 Qy 2277 MAVMMNTLGRBAQAQSDAQPSSQVAVADSKEKDTSHBMVVAACCFLYCFGCTGROKAM 2336

Db 2172 MEVMANVLG-----GGESEK-ITPFRKMANCCRFICYCRISRONOKAM 2214
 Qy 2337 FDHPDLLENSNILLRPSRLRGSTPLDVAVSSIMMENTELALAREHYLEKIAVYLSRGL 2396
 Db 2215 FDLHSTILERSISGLASPAIRGSGTPLDVAASVMDNDELALALREBDELEVAVYLAGGCL 2274
 Qy 2397 QSNSELVEKGYPDLDGMPVEGERYDPLFRCVWANGSEVSEENANLYRLLIRPECLGPA 2456
 Db 2275 QSCOMLVSKGYPDIGNVPGEGERYDLFRRPAVFCNGSEVENANVVRLLIRPECGFPA 2334
 Qy 2457 LRGE-GEGLIKALVDANKSERIADRRKLRBEMQEBDVNFSHLPES-----DEDE 2506
 Db 2335 LRGEKNGLLAAMEBAIKIAE-----DPSDGGSPFGSSKTLTDTEEBD 2379
 Qy 2507 DVIDTGAILNFCYTVLDLGRCAPAGVIALGKNSLRARALIRSLVPLEDLOGLVSLR 2566
 Db 2380 DTHMGALNTFTFALIDILGRCAPEMHLIHAGGAIRRSILRSLIFPGDLVGIVISTA 2439
 Qy 2567 FTLANPAGSEERKSDMPGSLRPGHQSQVGLFLERYGIEFQBLFYKLEBAFLPDLRAA 2626
 Db 2440 FQMPITAKQGNVYBPMASGFCPDHKAAMVLPIDRYVYGIEVQDFLHLLEVGFPLDRAA 2499
 Qy 2627 TMLDRNDGESDMALSNRTYIGNSIIPLIKHAIFYNEANVYSLDADTHTYRSLSKR 2686
 Db 2500 ASIDTAAISATDMALNRYLCTAVVPLTRCAPLFGAETHASLIDSLHTYRSLSKG 2559
 Qy 2687 MLTKGQREAVSDFVLVLTSMOPSMCLKRLKRLTVVYSKSEYTVVALRLLTYHERCAK 2746
 Db 2560 SLTKAQDSTLEVCLLSICQULRSMQHLRRLVFDPLNBSAKMPLKLLNHYERCKW 2619
 Qy 2747 YGSGTAGAGAFGASDSEKRLTMPLFSNIFDSLKNDYBPLFGKALPCLIAIGCALP 2806
 Db 2620 YLCLPG-GMNPFGAABEBELHLSRKLFWGIFDALISQKXQBLFKALPCLSAVAGALP 2678
 Qy 2807 DYLSKNYDEDFYKQAPAGDLNPOYDPOPIPTSSVALNNDLTVQKSESHYDHAKAS 2866
 Db 2679 DY-MESNYVSM--EKQSSMDSBG-NFNPQVPTISNIIIPKLEYFINKAESHSDQMS 2734
 Qy 2867 RKLENGVVEGMSDSQKTHPLKPYNMLNDYKERYKBPVRSLLKALLAIGSVSESEV 2926
 Db 2735 DKLANGITVGEIYSDSKLOPLMKPYKLSEKKEIYRWIKSLTKMLANGRIKTR- 2793
 Qy 2927 DIPSNRRSMRQSKSGRPPEIVTDSATPFDPNPHVPDNTNLTLSREMOMARLADNA 2986
 Db 2794 ---EGDSMLNNTRRISQTSQSVDA--HGSPRAIDMSNTLISDLDLHAAEMKAEVNT 2848
 Qy 2987 HDIWAKKKEEL 2998
 Db 2849 HNIWAKKKLEL 2860

RESULT 9
 ID RYR2 RABIT STANDARD; PRT; 4969 AA.
 AC P30957;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Ryanodine receptor 2 (Cardiac muscle-type ryanodine receptor) (RYR2)
 DB (RYR-2) (Cardiac muscle ryanodine receptor-calcium release channel).
 GN Name=RYR2;
 OS Oryctolagus cuniculus (Rabbit).
 OC Buiarvota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
 OC Mammalia, Eutheria, Euarchontoglires, Glires, Lagomorpha, Leporidae;
 OC Oryctolagus.
 OC NCBI_TaxID=9986;
 RN 1;
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Heart muscle;
 RX MEDLINE=90337947; PubMed=2380170;
 RA Otsu K., Willard H.F., Khanna V.K., Zorzato F., Green N.M.,
 MacLennan D.H.;
 RT "Molecular cloning of cDNA encoding the Ca2+ release channel

RT (ryanodine receptor) of rabbit cardiac muscle sarcoplasmic
reticulum.";
RL J. Biol. Chem. 265:13472-13483 (1990).
[2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8841406;
RA Miehida K., Otsu K., Hori M., Kuzuya T., Tada M.;
RT "Cloning and characterization of the 5'-upstream regulatory region of
the Ca(2+)-release channel gene of cardiac sarcoplasmic reticulum.";
RL Eur. J. Biochem. 240:408-415 (1996).
[3]
RP PHOSPHORYLATION SITE SER-2809.
RX MEDLINE=91250425; PubMed=1645727;
RA Wichter D.R., Kovacs R.J., Schulman H., Cefali D.C., Jones L.R.;
RT "Unique phosphorylation site on the cardiac ryanodine receptor
regulates calcium channel activity.";
RL J. Biol. Chem. 266:11144-11152 (1991).
CC -1- FUNCTION: Communication between transverse-tubules and
sarcoplasmic reticulum. Contraction of cardiac muscle is triggered
by release of calcium ions from SR following depolarization of T-
tubules.
CC -1- SUBUNIT: Homotetramer (Potential).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- TISSUE SPECIFICITY: Heart and brain.
CC -1- MISCELLANEOUS: The calcium release channel is modulated by calcium
ions, magnesium ions, ATP and calmodulin.
CC -1- MISCELLANEOUS: The calcium release channel actively resides in the
C-terminal region while the remaining part of the protein
constitutes the 'foot' structure spanning the junctional gap
between the SR and the T-tubule. It is possible that the foot
structure interacts with the cytoplasmic region of the
dihydropyridine receptor.
CC -1- MISCELLANEOUS: Ryanodine is an alkaloid that binds to the Ca-
release channel in junctional SR and modulates its activity.
CC -1- SIMILARITY: Belongs to the ryanodine receptor family.
CC -1- SIMILARITY: Contains 1 EF-hand domain.
CC -1- SIMILARITY: Contains 5 MIR domains.
CC -1- SIMILARITY: Contains 3 SPRY domains.

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between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

CC EMBL, M59743; AAA31179.1; -, mRNA.
DR PIR; A37113; A37113.
DR InterPro; IPR000659; Ca-rel_channel.
DR InterPro; IPR01682; Ca/Na_pore.
DR InterPro; IPR01192; EF-hand_type.
DR InterPro; IPR002048; EF_hand_Ca_bd.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR003608; MIR.
DR InterPro; IPR003032; Ryanodine_recept.
DR InterPro; IPR001215; Ryanodn_recept.
DR InterPro; IPR009460; Ryanrecept_TM4-6.
DR InterPro; IPR003877; SPRY_receptor.
DR PANTHER; PTHR1715:SF1; Ryanodn_receptor; 10.
DR Pfam; PF000036; efhand; 1.
DR Pfam; PF000520; Ion_trans; 1.
DR Pfam; PF02815; MIR; 1.
DR Pfam; PF06459; RR_TM4-6; 1.
DR Pfam; PF01365; RYDR_ITPR; 2.
DR Pfam; PF02026; RYR; 4.
DR Pfam; PF00622; SPRY; 3.
DR PRINTS; PR00795; RYANODINER.
DR PRODOM; PD000012; EF-hand; 1.
DR SMART; SM00054; Efh; 2.
DR SMART; SM00472; MIR; 4.
DR SMART; SM00449; SPRY; 3.
DR PROSITE; PS50222; EF_HAND_2; 1.
DR PROSITE; PS50919; MIR; 5.
KW Calcium channel; Calcium transport; Calmodulin-binding;

KW Glycoprotein; Ion transport; Ionic channel; Multigene family;
FT Phosphorylation; Receptor; Repeat; Transmembrane; Transport.
KW TOPO_DOM 1 3090
FT TRANSMEM 3091 3110
FT TRANSMEM 3154 3172
FT TRANSMEM 3941 3960
FT TRANSMEM 3979 3996
FT TRANSMEM 4234 4257
FT TRANSMEM 4295 4315
FT TRANSMEM 4501 4521
FT TRANSMEM 4580 4602
FT TRANSMEM 4722 4742
FT TRANSMEM 4770 4788
FT TRANSMEM 4812 4829
FT TRANSMEM 4847 4869
FT DOMAIN 110 165
FT DOMAIN 172 217
FT DOMAIN 225 280
FT DOMAIN 286 345
FT DOMAIN 351 408
FT DOMAIN 670 808
FT REPEAT 853 966
FT REPEAT 967 1080
FT DOMAIN 1098 1221
FT DOMAIN 1423 1561
FT REPEAT 2693 2811
FT REPEAT 2813 2926
FT DOMAIN 4024 4059
FT REGION 853 2926
FT REGION 2619 3016
FT REGION 2775 2807
FT REGION 2877 2898
FT REGION 2998 3016
FT MOD_RES 2809 2809
FT CARBOHYD 4105 4105
FT CARBOHYD 4796 4796
SQ SEQUENCE 4969 AA; 565073 MW; FF6E084B974BBAD CRC64;
Query Match 43.0%; Score 6770.5; DB 1; Length 4969;
Best Local Similarity 45.6%; Pred. No. 0;
Matches 1401; Conservative 530; Mismatches 851; Indels 291; Gaps 58;
QY 4 ARGASGDDVDFLRTEEDVLCSTAT---GSRVCLAEFGNRRHLENIAD-KNIPP 58
2 ADGEGE-DEIQFLRTDDEVLCATATIKHQOKCLAEFGNRLCFLESTNSKNVPP 60
DB 59 DISQCFVTEQALSTRALQELVTAAGSENGK-----TSGHRTLYGNMI 104
61 DISCTFVLEQSLVLRALQELM-ANTVERSEGVQVDEKRFMMKTAQGQGHRTLLYGHAI 119
QY 105 LIRHLNSDMYLAQLSTS--SSQDKLAFDVLQOHSQGEACMTLHPASKORSEGEKRVGD 163
120 LIRHVSQMYLCCLTSTSRSTDKLAFDVLQEDTGEACMTLHPASKORSEGEKRVGD 179
DB 164 DLIIVSVATERYLHTTKENEVSIVASPFVTHWSVQPYGTGISRMKYGVYFGDYLRF 223
180 DLIIVSVSERYLHTSYGNGSLHVDAAFOQTLMVSAFISGSEAAQ--GYLIGGDVLRLL 237
QY 224 HGG-DECTIPSTWKDGGQNIIVYEGGSVMSQASIMRLRLARKTKMAGFIWTHPMKI 282
238 HHGMBECLTVPSGHEGEORRTVHYEGGAVSVHASSLMLETLRLVAWSSSHLRWQGFPL 297
QY 283 RHITGRYLGAVDQNELYLVSRREATTASCAFLQOEKQDKQKQVEDKDLVYGAPIIKY 342
298 RHVTGKTLSDMEDKNLLMDKEKADVSTATPSSSEKLDGVR-KVDDMGTSSEIKY 356
DB 343 GDSIVIVQHSSETGLMSKSYETTKKKGVKYEKKQAILHEEGKMDGLDFSSQSEESRT 402
357 GDSICVIGHVDPLGLWLTQSVDVKSVRMSIQRK-AIMHHEGHMDGLNLSRQHEESRT 415
QY 403 ARVIRKCSLPTKFNGETLQENRRHSMFPASVNL--GEMVCEEDLINTYQAQDEDEME 460
416 ARVIRSTVFLFRFRIGDALSKAKAS---SYDLPIESVSLSDLDLIGYHPDDEHLE 471

DB 2440 AFQMPRTIADGNVNEEDMSAGFCBPKAAVTLDRYGLIEVDFLHLIEVGLFDLKA 2499
QY 2626 ATWLDNDGCESDMALSMNRYIGNSILPLLKHAAYNEAENYASILDATLHTVRLSKN 2685
DB 2500 AASLDTPAALSATDMALANRYLCTAVLPILTRCAPIFAGTEHNASLIDSLHTVYRLSG 2559
QY 2686 RMLTKQREAVSFVYALTSANOPSMILKLRKLTVDVSKLSAYTTVALRLTLHYERCA 2745
DB 2560 CSLTKQRDSIEVCLISICQGLRPSMOMHLRLRLVDPVLNHAQMPKLTNNHYERCW 2619
QY 2746 KYVGSFGAGGAGFASGASDEKRLTMMLFNSIPDLSKMDYEPRLFGKALPCLIAICALP 2805
DB 2620 KYICLPFG-GWGNFGAASBEELHLSRLKFWGCI FALSQCKYQGLFALPCLSAVAGALP 2678
QY 2806 PDYSLSKNYDDEFYGEKQAAGLDNPQYDPOPIINTSSVALNMDNTLVOKFSEHYDAMA 2865
DB 2679 PDV-MESNTVSNM--EKQSMDESG-NFNQPPVDTNIIIPELGEYFIKVAHSHDXKS 2734
QY 2866 SKRIENGWYVGGESGSDSQKTHPLKRYNNMLNDYKERYEPRESIKALLAIGWSEHSE 2925
DB 2735 MDKLANGWYGEIYSDSKIQPLMKRYKLSEKEKIYWPFIKESIKTMLAMGWRTERR 2794
QY 2926 VDIPSNNRSMRQSGRPREIYVDSATPPFYNDHPYDMTNLTLSREMOWAEEFLAN 2985
DB 2795 ---EGDSMALYNKRIKISQTSVSDAA--HGYSPLAIDMSVNTSLDLHAAVEMMAEN 2848
QY 2986 AHDIWAKKKEEL 2998
DB 2849 YHNIMAKKKKTEL 2861

RESULT 10
RNR2_HUMAN
ID RNR2_HUMAN STANDARD; PRT; 4967 AA.
AC Q92736; O15411;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Ryanodine receptor 2 (Cardiac muscle-type ryanodine receptor) (RyR2)
DE (RyR-2) (Cardiac muscle ryanodine receptor-calcium release channel)
DE (hRyR-2).
GN Name=RyR2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND ALTERNATIVE SPLICING.
RC TISSUE=Heart muscle;
RX MEDLINE=96404895; PubMed=8809036;
RA Tunwell R.E.A., Wickenden C., Bertrand B.M.A., Shevchenko V.I.,
RA Walsh M.B., Allen P.D., Lai F.A.,
RT "The human cardiac muscle ryanodine receptor-calcium release channel:
RT Identification, primary structure and topological analysis.",
RT Biochem. J. 318:477-487(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 9-87 AND 533-681, DEVELOPMENTAL STAGE, AND
RP INDUCTION.
RC TISSUE=Heart muscle, and Myometrium;
RX MEDLINE=97220386; PubMed=9148749;
RA Awad S.S., Lamb H.K., Morgan J.M., Dunlop W., Gillespie J.I.,
RT "Differential expression of ryanodine receptor RyR2 mRNA in the non-
RT pregnant and pregnant human myometrium.",
RT Biochem. J. 322:777-783(1997).
RN [3]
RP NUCLEOTIDE SEQUENCE OF 4292-4479, AND TISSUE SPECIFICITY.
RC TISSUE=Cerebellum, and Hippocampus;
RX MEDLINE=98268728; PubMed=9607712; DOI=10.1016/S0306-4522(97)00612-X;
RA Martin C., Chapman K.E., Seckl J.R., Ashley R.H.,
RT "Partial cloning and differential expression of ryanodine
RT receptor/calcium-release channel genes in human tissues including the

RT hippocampus and cerebellum.",
RN Neuroscience 85:205-216(1998).
RN [4]
RP VARIANTS VTSIP LEU-2246; SER-2474; IYS-4104 AND CYS-4497.
RX PubMed=11208676;
RA Priori S.G., Napolitano C., Tiso N., Memi M., Vignati G., Blaise R.,
RA Sorrentino V.V., Danieli G.A.,
RT "Mutations in the cardiac ryanodine receptor gene (hRyR2) underlie
RT catecholaminergic polymorphic ventricular tachycardia.",
RT Circulation 103:196-200(2001).
RN [5]
RP VARIANTS PPVT SER-2328; ARG-4201 AND PHE-4653, AND VARIANT ARG-2958.
RX MEDLINE=21112862; PubMed=1157710.
RA Laitinen P.J., Brown K.M., Pilipo K., Swan H., Devaney J.M.,
RA Brahmabhat B., Donarum E.A., Marino M., Tiso N., Viltasalo M.,
RA Toivonen L., Stephan D.A., Kontula K.,
RT "Mutations of the cardiac ryanodine receptor (RyR2) gene in familial
RT polymorphic ventricular tachycardia.",
RT Circulation 103:485-490(2001).
RN [6]
RP VARIANTS ARVD2 PRO-433 AND ILE-2386.
RX MEDLINE=21096894; PubMed=1159936; DOI=10.1093/hmg/10.3.189;
RA Tiso N., Stephan D.A., Nava A., Bagatlin A., Devaney J.M., Stronchi F.,
RA Lardere G., Brahmabhat B., Brown K., Baice B., Muriago M., Basso C.,
RA Thiene G., Danieli G.A., Rampazzo A.,
RT "Identification of mutations in the cardiac ryanodine receptor gene in
RT families affected with arrhythmogenic right ventricular cardiomyopathy
RT type 2 (ARVD2).",
RT Hum. Mol. Genet. 10:189-194(2001).
RN [7]
CC -1- FUNCTION: Communication between transverse-tubules and
CC sarcoplasmic reticulum. Contraction of cardiac muscle is triggered
CC by release of calcium ions from SR following depolarization of T-
CC tubules (By similarity).
CC -1- SUBUNIT: Homotetramer (Potential).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q92736-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q92736-2; Sequence=VSP_005953;
CC -1- TISSUE SPECIFICITY: Heart muscle, brain (cerebellum and
CC hippocampus) and placenta.
CC -1- DEVELOPMENTAL STAGE: Expressed in myometrium during pregnancy.
CC -1- INDUCTION: By TGF-beta.
CC -1- DISEASE: Defects in RyR2 are the cause of familial arrhythmogenic
CC right ventricular dysplasia 2 (ARVD2) [MIM:600996]; also known as
CC arrhythmogenic right ventricular cardiomyopathy 2 (ARVC2). ARVD is
CC an autosomal dominant disease characterized by partial
CC degeneration of the myocardium of the right ventricle, electrical
CC instability, and sudden death. It is clinically defined by
CC electrocardiographic and angiographic criteria; pathologic
CC findings, replacement of ventricular myocardium with fatty and
CC fibrous elements, preferentially involve the right ventricular
CC free wall.
CC -1- DISEASE: Defects in RyR2 are the cause of an autosomal dominant
CC form of stress-induced polymorphic ventricular tachycardia (VTSIP)
CC [MIM:604772]; also known as catecholaminergic polymorphic
CC ventricular tachycardia. VTSIP is a genetic arrhythmogenic
CC disorder characterized by stress-induced, bidirectional
CC ventricular tachycardia that may degenerate into cardiac arrest
CC and cause sudden death.
CC -1- DISEASE: Defects in RyR2 are a cause of familial polymorphic
CC ventricular tachycardia (PPVT) [MIM:192605]. PPVT is an autosomal-
CC dominant, inherited disease with a relatively early onset and a
CC mortality rate of approximately 30% by the age of 30 years.
CC Phenotypically, it is characterized by salvos of bidirectional
CC and polymorphic ventricular tachycardias in response to vigorous
CC exercise, with no structural evidence of myocardial disease.
CC -1- MISCELLANEOUS: The calcium release channel is modulated by calcium
CC ions, magnesium ions, ATP and calmodulin.
CC -1- MISCELLANEOUS: The calcium release channel actively resides in the
CC C-terminal region while the remaining part of the protein

CC constitutes the 'foot' structure spanning the junctional gap
CC between the SR and the T-tubule. It is possible that the foot
CC structure interacts with the cytoplasmic region of the
CC dihydropyridine receptor.
CC -1- MISCELLANEOUS: Ryanodine is an alkaloid that binds to the Ca-
CC release channel in junctional SR and modulates its activity.
CC -1- SIMILARITY: Belongs to the ryanodine receptor family.
CC -1- SIMILARITY: Contains 1 EF-hand domain.
CC -1- SIMILARITY: Contains 5 MIR domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL/ X98330; CAA66975.1; -; mRNA.
DR EMBL/ Y08218; CAA69395.1; -; mRNA.
DR EMBL/ X91869; CAA62975.1; -; mRNA.
DR EMBL/ AJ002511; CAA05502.1; -; mRNA.
DR PIR/ S72269; S72269; Homo sapiens.
DR EMBL/ ENSG0000019826; Homo sapiens.
DR HGNC; HGNC:10484; RYR2.
DR MIM; 180902; -.
DR MIM; 600996; -.
DR MIM; 604772; -.
DR MIM; 192605; -.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0015278; P:calcium-release channel activity; TAS.
DR GO; GO:0006936; P:muscle contraction; TAS.
DR GO; GO:0008016; P:regulation of heart contraction rate; TAS.
DR GO; GO:0007165; P:signal transduction; NAS.
DR InterPro; IPR000699; Ca-rel_channel.
DR InterPro; IPR01682; Ca/Na_pore.
DR InterPro; IPR011992; EF_Hand_Type.
DR InterPro; IPR02048; EF_Hand_Ca_Bd.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR003608; MIR.
DR InterPro; IPR003032; Ryanodine_recept.
DR InterPro; IPR01215; Ryanodn_recept.
DR InterPro; IPR009460; Ryanodn_recept.
DR InterPro; IPR03877; SPRY_receptor.
DR PANTHER; PTHR13715.SF1; Ryanodn_receptor; 10.
DR Pfam; PF000036; ehand; 1.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF02815; MIR; 1.
DR Pfam; PF06459; RR_TM4-6; 1.
DR Pfam; PF01365; RYDR_ITPR; 2.
DR Pfam; PF02026; RYR; 4.
DR Pfam; PF00622; SPRY; 3.
DR PRINTS; PR00795; RYANODINER.
DR PRODOM; PD000012; EF-hand; 1.
DR SMART; SM00054; EFh; 2.
DR SMART; SM00472; MIR; 4.
DR SMART; SM00449; SPRY; 3.
DR PROSITE; PS50222; EF_HAND_2; 1.
DR PROSITE; PS50919; MIR; 5.
KW Alternative splicing; Calcium; Calcium channel; Calcium transport;
KW Calmodulin-binding; Cardiac myopathy; Disease mutation; Glycoprotein;
KW Ion transport; Ionic channel; Multigene family; Phosphorylation;
KW Polymorphism; Receptor; Repeat; Transmembrane; Transport;
KW TOPO_DOM; 1; 3089; Cytoplasmic (By similarity).
FT TRANSMEM 3090 3109 M' (Potential).
FT TRANSMEM 3153 3171 M1 (Potential).
FT TRANSMEM 3940 3959 M1 (Potential).
FT TRANSMEM 3978 3995 M2 (Potential).
FT TRANSMEM 4233 4256 M3 (Potential).
FT TRANSMEM 4294 4314 M4 (Potential).
FT TRANSMEM 4500 4520 M5 (Potential).
FT TRANSMEM 4578 4600 M6 (Potential).
FT TRANSMEM 4720 4740 M7 (Potential).
FT TRANSMEM 4768 4786 M8 (Potential).

FT TRANSMEM 4810 4827 M9 (Potential).
FT TRANSMEM 4845 4867 M10 (Potential).
FT DOMAIN 110 165 MIR 1.
FT DOMAIN 172 217 MIR 2.
FT DOMAIN 225 280 MIR 3.
FT DOMAIN 286 343 MIR 4.
FT DOMAIN 351 408 MIR 5.
FT DOMAIN 670 808 SPRY 1.
FT REPEAT 853 966 1.
FT REPEAT 967 1080 2.
FT DOMAIN 1098 1221 SPRY 2.
FT DOMAIN 1423 1561 SPRY 3.
FT REPEAT 2692 2810 3.
FT REPEAT 2812 2925 4.
FT DOMAIN 4023 4058 EF-hand.

Query Match 43.0%; Score 6769; DB 1; Length 4967;
Best Local Similarity 45.6%; Pred. No. 0;
Matches 1399; Conservative 536; Mismatches 854; Indels 276; Gaps 58;

4 ARGASRDVSPFLRTEDMVCISCTAT---GSRVCLAAEGFGRHGFLENIAD-KNIIP 58
2 ADGSEGR-DEIQFLRTDEVVLCCTATIHKEQQCLAAEGFGRHLCFLESTSKVNP 60
59 DLSCVFVIEQALSVRALQELVLTAAAGSETGK-----TGSGRHTLLYGNAI 104
61 DLSTCTFLBQSLSVRALQELT--ANTYKESRGQVDVEKKMKMTAGCGHRTLLYGRAI 119
105 LLRLHNSDMYIACISGS--SSQDKLAPVGLQDSQSGACWTTLHPASKORSSEKRVGD 163
120 LLRLHSYGMVLCISSTSRSSSTDKLAIPVGLQEDTGTGACWTTIHPASKORSEKRVGD 179
164 DLLIVSVATRYVLTHTKENBSYINASFHTHMSVOPGTGISMKVYVFGGVDLPFF 223
180 DLLIVSVSEKRYLLTSGNSLHVDAPQOTLMSVAPLSSGSAQ--GYLIGVDLALL 237
224 HGG-DECLTPTWTXGQGNIVVYEGSGVMSQARSIMRLTAKTNAAGFINVHPRI 282
238 HGHMDECLTVPSGSHGEQRRTVHYEGGAVSVHARSIMRLTAKTNAAGSHIRNGQPRRL 297
283 RHITTGRLGVNDQNELYLSREBAITTASCAFCIRQEKDDQKQVLEDKOLEVIGAPITKY 342
298 RHVTYTKXLSLMBEKNLLAMDKEKADVSTAFTRSSK-EKLDVGRKVDGKMTSEIKY 356
343 GDSVTVIOHSEGTGLMLSYKSYETKKKGKGVKESQALIHESGKDDGLDPSRQSEBSRT 402
357 GDSVCTYIOHVDGTMLTYSQVDVSVRSGSIQR-ALMHEGHMDGISTSRSHESRT 415
403 ARVIRKSSSLPTKEFINGLETLOENRRHSMFPASVNLGEMWCLDLINYPADPEDEHE 462
416 ARVIRSVPLFENRIRIGLDALSKKAKAST--VDLPISVSLSQDLIGFRRPDEHLE 473
463 EKQKKFALNRNRODLFOEBGILLNILEAIDKINITYSQGFLAGFLADESGQSWEMISGY 522
474 DKQNRRLAKNRQVLFQEBGMINVLECIDRLAHYSSAARPAD--VAGREAGESKSIINS 532
523 LYQLLAIIIGNHTNCAQFANSRLNMLFSLSGQAAGEGTMCDVHLCULIDPEALNM 582
533 LYELLAALIRNRNCAQFSGS--LDWLISRL--ERLEASSGILEVLHCVLVESEPALNI 588
583 MRDEHIKITYLSLEKGRDPVLDVLCSLCYGNGVAARSSQNNICDYLTPKNTLLQYAL 642
589 IKEGHIISISLDRGRNKHVLDVLSLCYCHGVNARSNHLCDNLIPRRDLLQTRL 648
643 VDHVSVRPNI FVGRVSGSAVYRRVFEVMTDIEK--TTHMPLIRIGMANTTYVYPYG 701
649 VNHVSNRPNIFLGVSBSAQYKKMYELMWDHTEPRVTAEAATHLRVGMASTEYSYPYG 708
702 GGEKMGNGVDDLLXSYGPDGAYLMSGKRTPVNRTAABRYTIKKGVIGALALTYPI 761
709 GGEWEGNGVDDLLFSYGPDGLHMSGIARTVSPN--QHLTLTDVVISCLDLSASI 766
762 NFMENGVAVTGSFTNPNLBMGFPPVVISCSKSLSCRFLLGEGHGLRYAAPEGYSPLVEST 821

[illegible]


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Db      1410 LADDDRDYDFLMQSTSTYYSVRIFFPGQEPANVWVWMTTSDFOYDTCGFDLDRVRYTVTL 1469
      1593 TDYDVBVENVWNSQCMVRADSLVNVMAEATKAKASQGMFQCSVDTSVGSFPCBG 1652
      1470 GDEKGVHBSIKSNCTMCA---GESMSPGQGRN--NGLEIGCVVDAAISGLTLTFANG 1524
      1653 KQSPFKMPEPTKLPALFVEATSKELIQIEIGRSATSLPLSAVALPTSDKHVLPQPP 1712
      1525 KEISTYVQVPSIKLPPAVPAQATSPVQFELGRINWNPILASGLEFSKHKNPVQCP 1584
      1713 RLKVQCLKPHQWARPVNSTQVHALKSIDIRGWSMLCEDAVSMLAHIPEEDRCIDLEP 1772
      1585 RLHVQELSHVLSMRMPQFLKVDVRSISERQGLVQCLDPLQFMSLHIPEENSVDLLEL 1644
      1773 IEMDKLSFHSHTLTYALCYOSNYRAAALCTHNDQKLYALIOSQVNSGFLRQGFYD 1832
      1645 TEGEBLLKFPYHTLTRYSAVCALGNHRVALALCSHVDLPQLYAIENKYPGLIRAGYD 1704
      1833 LLLALHLSHATTMEACKNFVILPLGPELKA--LYEPPDMGHSLSL-OTESVAPQMKMT 1689
      1705 LLLDILHSYATARLMMNNEYIVPMETKSTITLFPENCKGGLPGIGLSTSLRPNQPS 1764
      1890 DIASITEISN--LYSPPELEVARBFVQALABAVETNOVANDPVGSSNENLPLPLI 1946
      1765 --SPFSVISNECYQSPFPDLIKGKTIOMLTEAVGEGSLNARDVGGTETFLFVPLI 1822
      1947 KLVDRLLVGMDEDEVEKLLIM-----TPEETWDSFDKE-----GKDR 1986
      1823 KLFYTLIMGI FHNEDLKHIQLIBSVFKEAATPEESDSTLEKESVDDAKLQGADEE 1882
      1987 -----HRKGLHMKVAGAKQWCVLLOHNDILOHRVEATIAFANDPVGDLQTDQLR 2040
      1883 AKGKRPKEGLQKLPKPVKQKMLQYLCDQVHRIEALVABDDVVALQDNQRF 1942
      2041 RYTBKQS-DLPSAVAAKTRBRCPPREQWNAILSPKLBBDKENCPCGEBELIARME 2099
      1943 RYNEVQALMSAALTARKTKBFRSPQBDIMLNLFK---DDKSCPCPEBIRQDLDD 1998
      2100 FHDTLMAHVSLLAQEPDAENQEPKAPGGLNYIINTVKELEB--AKAIEBPCK 2157
      1999 FHDLMTHCGIELDEDSLDGNSDLTR---GILLSVGRVYLLKKKQABKPVESDSK 2054
      2158 TPBEKTRKVLQITVNAABSOJETPLVEMPSLVRQYDAVGEILRALKTYVINAKT 2217
      2055 S--STLQQLSETWTRRAQSVLEDPFLVAMFLLRQDGLGSLVRLPKTTINGVS 2112
      2218 KLDVAEMWVGLSGIRALLPVQMSQEBEELMKRLMKNHTPFQHPDLIRVLRVHENW 2277
      2113 VEDTINMLASLGOIRSLLSVRMGKEBKMLIRGLGDIANNKVFQHNLMRALGMHETM 2172
      2278 AVMMNTYGRPAQAOQSDQPSQPVADSKSDKOTSHENVAACRFLCYFCTGRNQAMF 2337
      2173 EVWVNVVLG-----GSESKE--ITFPKVNACCRFLCYFCRISRONQAMF 2215
      2338 DHDPLLENSNIILSRPSLSTPTDVAAGSLMENTELALAHRYVEKIAVVISRGLO 2297
      2216 DRLSYLLENSVGLASPAKMGSTPLDVAALSVMDNNELALAKRPDLKRVRYLAGGLQ 2275
      2398 SNBELVEKGYPDGLMDPVEGERYLDPLRFCVWVNGSVEENANVIRLLIRPECLGAL 2457
      2276 SCQMLVSKYFPDIGNVVEGERYLDPLRPAVPCNGSEVERANVYVALLIRPECPAL 2335
      2458 RGE--GEGLLKAVDANKMSERIDRRKLREMEQSG--DVNFSPHLPESDEDEYDTGA 2513
      2336 RGEQGNGLLAMEBAIKIAR-----DPSRQGPSPNGSSKTLTTEBEDDTIHNGN 2386
      2514 AILNFTYTLVDLGRCPDAGVIALGKNSIRARATIRSLVPLEDLOGVSLRFTLNP 2573
      2387 AILNFTYTLVDLGRCPDAGVIALGKNSIRARATIRSLVPLEDLOGVSLRFTLNP 2446
      2574 AGEBRPKSDMPSGLIPGHKQSVGLFLERVYGIEQELFYKLLBEAFLPDLRAATMLDRND 2633

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Db      2447 KQGNVVEPDKSAGFCEDHKAAMVTLFDRYVGIQVDFLHLLEVGFLPDLRAASLDPTA 2506
      2634 GCESDNALSMKRYTIGNSILPLLIKHAFFYNEAENYASLDATLHTVYRLSKNMLTKGOR 2693
      2507 LSAIDMALNLRILCTRAVLEPLTRCAPLFRAGTEHHSLSDLSLHTYRLSKGSLTRQAR 2566
      2694 EAVSDPLVALTSAMQPSMLIKLRKLTVDVSKISEYTTVALRLTLHYERCAYYSTGA 2753
      2567 DSIEVCLLSICQLRSPSMQHLRLRVFDPPLINBAKMPILKLTNHYERCWCKYCLPG- 2625
      2754 GQAPGASDPEERKLTMMPLPSNIFDLSKNDVPEELFGKLPCLTIAGCALPPDYSLSN 2813
      2626 GWGNFGAASBEELHSRKLPFWGIFDALISQKRYQELFKLPLCLSAVAGALPPDY--MESN 2684
      2814 YDEPFYKEQAGADLNPQYDPPQINTSVSVALNNDLNTTYQKSEHYHDAMARKLENGW 2873
      2685 YVSM--EKQSSNDSEG--NPNPQVDTSNITTEKLEFPIFKAEHSHDKMSDKLANGW 2741
      2874 VYEGMSDSQKTHPLKPYNMLNDYKERYKEPRESLKALAIAGSVESHEVDIPSNR 2933
      2742 IYGEIYSDSKVQPLMKPYCLLSKEKEIYRWPILKESLKTMLARTWRTKTR----EGDS 2797
      2934 SSKRQSGSGRPELIVTDSATPVDNPHVDNTNLTLSREMONMARLADNADIAWK 2993
      2798 MALYNTRIRISQTSQVSDAA--HGVSPPRAIDMSVTLSDHAMEEMAEYHNIAWK 2855
      2994 KKEEL 2998
      2856 KKEEL 2860

RESULT 12
O6RNG_MOUSE PRELIMINARY; PRT; 4967 AA.
ID O6RNG_MOUSE PRELIMINARY; PRT; 4967 AA.
AC O6RNG_MOUSE PRELIMINARY; PRT; 4967 AA.
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cardiac Ca2+ release channel.
GN Name=Ry2;
OS Mus musculus (Mouse).
OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MBDLINE=99403027; PubMed=10473538; DOI=10.1074/jbc.274.37.25971;
RA Zhao M., Li P., Li X., Zhang L., Winkfein R.J., Chen S.R.;
RT "Molecular identification of the ryanodine receptor pore-forming
RT segment.";
RL J. Biol. Chem. 274.25971-25974 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Chen S.W.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF295105; AAC34081.1; -; mRNA.
DR Ensembl: ENSMUSG0000021313; Mus musculus.
DR MGI: MGI:9685; Ry2.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0016020; C: membrane; IEA.
DR GO: GO:0005262; F: calcium channel activity; IEA.
DR GO: GO:0005509; F: calcium ion binding; IEA.
DR GO: GO:0005219; F: ryanodine-sensitive calcium-release channel. . .; IEA.
DR GO: GO:0006874; P: calcium ion homeostasis; IEA.
DR GO: GO:0006816; P: calcium ion transport; IEA.
DR GO: GO:0006812; P: cation transport; IEA.
DR InterPro: IPR000699; Ca-rel channel.
DR InterPro: IPR001682; Ca/Na pore.
DR InterPro: IPR002046; EF_hand_Ca_bd.
DR InterPro: IPR005821; Ion_chan.
DR InterPro: IPR003608; MIR.
DR InterPro: IPR003032; Ryanodine_recept.

```


Qy	1891	DLILIALHSHAATMEAKCKNRPVILPDEPLKA--LYEPMGHSLAST--QTESRPMOK	1887
Dp	1704	YDLIDLHSSSYAIRLMMNNEFFVPMTEERTSITLLPDEKNGKGLPGIGLSTSRPWR	1763
Qy	1888	MTDIAESIETISN--LYSPYFPLEVAEFPYMOALAEVETNOVNRDPVGSNENLPLP	1944
Dp	1764	FS--SPSPVJISNOCYOYSPERPDILAKNTIOMLTEAVKGSLSHARPVGSTTEFLVP	1821
Qy	1945	LIKLVDRLLVGMNRDEVEKLLIMTNPETW-----DPSFDKE--19822	
Dp	1822	LIKLPYTLILINGIFINEDLIKHLQILRPSVPEKAAVPEEGGTPEKEISIDAKLEGEEB	1881
Qy	1983	--GDEHKKGLHMMAGACLOMCOYUOLHNDIOLBRVAVIATAFADPFQDLOTOLR	2040
Dp	1882	AKGGRPRRPGGLQMKLPVPKLOMCLLOYICDCVRRIRIATAVAFSDPAKQODNORF	1941
Qy	2041	RYTEIKOS-DLPSAVAACKTRRPFRCPRRCONAALISFGLHEEDKENDPCCEELIARNE	2099
Dp	1942	RYNEVMOALNNASALTARKTEPSPRPOEQIMLNNFK-----DDXSEPCPEEIRDOOLD	1997
Qy	2100	FHDITMAVSLHALQEPDPAENQEBEAKPAGFKLNIINTVKELBEEAKAIEEPPKXT	2159
Dp	1998	FHEDLMTGCIELDEBGSIDGSNDLITR-----GRLLSYERKTYLKK--KOAEKPVASDS	2051
Qy	2160	EE--KFRVVLQTIYNMAEBOIEFRKLVREMFSLVNOYONAVGELLPALEKTYVINAKT	2217
Dp	2052	RKCSLQOOLISETWRAQESVIBEPPELVRAMFVYLHNOYOGIGLVALPKYTINGVS	2111
Qy	2218	KLDVAEMVVGJSQIRALLPYOMSOEELERKRLMKLVNNTPFQHPDLIVLRVHEVM	2277
Dp	2112	VEDITNINLASGOIRSLISVYMGKEEKCLMRGLADIVNNKVFYOHPLYMALGHEVM	2171
Qy	2278	AVMMNTLGRRAQASDAOPSSQPAVADESKEXTSHENVACRFLCYFCRTGRONQXMF	2337
Dp	2172	EVMMNVVVG-----GSESKX--ITPRKVANCCRFICYFCRISRONQXMF	2214
Qy	2338	DHFPPLLENSIILSRPSLRGSTPLDVAVSSLMTEALALRHYLEK--IAVTLSRGL	2386
Dp	2215	DHLVYLENSVGLASPMRGSTPLDVAAVMDNNEIATLARREPDLEKVAARYAIAAGCL	2274
Qy	2397	QSNSEIVEKGPDPDGMDFVEGERYLDLPRFCVMNNGSEVENANULVRLIRREPCGPA	2456
Dp	2275	QSCOMLVSKGPDJGMNPFVEBERYLDLPRVAFNGSESVENANVVALIRREPCGPA	2334
Qy	2457	LRGB-GBGLIKAIYDANKMSERIDRRKLRMEBOGDVNFPHLPES-----DEDE	2506
Dp	2335	LRGBGNGGLLAMEAETKIAE-----DPSRGRPSTGSSSKTLIDEEED	2379
Qy	2507	DYIDTGAAILNFCTYLDLGRCAPDAGVIALGKNESIRADALIRSLVPELDLOGVLSLR	2566
Dp	2380	DTIHNGAIAIMFYAALIDLGRCAPEMELIHAGKEAIRISIRSLIRPLGDLGVISIA	2439
Qy	2567	FTLNNPAAGEBRPSDMSGILPHGKOSVGLFERYVGTIEROELFYGLLEBAFLPDIAA	2626
Dp	2440	FQMTTIAKOGVNERBDSAGFCPDHKAMAVFLDVVGIEVQDFLHLEGFRLDIAA	2499
Qy	2627	TMLDRNDGCEBDMALSMNRVYIGNSILPLLIKGAAFYVNEAEVAYASLDATITVYRLSKOR	2686
Dp	2500	ASLDOTALASIDMALALNRYCTAVLPLRTTCARLPAGTEHNASLISLMTIVYRLSGC	2559
Qy	2687	MLTYGOREAVSDFLVALTSAMOPSMLKLRKLTVDVSKSEYTTVALRLTLHYERCAK	2746
Dp	2560	SLTRAQORSDISEVCLISICGOLRPSMMOHLRLVFDVPLINEHAKMPLKLTNNHYERCMK	2619
Qy	2747	YUGSTAGCGGAFGASDEEKRLTMMLEPNISIDSLSKMDYEBELRGSKLPCILAGCALP	2806
Dp	2620	YYCUPG-GWNGFGAASBEELHLSRGLFGIGTIDALISQKYEOLBFLGALPCISAAVAGALP	2678
Qy	2807	DYLSIKNYDDEFYGEKAAGDLNDPQYQPOEINTSSVALNNDLNTIYQFSEHNDAAAS	2866
Dp	2679	DY-MESNVVSM--EKOSMSDEG-NFRPQYVDVTSNITIPKLEFYINKVAHSHDKSM	2734
Qy	2867	RKIENGWVGGGMSDQKTHPRLKPYNMLANDYEKERYKEPVRESUKALALAGMSVERSEV	2926

Dd 2735 DKLANGMYIGSEIYDSSKIQPMPKEPTVGLSLEKEKEIYRWIKSLKTMLMWGRIETR- 2793

Qy 2927 DIPSNNSMNRÖSKSGRPPEIVTDSATFPDYNPHEVDNTNLTLSREOMMAERLADNA 2986
 ::
Db 2794 ---BGSDMALYNRRIRRSISQTSQVSIDAA--HGVSFPAIDMSVTLSRDLLHAMAMEMALeny 2848

Qy 2987 HDIYAKKKKEEL 2998
 | : ||||| |

Dd 2849 HNIWAKKKCKEEL 2860
 | : ||||| |

RESULT 13

OSVWP1_HUMAN
ID OSVWP1_HUMAN PRELIMINARY; PRT; 4965 AA.
AC OSVWP1;
DT 01-FEB-2005 (TREMBLrel_29, Created)
DT 01-FEB-2005 (TREMBLrel_29, Last sequence update)
DT 13-SEP-2005 (TREMBLrel_31, Last annotation update)
DE Ryanodine receptor 2 (Cardiac).
GN ORFNames=RP4-62637.1-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
CC Homo.
OK NCBI_TaxID=9606;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RA Wall M.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RN NUCLEOTIDE SEQUENCE.
RA Coville G.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RN NUCLEOTIDE SEQUENCE.
RA Moore M.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [4]
RN NUCLEOTIDE SEQUENCE.
RA Pearce A.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [5]
RN NUCLEOTIDE SEQUENCE.
RA Griffiths C.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [6]
RN NUCLEOTIDE SEQUENCE.
RA Clark S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [7]
RN NUCLEOTIDE SEQUENCE.
RA Tracey A.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1-SUBUNIT: Myosin is an hexamer of 2 heavy chains and 4 light chains
 (by similarity).
CC -1-DOMAIN: Each of the four internal repeats contains five
 hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
 positively charged transmembrane segment (S4). S4 segments
 probably represent the voltage-sensor and are characterized by a
 series of positively charged amino acids at every third position
 (by similarity).

DR EMBL; AL391809; CA114440.1; -; Genomic DNA.
DR EMBL; AL442065; CA115350.1; -; Genomic DNA.
DR EMBL; AL513130; CA115936.1; -; Genomic DNA.
DR EMBL; AL356773; CAH73928.1; -; Genomic DNA.
DR EMBL; AL445473; CAH71393.1; -; Genomic DNA.
DR EMBL; AL365332; CAH71369.1; -; Genomic DNA.
DR EMBL; AL359924; CA122065.1; -; Genomic DNA.
DR EMBL; AL513130; CA122065.1; JOINED; Genomic DNA.
DR EMBL; AL359924; CA114440.1; JOINED; Genomic DNA.
DR EMBL; AL356773; CA114440.1; JOINED; Genomic DNA.
DR EMBL; AL365332; CA114440.1; JOINED; Genomic DNA.

Qy 1057 DPTGEOHALLLEASKQKQADFTTTRAEKRYAVSSGKWFPEFELITAGPMKVGMAHDM 1116
Dy 1063 EAP--DQHAARAEVCSGTGERFRIFRAEKTYYAVAGRWFEFETVITAGDMRWGMSRQGC 1120
Qy 1117 ARGMMLODENSMAFDGNEEKYVSGNTESFGKQMAVDVGVPLDLIDKTIISPLNEL 1176
Dy 1121 QPDELGSDEDAFAFDGFKQRMHOGN-EHYGRSQADVDVGCWDMNHEHTMPTLNEBI 1179
Qy 1177 LMDALGETTPADVO-GDNFVPACTIAGVOKARLYTGODVNTLKKFTTCGLQEGEPFCV 1235
Dy 1180 LLDSSGSLAKDPDVGDFPIVCSLGYAVQGRMFGVDSTLKFITCGLOEGEPFPAV 1239
Qy 1236 NMKQDVHTMYTKDQPIFENTDEMIDTRIDVTRIPASDTPPCLKISHTFETMEKANE- 1294
Dy 1240 NTNRDITWMLSKRLPQFQVPSNHE-HIETRIDGTIDSSPLCKATYQSGS-QUSNTDI 1297
Qy 1295 -PLSLSPVTCNNEIIDEAKARRWEIKRQOILMKAVAEQMAHIDQMRSGF--TM 1351
Dy 1298 MFYLSMPEIBCAEYF-----SKTVAGGLFG-----AGLFGPK 1329
Qy 1352 NDIGLHYEDNOBELPSGKMKRLPSRPPKSGMTRGVITQNYNNLOPGOVGMHSTSEA 1411
Dy 1330 NDLEDYDADSPPEVL---MKTAA-----HGLVPEPRVD----- 1358
Qy 1412 EMATYDLGAQGLTPDDKKOKRGRSPFKFRSGKSSDRAKSRKSTPDPSPDTEVSPER 1471
Dy 1359 -----KDXEA----- 1368
Qy 1472 GARRPNPOIKVSOANQRYNGNANPGRNLVGSQVGLMAMTPTODRKOMTTSTLAQSTTE 1531
Dy 1369 NNHMDYOAEKPSRLKQRETLRRTKP-----DYSTSHSARLTED 1406
Qy 1532 TVNGEIPBAECLLINEFYGVRIYQODPTHVYIQTWTOYHLHSQFNQSKVTKSSVI 1591
Dy 1407 VLADRDYDPLMOTSTYTYISRIYFGQSPANVWGMITSDFHQDTGTDRAVATVVT 1466
Qy 1592 ITDDYDRVENVNQSCYMNABDELXNEMAEATKAGASQGMFIGSVDTSGVSFTCE 1651
Dy 1467 LGDEKGNKHESI KSNCCYMWCA---GEMSPGQGRN-NNGLEIGCVVDAASGLTFLAN 1521
Qy 1652 GKDTSPFKMEBETKLPALITVEATSKELQIEGRATSLPLSAAVLPSTDKAVIPDP 1711
Dy 1522 GKELSTYQVPEPSTGLPFAVPAQATSNNVQFELGRINQVPLSAGLFKSHKNEVPQCP 1581
Qy 1712 PRLVQCCLPKQMAVBNOSLOVHALKLSDRGMSMLGEDAVSMALHIPREDICITLE 1771
Dy 1582 PRLVQFLSHVLSMSPNQPLKVDVSRISERQGMVQCLDPLQFWSLHPEENRSVDLLE 1641
Qy 1772 PIEMDKLSFHSHTLTLYAALCYOSNYRAAHLCTHVQKOLLYAIOGQVSGPLRQGFY 1831
Dy 1642 LTBQBELKPYHTIKLYSAVCALGNHVAHLCHVDEPOLLYAIENKTPGILLRAGY 1701
Qy 1832 DLLIALHESHATTWACKNEFVJPLGPELKA--LYEBPDNGHSIRSL-QTESVAPQMK 1888
Dy 1702 DLLIDHLSYATARLMANNEXIYVMTBETKSTITLFPDENKKGGLPGIGLSTSLPRMQF 1761
Qy 1889 TDIBASTIEISN---LYGPFYPLVABRFVQALABAVTQVNHNDVVGSSNEULFPL 1945
Dy 1762 S--SPSPVSIENECYQSPBPPLDILKSKTIQMLBAVKEGSLHARDPVGITTEFLFPL 1819
Qy 1946 IKLVDRLLLVGMMDDEVEKLLIM-----TNPBTWPSFDGE-----GKD 1985
Dy 1820 IKLFTTLIMGI FHNEDLKHILQILIEPSVFKBAATPEESDTEKELSVDDAKLOGAGEE 1879
Qy 1986 E-----HRKGLHMKMAEGAKQWCVYLLOHLNDIQLHRRVEALITAFADPVGDLQTDQL 2039
Dy 1880 EAKGQKRPKEGILLQKRLPEPVQLQWCLLOYLCDQVHRRITAIYAFSDDFAKQADQOR 1939
Qy 2040 RRYETIKOS-DLPSAVAAKTRERFCPREROMALSTFKHLEEBKENCPCGEHELIAAMN 2098
Dy 1940 FRYNEVMOALNMNSALTARKTKEFRSPQEOJNMLNFK---DDKSSCPCEBEKIRDLL 1995
Qy 2099 EFHDTLMHVSILHALQEPDAENQBPRAKPGAFGLYNIINTVKLEEE--AKAIEBPBK 2156

Dy 1996 DFHEDLHTHCIGIELEBDSLDGNSDLTIR-----RRLSLVEKVTYLLKKQAEKPEVSDSK 2051
Qy 2157 KTRPEKPKVLIQITVNMABESQIETPKLVEMFSLVROQDVAAGELIRALEKTYVINAK 2216
Dy 2052 KS--STIAQLISETWKMAQSVIEDPELVAMVLLHRODGGIGVLRALPKTYTINGV 2109
Qy 2217 TKLDVAEMWVGLSQIRALLPVQMSQEBEELMKRLMKLVNNHTFQPHDLIRLVHENV 2276
Dy 2110 SVEDTINULASLQIRSLSTRMKGEBEKLMI RGLGDIIMNKVYQHPNMLRALGMHEBT 2169
Qy 2277 MAVMNTYGRPAQASDAQSSQPVABDSKQTSHEWYVACCFPLCYFCGTGQONQAM 2336
Dy 2170 MEWVNVTVG-----GGSKSK-IYFPKRVANCCFPLCYFCRISHQONQAM 2212
Qy 2337 FDHPDPLENSNILLRSPSLRGSTPLDVAYSALMENTELALAEHYLEKIAVYLSRGL 2396
Dy 2213 FDLHSTYLENSSVGLSAPMKGSTPLDVAASVMDNNEELALAEHPDLEKVRILAGGGL 2272
Qy 2397 QSNSELVEKGYPDLGMPVBEGERYLDPLFCVWVGSVEENANLVIRLLIRRECLGPA 2456
Dy 2273 QSCQMLVSKGYPDIGMNPVEGERYLDPLRFVAFPCGSSVEENANVYVLLIRREPCBPBA 2332
Qy 2457 LRGE-GEGLKAIYDANKMSERLADRRKLREMEQBG---DVNFSHPLPESDEBDYDUTG 2512
Dy 2333 LRGEQNGLLAAMEAIIKAE-----DPSRDGSPNAGSSKTYLDEEBEDDTIMG 2383
Qy 2513 AALNPFYCTIYDLGRCAPDAGVIALGNESLBARILRSIVPLEDIOGVSLRPTLNP 2572
Dy 2384 NAITFTYSALIDLGRCAPEMHLIAGKEAIRSIIIRSLIPGLDLGVASIVAQMTI 2443
Qy 2573 AAGEERPKSDMPGSLIPGHKQSVGLFLERVYGIETQBLFYKLBEAPLPDRAATMLDRN 2632
Dy 2444 AKQGNVVEPDMASGCPDHKAAMVLFDRVYGIIVQDPLHLLEVGFLPDLRBAASLDTA 2503
Qy 2633 DCGSDMALSNRYIIGNSILPILIKHAYFYNEBENVASLDATHTVTRLSKRMVLYGQ 2692
Dy 2504 ALSATDMALAINRYLCTAVLEPLTRCAPLFGTEHHA SLIDSLHTVTRLSKGSILTYAQ 2563
Qy 2693 REAVSDPLVALTSMOPSEMLKLKRLTVDSKLSERYTVALRLTTHYERCAKYGSTG 2752
Dy 2564 RDSLEVCLLSTCGQRPSPMOMHLRLVFDVPLNEHAKMPLKLTNHYECMKTYCLPG 2623
Qy 2753 AGOGAFGASDEBERLTMWLSNIPDSLSKMDYEBELFGKALPCLIAIGCALPPDYSLSK 2812
Dy 2624 -GKNGFGAASBEELHSKRLFWMGIFDALSQKXYQELFKLALPCLISAAAGLPPY -MES 2681
Qy 2813 NYDDEFYGKEQAAQDLNDPOYDPOPIINTSSVALNNDLNTIVQKSEHYHDAASKIENG 2872
Dy 2682 NYVGMN--EKQSMDSBG-NFNPOVPDTSNITIEKLEYFINKYAEHSHDKMSMDKLANG 2738
Qy 2873 WYBEGMSDOSKTHPRKLPKPYMLNDYERKKEPPEBESLKLALIGSVHSEVDIIPSN 2932
Dy 2739 WYBGIYSDSKSVPLMKPYKLISEKEKEIYRWPKSLKMLMGMWIEKTR-----EGD 2794
Qy 2933 RSSMRBOSKSGRPEPITVDSATPDVNPVPHVDVNTLTSREOMWABRLADNAHDIYAK 2992
Dy 2795 SMALYNKTRRISQTSQVSVDAH--HGSPRAIDMSVTLSSDLAMAMEMALENTHINIAK 2852
Qy 2993 KKEKEL 2998
Dy 2853 KKKMEL 2858

RESULT 14
Q91313 RANCA
ID Q91313 RANCA PRELIMINARY; PRT; 5037 AA.
AC Q91313
DT 01-NOV-1996 (Tremblrel. 01. Created)
DT 01-NOV-1996 (Tremblrel. 01. Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26. Last annotation update)
DE Rymodine receptor alpha isoform.
GN Name=PROG-ARR;

O6	Rana catesbeiana (Bull frog).
OC	Euryxyleta; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana;
OX	Aguaruna.
NCBI_TaxID=8400;	[1]
NP	MUCLEOTIDE SEQUENCE.
RP	TISSUE=Skeletal muscle;
RC	MEDLINE=94274714; PubMed=8006029;
RA	Oyamada H., Murayama T., Takagi T., Ino M., Iwabe N., Miyata T., Ogawa Y., Endo M.;
RT	"Primary structure and distribution of ryanodine-binding protein isoforms of the bullfrog skeletal muscle.";
RL	J. Biol. Chem. 269:17206-17214(1994).
CC	-1- DOMAIN: Each of the four internal repeats contains five hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one positively charged transmembrane segment (S4). S4 segments probably represent the voltage-sensor and are characterized by a series of positively charged amino acids at every third position (By similarity).
CC	EMBL; D21070; BAA04646.1; -; mRNA.
DR	PIR; A54161; A54161.
DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0015020; C:membrane; IEA.
DR	GO; GO:0005262; F:calcium channel activity; IEA.
DR	GO; GO:0005509; F:calcium ion binding; IEA.
DR	GO; GO:0004872; F:receptor activity; IEA.
DR	GO; GO:0005219; F:ryanodine-sensitive calcium-release channel. . ; IEA.
DR	GO; GO:0006874; P:calcium ion homeostasis; IEA.
DR	GO; GO:0006816; P:calcium ion transport; IEA.
DR	GO; GO:0006812; P:cation transport; IEA.
DR	InterPro; IPRO00659; Ca-rel_channel.
DR	InterPro; IPRO01992; EF-Hand_pore.
DR	InterPro; IPRO11982; EF-Hand_Cys.
DR	InterPro; IPRO02048; EF_hand_Ga_bd.
DR	InterPro; IPRO05821; Ion_trans.
DR	InterPro; IPRO03608; MIR.
DR	InterPro; IPRO03032; Ryanodine_recept.
DR	InterPro; IPRO01215; Ryanoda_receptor.
DR	InterPro; IPRO09460; Ryandrecept_TM4-6.
DR	InterPro; IPRO03877; SPRY_receptor.
DR	pfam; PF00520; Ion_trans_1.
DR	pfam; PF02815; MIR; 1.
DR	pfam; PF06459; RR_TM4-6; 1.
DR	pfam; PF01365; XYR_ITPR; 2.
DR	pfam; PF02026; RYR; 4.
DR	pfam; PF00622; SPRY; 3.
DR	PRINTS; PR00795; RYANODINER.
DR	PRODOM; PD000012; EF-hand; 1.
DR	SMART; SMART472; MIR; 4.
DR	SMART; SMART449; SPRY; 3.
DR	PROSITE; PS00919; MIR; 5. Ion transport; Ionic channel; Receptor; Repeat; Transmembrane; Transport.
KW	SEQUENCE 5037 AA; 571291 MW; FF263948A51C3ABF CRC64;
SQ	
Query Match	41.5%; Score 6534.5; DB 2; Length 5037;
Best Local Similarity	44.3%; Pred.No.0;
Matches 1371;	Conservative 539; Mismatches 875; Indels 311; Gaps 64;
OY	4 AEGASSEDVVSFLRTDMDCLSTAT---GERVCLAAGFGNNHCFLENIAD-KNIP 58
Dd	2 AEGECE-DEIOPLATEDDVVLQGSAITRKENLKKMCGVEGGRNLCTYSTSNANP 60
OY	59 DLSCVPPIEALSVRALDELV---TAAGSETKGTSGRHRTLTYGNALLRHLSNDYL 115
Dd	61 DLACCPFLLESLSRALQENMLANTVENGSSEO--GGSHHTLLYGAILLRHGSDMYL 118
OY	116 ACISTSS-SORLAFDVGLOOHSGEAQMTHLPASSKORSSEGEKYRVGDILLIVSVATER 174
Dd	119 CCUTTSRSULTKLAFVDGLQEDASEAKMTWHPSKSRSGEKYRIADDILLVSSESR 178
OY	175 YIAHTTKEENVISVNASPVHTMSVOPTGTISRKKYGVYEGGDVARPFHHG-DECLTP 233

Db	179	YHJSTASGDQVNASFWQJTMNNPITSGEIAE--GYVVGQVLRLEFGHMDCLTIS	236
Qy	234	STWTDDGSONLVVEGSGVMSOARSIMTELARTMACGFINNYPMIRHITTRRYICV	293
Db	237	STDOGEERRIPIHIEGAVCHANSIMSEPLRISGSHRMKGFPAARHNTTRILAR	296
Qy	294	NDONELVYVSEBEATTASCAFLQROEKDQOVLEDKOLEVIAGPIIKYGDSTVIOHSE	353
Db	297	EEERGLVVDAEKANTRKATACFRISK-EKUDVAPKRDIEGMGRADIKGSGSMCVQJNV	355
Qy	354	TGLMSTYSYETKKGKGVKEKOAIIHEGKMDDGLPSSQBEESTARATKCSLSIF	413
Db	356	SGMLTYAAASOKVARIQPIKRX-ALHQEGHMDALSLRSQREBSQAARVIYSTAGLF	414
Qy	414	TKFINGETTLOENRHSWFASVNLGEBWMLCEIDINVFAOPDEMEHEBKONKRALRN	473
Db	415	NIFIKGDSLNGKNKPSKPT-SLPIDWVLLTLODIIQYFQHEELQJHEBKOTKURSLKN	473
Qy	474	RODLFOEBEGLIINLLEAIDKINVTISQGLAGFLAGESGOSWEMISGTYLQTLAAITKG	533
Db	474	RQNFQEBEGLISQVLDICIDRLNVSTAHFABF-AGEBAASMKRIVNLVELLASTLRG	532
Qy	534	NHTNCAOPANSRNLNWLFSRLGS-QASGEBCMLDYTHCVTIDSPALNMRDEHIKYL	592
Db	533	NRSNCALF--SNNDWVWVSKIDRLIEAS---SGILEVLCVLIBSEPEVLIINIKKHIIKSI	587
Qy	593	SLEKHGDDPYVLVLCGLCVGNQVAVARSNNICDYLLPQKNIILLOFALVDHSSVAPN	652
Db	588	SLDHGHRNKVLDVLCGLCVGNVAVARSNNILTENILPRDLLOTRMNAVYISMRPN	647
Qy	653	IFVGRVGEASARKKMEYEVTNDHIEK-TTHMPPHRIQMANTTGYVYPGGGEKVGNGV	711
Db	648	IYFGCSGSTQFKKMGFEVIVDOYEPFYTAATHLRVGMALTEGSPYRGAEGEGANGA	707
Qy	712	GDDIYSGFDGAYIWMSSGKTPVNRTHAEEPIRKGDVIGCALDUTPIINFMNGRAYT	771
Db	708	GDDIYSPAFDILHIMS-GYVCRAVASH-NQHLILRADVDVSCCLDUTVPSISFRFNGHVQ	765
Qy	772	GSFNFNPLEGMPFVVISGSSKLSORFLGSEHGLRYAAREGSPVLSLPOOLISER	831
Db	766	GMFENFNLDGFFPVSSFSPEIKIRFLGNGHGFKLPPRGVAPAYEALPRDRARVER	825
Qy	832	CFYF-----GNLSKRALAGPRLVODDTFAVPRPVDTLOITTEPTYEQRIDKLAENIHEWA	887
Db	826	IKEYKHVDGI--RNLGPTKKSJSHTEFVPRVDVTQVLPRLHERIREKLAENIHEMA	883
Qy	888	MNKIEAGMGTQDQREDLHKIHPCLVPPERLPPRAEKRYDIOQAVOTLKTIALGYIISI--	945
Db	884	LTRIEQMTWGPRIDDDKRLHPCLLDHSPLEPERANNILMMSGETLKTLLALGCHVAD	943
Qy	946	DKPARIARNRLPHREPMOSGVYAPRLDISAVLTTPRMBELVQOLENTHNLMAREIO	1005
Db	944	EKAENELKTKLP-KTMMSSNGVYAPRLDISHVLTTPRQNTLVKCLAHNGHNVMRDVO	1002
Qy	1006	QGMWYGLNEDSDMRSPLHVPYPKVDAIKAANDTASETYRTLVLVGYMLDPRTEQHE	1065
Db	1003	QGMWYSLIIOIKNKNRNLVYVLLDEKTKTNDSLCEAVRTLMGVOYNIERP--DEBS	1066
Qy	1066	ALLIEASKQKOADRTYRAEKNAVVSQKTYFEBEILTAGPMRYGMAHADMAPGMLGOD	1125
Db	1061	SAOGGIIKTPRAERMRIRFRAEKSYAVKSGKTYFEEFAVTTGEMRGVMARBYVRPVELCAD	1120
Qy	1126	ENSWAFPGVNBKEKYSGNTBSPGQOMVGVDPVUGFLLIDKTIISPSINGELMALGETT	1185
Db	1121	ELAVFNGHNGQORNHG-SEPFNGNWPBGDVVGCMIDLTENNINFTLNGEMLIGDSGSDV	1179
Qy	1186	TFADVQ-GDNFVPACTIGVQOKALTYGQDNTLAKTYTTCGLQGEYEPFCVNMKRDVTH	1244
Db	1180	AFKQIEGEGEIPVCSIGMSQVGLNIGQVGSIRYTLICGLQGEFPERFALNMGREITW	1239
Qy	1245	YTKQOPIFENTDEMIDTRIDVTRIPAGSDPPCKISJHNTETMEKANWE--FLRLSLPV	1302

Db 1240 FSKSLPQFANV-SADHIEVSRI DGTVDNPPCLKTHTKTFGS-QNSNTDMLPFRLSMPV 1297
 Qy 1303 ICHNEFIDEABKARWVEIKORQOILMKAEVAEQMRAHIDQIMSGETMADIKGLHYEDN 1362
 Db 1298 ----EFETPKCTPGATPLTRSFITVEEYQDVDMSEF-BVLKKAARKIEA-----TN 1348
 Qy 1363 QEBLPSKMKRLPSRPPKGSMTKGVITIQVNNLQPCQVNGMHRSTSEAMAKYDLGAOG 1422
 Db 1349 BKOL-----AKETPEPEPK----- 1362
 Qy 1423 LTRDDKDKKRGKRPFKFRSKGESSDRAKS-----KSKTPDPESDTEVSPERGARRPNP 1478
 Db 1363 --BENEED-----TTTEKTKKRGFLFKPKKPAFISTPVP----- 1396
 Qy 1479 QIKVQANQRYNGNNAKPSRTNLVGSQVGLNMAPTQDRKQMTSTLAQATETVGNIEF 1538
 Db 1397 -----TPRLMKEVVPPDRD 1411
 Qy 1539 DAECCLKINBYFYGVARYPGODPTHVYIGWVTTQYHLHSDPNQSKVTKASVITDDYR 1598
 Db 1412 DPEIIRNTTYYYSVAFAGQEPFGVWIGWVTPDYLIDMNFDMKVRNATITMGDDKN 1471
 Qy 1599 VVENNRQSCYMRADLYNEWMAEATKAGASQMGFCSDVDTSGSVSTCEBKDTSEK 1658
 Db 1472 IFNSIRNSCYMWGSGFSSNNTQ---QARVRKEDLVGCLIDLATGLMTETANGKEVNTF 1528
 Qy 1659 FKKEPETKLPATFVETSKEIILQIBLGRATSLSPLSAVLPTSDKHVITQOPRPLKYOC 1718
 Db 1529 FOVEPNTKFPFAVFPVPLSOTLFOFELGKKNIMPISAMFRSSKSPVQCCPRLLVOV 1588
 Qy 1719 LKDHQAVRPNOSILOVHALKLSDIGMSMLCEBAVSMALHIEBDCIDILBIEMDKL 1778
 Db 1589 LKVVMSRBMNDFLKAVESSKVSDBHGMVCECTPLWMMALHIEBDCIDILBIEMDKL 1648
 Qy 1779 LSHFSHTLYAALCTQSNTRAAHALCTHYDQOKLYAIOQVSGELRGCFDOLIALH 1838
 Db 1649 LKHNYHTLKLKCYCVCALGNRVAHALSHYDESQILYTISSNNLSGILRSGFYDLISIH 1708
 Qy 1839 LSEHATTEMAKCKRBFVPLGRBLKA---LYEBPMGHSLSRL-QRESVRPQMTDIAESI 1895
 Db 1709 LBSAKGRMTMNSBFIYPMDDQTSITLFPENENKQHLPGVGWSTCLRPALHSHTC-FV 1767
 Qy 1896 TEISNLY--SPYFPLVAREEFVQALAEAVETQVNHNDPVGNSNEMFLPLIKLYDRL 1953
 Db 1768 STISELYHSPFYPLDLIKTKALINLTSVQDGGQHRDPEVGSVERQFVPLKLISTL 1827
 Qy 1954 LVGMNDEDEVKLLIMTNPETW---DSFD----- 1980
 Db 1828 IMGVFQDDVVRHILKMLEPNVFSBEPDAEGGEBGEKATEKGGEEVEGEGQEKTED 1887
 Qy 1981 -----KEGDERHKGILIMKMAEGATQMCYLLQHLNDQLAHRVBAITAPA 2027
 Db 1888 GBEKTYEDGABAKESBEALBEGLOMKLPESVQLQMCNLQYFCRELDHRVEAITAFS 1947
 Qy 2028 HDEVDGLQTDQLRRYETIKOS-DLPSAVAKKTRFPCPREQMNALISFKHLEEDKEN 2086
 Db 1948 ERMDLSQTNQRRKRYKELMAFTMSALETARKTRERFPQEOINLTVNKNIPBEE--- 2004
 Qy 2087 CPCGSELIAKMNFPDHTLMAVSLHALQEPDALENOSPRAKPAFGCLYNIINTVKELE 2146
 Db 2005 YPVEBIEIRDEHIDFHDILAHCGVHM-----EGEBEBOGDTSLARRLLSLVEKIKLRG 2059
 Qy 2147 EAAQIEBPPKCTBEK---PRKVLQIYVMAESQJETKLYREMSSLLVROYDAVEL 2203
 Db 2060 KKGSPBEPBEOBEPKTTLOELISHTMVMAOESFQNPBELVRVMSLSLHROYDIGEL 2119
 Qy 2204 IRALREKTYVNAKTKLDVAEMVGLSQIRALLPVMQSOEBSBLMRKCLMTLVNNHTFQH 2263
 Db 2120 IRAMPKAYTTINAVSVEBTNNLBSLGLSRLILYQMBPEENMLIGSIGIMNNKYFYQH 2179
 Qy 2264 PDLIRVLRVHENVAVMMNTLGRBAQASDAQSPVASDSKREKOTSHENYVACCFCLC 2323
 Db 2180 PNIMRALGHEJTWJEMVAVNLG-----GSESKE-IRPRKQVNTCCRFCLC 2222

Qy 2324 YFCRTGRONOKAMFDEHDFLENSNILLSPRSRGSTPLDVAVSSLMTELALAREHY 2383
 Db 2223 YFCRISQNRQAMFPHLSYLENSIGTL---GMRGSTPLDVAASVIDNNEMLALAOEOD 2279
 Qy 2384 LEKIAVYLSRQGLQNSSELYEKYPDIGWDPVEGERYLDPLRCVWNGESVEBNANLV 2443
 Db 2280 LKRVSYIACGGLQSCPMILAKGYPDIGMNPVGERYLDPLRAVFNNGESVEBNANLV 2339
 Qy 2444 RLIRREPCGPAIRGE-GRGLKAIYDANKSERIA-----DPRKIREMOBEDVN 2494
 Db 2340 RLIRREPCGPAIRGEGNGLGALIDAIRISBDEPRDGPYKDBRR---ELYGG-- 2393
 Qy 2495 FSHLPESDEDEYDITGAAILNFYCTLYDLGRCAPDAGVIALGKNESTPRABAILRSV 2554
 Db 2394 -----EBHEENRVHGNAINSFYALIDLRCAPEMHLIQAGKEALRIAILRSV 2447
 Qy 2555 PLBEOGLVLSRPTLNNPAAGBE---RPSDMPGSLIPGHOSVGLFLERYGIEFOEL 2610
 Db 2448 PIEDLVGVISL--PLQIPAFGKQNTIEPK--MSASFVPDHKAPMVLFLDRVYGDIDQDF 2503
 Qy 2611 FYTLREAPLPLDRAATMTDRNDGCSBDMALSMNRYGNSILPLILKHAIFYNBAEYAS 2670
 Db 2504 LQVLEVGFLPDRRAAASLDYAAPSTTEMLANNRYLCSAVLPLITCAPLFGTEHRAI 2563
 Qy 2671 LIDATLHTVRLSKNMLTKGREAVSDFLVATLSMOPSMILKRLKTLVDVSKLSEYT 2730
 Db 2564 MDSMLHTITRLSRGSLTQAQDVIBECMLGCLPLRBSMLQHLRLVFDVPIINFS 2633
 Qy 2731 TVALRLITLHYERCAKYSGTAGQAGFASDSBEKRLTMALFNSIPDSLSKNDYBELF 2790
 Db 2624 KMLPLKLTINHYERCMKY--CLPTGMANYGVSSBEEHLTRKLFMGIPESILAHKRFDAELY 2682
 Qy 2791 GRALPLCIAIGCALPPDYSLSKRYDDEFYKEQDAAGLD-NPOYDPOPIITSSVYALNNDL 2849
 Db 2683 KITMPCICALAGAIIPDY-----VDASYSSTKTKKASVDABGNFDPPEVETLNVILPEKL 2737
 Qy 2850 NTIVOKSEBHYHAPAMASRKLENGMVYGEGSDQKTHPRKLPYMLNDYKERYKEPVRE 2909
 Db 2738 DGFINKYAEHTHDKMAPEKIQNNWSYGETIDEBAKTHPMLRPKTTBSKDEKIYRWPIKE 2797
 Qy 2910 SLKALLAIGMSVE---HSEVDIPSNRKSNSRROSKSGR--PREIYDTSATPDPYNHVP 2964
 Db 2798 SLKMLAMEWLVKAREGEED-RTEKKTKRKISQNAQCYDDMVQJ-----FSPTPI 2849
 Qy 2965 DMTNLTLSREMQMARLADNADINAKKKKEBLVT 3000
 Db 2850 DLTGTLISRELQMAEQLAENYHNTWGRKKKVELET 2885

RESULT 15
 RYRL_PIG
 ID_RYRL_PIG STANDARD; PRT; 5035 AA.
 AC P16960;
 DT 01-NOV-1990 (Rel. 15, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ryanodine receptor 1 (Skeletal muscle c-type Ryanodine receptor) (RYRL)
 GN Name=RYRL; Synonym=SRC;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Suidae; Suidae;
 OC Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP NCITROTIDE SEQUENCE. TISSUE=Skeletal muscle;
 RC RYRL=Norwegian Landrace; TISSUE=Skeletal muscle;
 RX MEDLINE=93036581; PubMed=1329581; Pubmed=1329581;
 RA Harbitz I., Kristensen T., Bosnes M., Kran S., Davies W.;
 RT "DNA sequence of the skeletal muscle calcium release channel cDNA and
 verification of the Arg615-->Cys615 mutation, associated with porcine
 malignant hyperthermia, in Norwegian Landrace pigs";

RL Anlm. Genet. 23:395-402(1992).
 RN [2]
 RA NUCLEOTIDE SEQUENCE OF 1129-2801.
 RP Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RA NUCLEOTIDE SEQUENCE OF 1129-2643.
 RC STRAIN=German Landrace; TISSUE=Liver;
 RX MEDLINE=94117003; Pubmed=8288381;
 RA Leeb T., Schmolz S., Brem G., Brenig B.;
 RT "Genomic organization of the porcine skeletal muscle ryanodine
 receptor (RYR1) gene coding region 4624 to 7929";
 RL Genomics 18:349-354(1993).
 RN [4]
 RP NUCLEOTIDE SEQUENCE OF 4785-5035.
 RX MEDLINE=91065640; Pubmed=2174405;
 RA Hasbiter J., Chowdhary B., Thomson P.D., Davies W., Kaufman U.,
 RA Kran S., Gustavsson I., Christensen K., Hauge J.G.;
 RT "Assignment of the porcine calcium release channel gene, a candidate
 for the malignant hyperthermia locus, to the ep11--p21 segment of
 RT chromosome 6.";
 RL Genomics 8:243-248(1990).
 CC -1 FUNCTION: Communication between transverse-tubules and
 sarcoplasmic reticulum. Contraction of skeletal muscle is
 triggered by release of calcium ions from SR following
 depolarization of T-tubules.
 CC -1 SUBUNIT: Homotrimer (Potential).
 CC -1 MISCELLANEOUS: The calcium release channel is modulated by calcium
 ions, magnesium ions, ATP and calmodulin.
 CC -1 MISCELLANEOUS: The calcium release channel actively resides in the
 C-terminal region while the remaining part of the protein
 constitutes the 'foot' structure spanning the junctional gap
 between the SR and the T-tubule. It is possible that the foot
 structure interacts with the cytoplasmic region of the
 dihydropyridine receptor.
 CC -1 MISCELLANEOUS: Ryanodine is an alkaloid that binds to the Ca-
 release channel in junctional SR and modulates its activity.
 CC -1 SIMILARITY: Belongs to the ryanodine receptor family.
 CC -1 SIMILARITY: Contains 5 MIR domains.
 CC -1 SIMILARITY: Contains 3 SPRY domains.

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 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

 DR EMBL, X62880; CAA44674.1; ALT. SEQ. mRNA.
 DR EMBL, X68247; CAA48318.1; -, Genomic DNA.
 DR EMBL, X69465; CAA49225.1; -, Genomic DNA.
 DR EMBL, M32501; AAA31022.1; -, mRNA.
 DR InterPro: IPR000659; Ca-rel channel.
 DR InterPro: IPR001682; Ca/Na pore.
 DR InterPro: IPR011992; EF-Hand type.
 DR InterPro: IPR002048; EF-hand_Ca_bd.
 DR InterPro: IPR005821; Ion_trans.
 DR InterPro: IPR003608; MIR.
 DR InterPro: IPR003032; Ryanodine recept.
 DR InterPro: IPR001215; Ryanodn_receptor.
 DR InterPro: IPR009460; Ryanrecept_TM4-6.
 DR InterPro: IPR003877; SPRY_receptor.
 DR PANTHER: PTHR13715.SF1; Ryanodn_receptor; 10.
 DR Pfam: PF00520; Ion_trans; 1.
 DR Pfam: PF02815; MIR; 1.
 DR Pfam: PF06459; RR_TM4-6; 1.
 DR Pfam: PF01365; RYR_ITPR; 2.
 DR Pfam: PF02026; RYR; 4.
 DR Pfam: PF00622; SPRY; 3.
 DR PRINTS: PR00795; RYANODINER.
 DR Prodom: PD000012; EF-hand; 1.
 DR SMART: SM00472; MIR; 4.
 DR SMART: SM00449; SPRY; 3.
 DR PROSITE: PS50919; MIR; 5.

Query Match	Best Local Similarity	41.0% Score 6453.5; DB 1; Length 5035;	Matched 1367; Conservative 531; Mismatches 894; Indels 303; Gaps 63;
QY	5	EGGASBEDDVSFLTEDMVCISCTAT---GERVCLAAEGHNRHCFLENIAD-KNIPPD 59	
DB	3	DGGEGE-DEVOFRTDDEBVVLQCNATYIKQLKCLAAEGGNRLCFLEPTSNANQVPPD 61	
QY	60	LSQCVFVTEQLSTRALQELV---TAGSEFGKKTSGHRTLYGNAILRLHNSDWYLA 116	
DB	62	LAICFVTEQSLSTRALQEMIANTVAGVSSQ---GGHRTLYGHAILHNSHWYLS 119	
QY	117	CLSTSSSO-DGLADPVGLQHQSEGLCMWTLHPASKORSBEKRYVGDIDLIVSATERY 175	
DB	120	CLTTSRSMITDGLADVLQGEATGEALCMWTLHPASKORSBEKRYVGDIDLIVSSERY 179	
QY	176	LHTTKENEVSIVNASFVHTWNSVOPYSTGISRMKGVYVFGADVLRPFHG-DECLTTPS 234	
DB	180	LHLSVASEGLVDVASFMQTLMMNPICSGCE---GVYVGHVLRPFHGMDECLTTPS 234	
QY	235	TWTYDGGGNTVYVGGGYSMSQARSLMKLELARTKAGGFIWYTHPMTIRHTTTRRYLGN 294	
DB	235	PADSDDDGRLVYVGGGVSCTARSLMKLELRLIWSGSHLWQGLRLRHVHTTTRYALI 294	
QY	295	DQNELVYVSRREATTASCAFLRQBDQDKVLDKULEVADPIIRKYGSTVYVHSET 354	
DB	295	EDQGLVVDVASKATKATKTSFCFRISK-BKLDITAKRVDVGGPPEIKYGBSLCVQGVNAS 353	

355 GLMLSYKTYETKKKGVKVEEKOALIHBEKGMDGLDERSQOESESTARVIRKCSLT 414
354 GLMLTYAPDPKALRLG-VLKKKALIHQBGMDDALSTTRCOEESQAAWVITAGLYN 412
415 KPIINGLETLOENRHSMEFA--SVNLGEMVNCLEBLLINYPAOPDEMEHEKONKPRALR 472
413 HPIKGLDSFGSKPRGSGAPAGTALPLEBGVILSLDLIGYFPPPSBEILOHEKQSKLRSIR 472
473 NRQOLFOEEGLMLILEADIKINVTSGPLAGLAGESQOSQEMISGVLXQLLAIIK 532
473 NRQOLFOEEGLMLILEADIKINVTSGPLAGLAGESQOSQEMISGVLXQLLAIIK 532
533 GNHNHCQAFANSNRLMPLSRIGS-QASGEETGMLDVHACVILDSPEALNMMDHEIKVI 591
532 GNANALF--SNMLDLVSKDLRLBAS---SGILEVLYCYLISBEPVLANTIQENHIKSI 586
592 ISLLEKRGDRPKVLDVLCSLCVGNVAVRSSQNNICDYLPPQKILLQYALVDHVSVR 651
587 ISLDDKGRNKHVLDVLCSLCVGNVAVRSSQNNICDYLPPQKILLQYALVDHVSVR 646
652 NIFVGRVGSANVYKRYEYVMDHEK-TTMMPHLARGMANTGYVYPPGGEGMGNG 710
647 NIFVGRVGSANVYKRYEYVMDHEK-TTMMPHLARGMANTGYVYPPGGEGMGNG 706
711 VGDDLXGYPGAVILMSGGRKTPVNRTHABEPIYRKGVIGCALDLYPIINFMNGYRV 770
707 VGDDLXGYPGAVILMSGGRKTPVNRTHABEPIYRKGVIGCALDLYPIINFMNGYRV 764
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765 QGVFAPPLNGLLFFPVVPSFSAQVKRFLDGGHGFKLPPGYAPCHEAVLPRRLALE 824
831 PCYFPGNISKRA--LAGPPLVQDDTAFTPTVYDTQITLPTYVBOIRKLAENIHEMAM 888
825 PIKEYREGRGPHLVGPRCSLSTHDFVPCPDVTOIYVPHLEIRKLEKLENIHEMAL 884
889 NKIAGMNGQORREDLHKIPCLVPEERLPRABKXYDQOLAVQTKTILAGYISL--D 946
885 TRIQOMYTGVPVRDNKRLHPLVDHSLPBERNYNOMSGEITKTLALISCHGMDE 944
947 KPARIIRVRLPNEPFQNGYKAPALDLSAVTLTPKMDDELVDQALANTHMLMAERIQ 1006
945 KAEINLAKTKLP-KTYMNSNGYKAPALDLSHVRLTPACTTILVRLABEIGHVMAWDRVAQ 1003
1007 GWYGLNEDSDMARSPLVPTPKVDDAIKANDTASERTLTVYGMLDPEPGEQHEA 1066
1004 GMSYSAVQDIPARBNPLVPRLLDEATKRSNRDLSQAVRLLGYGVNIBPDEPQOV 1063
1067 LLLBASQKQADFRYRAEKXVAVSSGKWPPEFELITGPMRVGMHADMAQMMMLGODE 1126
1064 ---BSQSRMDRVRLPRAEKSYAVQSGKWPPEFELITGPMRVGMHADMAQMMMLGODE 1119
1127 NSMAFDGNEBEKVYSGNTESFGKQWAVGVFLLDLDKTIISFSLNGLMDALGSETT 1186
1120 LAYFNGRGRQWHLG-SELFGRFQOSGDVVCMDLIENTIIIFTLNBEVLMSSDGSSTA 1178
1179 FRDIEVGDGFLPVCSLGGQVGHNLMDQVSLRFFALCGLQEGFEPALINMQRVVTWTF 1238
1187 FADVQ-GDNFVPACTLVGQKARLTYGQDVNTLKTFTTCGLQEGYEPFCVANKRDVTMY 1245
1246 TKQDPIFENTDEMTDIRIDYTRIPAGSDPTPLKTSNHTFERMER-AMBEPLRLSLPYIC 1304
1239 SKSLPQFEAV-PLEHPHYEVSVDGTVDTPCLRLTHHTWGSQNSLVEMLFRLSLPVOF 1297
1305 HNEPIDABKARWVEIKDROQILMKBAVEAQMPAHIDQIMSGFTMNDIKGLHYEDNOE 1364
1298 HOHPRCTA-----GAT----- 1308
1365 ELPSKMKRLPBRPPKSGMTRGVTTIQYNNILOPQVNGMHSRSTEAEMAKYDLAQGIT 1424
1309 -----PLAPP-----GLQF-----PAEDS-----ARAAR 1327

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1428 LNTTYYTSVAVFPAQBSQVWGVYTPDYQHDMNPDLTVRAVYTMGBOGNHSSL 1487
1604 NRQSCYVRADELVNEVMAEATYAKGASQMGFICGSVDTSGSVSFTCEGDKTSFKYMER 1663
1488 KCSNXYWGGDF---VSPQGGRIISHTDVLIGCLVDLATGMLFTANAGESNTEFOVER 1544
1664 ETKLPPALFYVATSKELIQTILGSAISLPLSAVLPYSDGVYPOPPRLKYOCIKRHO 1723
1545 NTKLFPVAVFVLPYQNYIOFELGKQKIMPLSAMFUSERKPAPOCPRLMOMLMEVS 1604
1724 WARYNOSLOVHALKLSIDRGSMLCEDAVSMALHITPEEDRCIDILEPIEMDKLSFHS 1783
1605 WSRPHNHLKAVETRAGERLGNVQCPPLTMALHITPEERCMIDIELSRDLQYHS 1664
1784 HTLTYALCYQSNYRAAHALCTHVQKOLLVYIQQSYMSGPLRGFYDLLIALHLSHA 1843
1665 HTLTYALVACLGNNRVAHALCSHVDAQILHLEDAHLPPRLNAGYDILLISIHLESAC 1724
1844 TTMEACNKEFVITPGPELICAL-----YEPDMGHSLSBL-QTESVRP----- 1884
1725 RSRSMSSEYVLPPTERRALTLPFGKRTNGRRHQLPVGVTYSLRPHHSAPCFV 1784
1885 -QMGMTDIAESITHSNLYSPPLVAREEVMOLAEVATNQVHNRDPVGSNENFL 1943
1785 AALPVGAAEAPRL---SPSILPEALRDALNMLGEAVDGGOHARDPVGGSVEFPV 1840
1944 PLIKLVRLILVGMNDEVEDVEKLLIMNPEW-----DSPFKEGDERK----- 1989
1841 PVKLTVSTLVMGIFGDEVDVQILKMLIEPVFTSEEBEEREBEEREBEEREBE 1900
1990 -----GLIMMAAGAKIOMCYLLOHLNDIOLRHRVAILI 2024
1901 ARBKDEKEEEREAEGEKEYLEBGLLOMCLPSEVKLOMNLLEYPCDOELQHVESIA 1960
2025 APANDFVDDLOTDOURY-TEIKOSDLPASAARKTRFRCPPEBOMNAIISFKLSEED 2083
1961 AFAERYVQKQANDKDRGIIMKAFPTMAETARTREFRSPBOQIMMLHFK--DGED 2018
2084 KENCPCGEBELIARMBEFDTLMAVSLHALQEPDAENQOBEAKGAFGLYNIINTYKE 2143
2019 EEDCPLPBEIRKODLEPHQDILLTHCGIOL-----EGESEEPBEBATLGSRLMSLEKVR 2073
2144 L-EBERAKIIEBP-KCTPEERKRYVLIQTIYNMAESQIEFPKLVRENFSLVROYDVG 2201
2074 VKKSEKSEEBEPABESYAOGLQELVSHTVRMQOEDVQSPBELVRAFSILHRYDGI 2133
2202 ELIALKETVYINAKTKLDVAMEMVGLSOIBALLPVQMSQSEEBELMRKLVNHTFE 2261
2134 ELRLPLPAAVYITSPESVEDTWSLBEGLQIISLLIVQGPBENIMTOSIGNIMNKVFY 2193
2262 QHPDLIRVLRVHEVMAVMANNTLGRRAQSDAOPSSQPVAVESKERTSHENVACRF 2321
2194 QHPNIMRLGHEHYEMEMVAVLG-----GGESEB-IRFPKMTVSGRF 2236
2322 LCYFCRTGRONQKAMFDFPULLENSNLSRPSLRGSTPLDVAVSSIMETELALARE 2381
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2382 HTLEKIANYLSRQGLQNSBELVKGYPDLGMDPVGESEYVLEFLRCVAVNGESVEENML 2441
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QY      2609  ELFYKLEBEAFPLDILRAATMLDRNDGCSDMALSMNRYIGNSIILPLIKHAYFYNEANY 2668
Db      2517  DFLHLVLDVGFPLPDRRAASLDYATFTTEMALALNRYLCLAVPLITKCAPLFAGTEHR 2576
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Search completed: April 14, 2006, 01:41:40
 Job time : 465 secs

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 Qy 343 GDSVIVOSHETGLMLSYKSYETFKKKGVGVEKKAQILHEEGMDGLDPSRQOEESEST 402
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 Qy 403 ARVIRKCSLLFTKEINGLETLOENRHSMPFASVNL-GBMWCLIEDLINYPAQDEME 460
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 Qy 461 HEKOKRPRALNRDOLFQEGILNLILEADIKINITYSGFAGLAGLADDESGQSEMS 520
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 Qy 521 GYLYOLALAIKGNHTNCAQFANSNRLNMLFSLGSOASGEGTMLDVLICVILDEPEAL 580
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 Db 647 RLNVHSSRPNFIFGVSSGSAQYKMYELMVDHTEPVTAEATLIRVGMASTEGYSBY 706
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 Db 707 PGGEKMGNGVDDLYSYGFDGHLMSGCIARTVSSPN-QHLRTDIVISCDLDSAP 764
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 Qy 820 SILPQOILSLERC-FYRGNLSKRALAGBPVODDPAFVTPPTDITQILPTVVEIRK 877
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 Qy 1353 DIKGLHYENQEBELPSSKMKRLPSRPKRGSTRTGVTIONVNNLOPQGVNGHRTSEAE 1412

Db 1315 -----SKTVPGCLPGAGLF-----GPKNDLEDDVADSD 1342
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 Qy 1532 TVGNELPDAECCLKINEYUGRIYPGODPTHVYIGWTTQYHLKDFNQSQKTSYI 1591
 Db 1409 VLADRDVDFLMQSTYTYSYRIFPGDEPANNWGMTSDHQDTGDFDLRVKRTVYT 1468
 Qy 1592 ITDDYDVVENVRNOSCYMVARDELINYEWAETKAGASQGMFIGSVDTSGVSFTCE 1651
 Db 1469 LQDEKGNHESIKNQCNVCA-----GSMSSGQGRN-NNGEIGCVNDAAGLLFTIAN 1523
 Qy 1652 GDOTSPFKMEPEYKLPFAIVFVATSKILLQIELGRSATSPLSAAVLFTSDKAVLPQFP 1711
 Db 1524 GKELSTYQVPESTKLPFAVFAQATSPIVVFQELGRIKVMPLSAGLFKSEHKNPVQCP 1583
 Qy 1712 PRLXVOCLKPHQMAVBNQSLQVHALKSLDRGSMGLCEDANVMSLHNTPEEDRCIDILE 1771
 Db 1584 PRLHVQFLSHVLMSHMPQFLKVDVSRISERQGMVQCDLPVQFMSLHNTPEENRSVDILE 1643
 Qy 1772 PIEMDKLSFHSHTLTLAALCYQSNYRAAALCTHVQKQLLVYAIQSYMSGPLRGCFY 1831
 Db 1644 LTBQELBELKFNHTLRISAVCALGNHVAALCHVDEPQLVYAIENKYMGLARTGY 1703
 Qy 1832 DLLALHLSHAATTMEACKNEFVILPGLBLK--LYEEDMGHSIRSL-QTESVRPQMK 1888
 Db 1704 DLLIIDIHLSYVATLMMNNEFIVPMTETKSTITFPENKKGHGPGLGISTSLRPMQF 1763
 Qy 1889 TDIASTEISN--LYSPYPLBVARBPWQALAEAVETNGVNRHDPGSGNENLPL 1945
 Db 1764 S--SPSPVINSNECYQYBEPFLDLKAKTTQMLTEAVAGSLHARDPVGTTBFLPVLL 1821
 Qy 1946 IKLVRLLLVGMARDEVEKLLIMTNPETW-----DPSFDK--BGKDH 1987
 Db 1822 IKLVFTLLIMGIFHNEDLRHLIQLEBVFQDAAPREBEGDTLEBSEVDTKLGAAGE 1881
 Qy 1988 -----RKGLIHKMAEGAKLQNCYLLQHLINDITQLRHVAITAPAHDPVGDILQDOL 2039
 Db 1882 EAKMGKRPEGLQMKLEBPVQLQMCILLOXCDQVHRIRBAIVAFSDPFAKIQDNOR 1941
 Qy 2040 RRYTEIKOS-DLPSVAAKTREFRCPRREONAILSPKHEEDKENPOGEELABRN 2098
 Db 1942 FRYNEVQALNNSAALTARKTEFRSPROBOITMNLNFK---DKSBCPCPEBTRDQL 1997
 Qy 2099 EFHDTLMAHVSILHALQEPDAAENOEPEAKPGAFGLVYNIINTVKELEEB--AKAIEBPPK 2156
 Db 1998 DEHEMLMHCGLIEDEDSLQNSDULTIR---GULLSLEVENYVLLKKKQOTKEPVBSDR 2053
 Qy 2157 KTBEEKFRKVLITQIVNNAEBSQIETPKLVBMESLVRQYDAVGBELIRALEKTYVINAK 2216
 Db 2054 KS--STLQOLISETVMAQESVIEDPELVAMFYLIRQYDGIQGLVYALPKTYTINGV 2111
 Qy 2217 TKLDVAEMWVGSLQIRALLPYQMSQEEBELMRKMLKVNHTTFQOHDILRVLAHNEV 2276
 Db 2112 SVEDTINILASIQIRSLISVRMGKEBEKMLIRIGDITMNNKVFQHPHMLALQNHETV 2171
 Qy 2277 MAVMNNTGARRAQASDAQPSQPAVBESKEKDTSEHNVVACCFYLCYFCRTGRONOKAM 2336
 Db 2172 MEVMNVNLG-----GGSKE-ITPRKAVANCRCFLCTFCRSRQNOAM 2214
 Qy 2337 FDHPDLLNSNILLSRPSLRGSTPLDVAYSLMENTELALALREHYLEKIAVYLSRGL 2396
 Db 2215 FDHLSYLLSENSVGLASPAWGSTPLDVAASVMONNELALALREPDLEKVVYLAGGL 2274
 Qy 2397 QSNSELYKGYPDUGMDVYBGERYIDELRFCYVNVNGSEVEBANAVITALLIRPECLPA 2456
 Db 2275 OSCQMLVSKGYPDIDGMNVEBGRYIDFLRFAVFCNGSEVEBANAVVLLIRRPBCFGPA 2334

Oy	2457	LRGE-GBGLKALYDANAMSERIADRRKLRMEBEGVNFENHLPES-----DEDE	2506
Db	2335	LRGGCGNGLLAAMEBAIKIAE-----PSSRDGSPPTSGSSKXTLDTTEED	2379
Oy	2507	DYITGAAIINFYCTVLDLGRCAPDAGVIALGNKSESIRARAIRSVLPLEDLQGVSLR	2566
Db	2380	DTIMGNALIMFYAALIDLLGRCAPENHILNAGGEARIRISIRSLIPLGDLVGVISIA	2439
Oy	2567	FTLNPPAAGEERPKSDMPSGLIPGHKOSVGLFLERVYGIETQELFYKLLBEAFLPDLRAA	2626
Db	2440	FQMPETIADQGVNVPEBMSAGFCPDHKAAMVFLDRVYGVIEVQDELHLLVEGLFPLDIRAA	2499
Oy	2627	TMIDRNDGCEBDMLSMRYIGNSILPLLIGHAYFYNMEAEVYASLLDATTHTVYRSLSKR	2686
Db	2500	ASLTPAALISATDMALALNRVLCYAVLPLTLTCAPLPAGTEHHASLLDSLHTVYRLSKGC	2559
Oy	2687	MLTKGQREAVVDPLVALTASAMQPSMLTLRLKRLTVDSYKLSRYTTVALRLTLTHYEECAK	2746
Db	2560	SUTKQGRSIEVCLLSICGQARPSMGHLLRLVLPDVLNENHAMKPLKLTNNHYECWK	2619
Oy	2747	YVSTGAGQGAFGASSDEEKLITMLPSNITDSISKDYBELFGKALPCLIAIGCALPP	2806
Db	2620	YYCIPFG-GWGNFGAASEEELHSRKLFWGIFDPAISQKKYEQBELFKALPCLISAVAGALPP	2678
Oy	2807	DYSLSKVNDDEFYGEQAGDLDNPQVQPOPIINTSSVALNNDLNTIYQKPEHHNDAMAS	2866
Db	2679	DY-MESNTVSNM--EKSSSMSECG-NFNPQVDYTSNIITPEKLEYFNKTAHSHDKMSM	2734
Oy	2867	RKIENGWYVGGESWDSQKTHPRLKPYNMLNDYEKERYKEPYRESIKALLAIGMSVSEHV	2926
Db	2735	DKLNGWITVGIISYDSBKIQPLMKRYKLSSEKEIYRWPIKESLKTMLANGWIRIBETR-	2793
Oy	2927	DIPSNNSSMRQSKSGGRPPEIYVDSATPPDYNPHPVDNTNLTLSREMMARLADNA	2986
Db	2794	--EGDSMALNRRRRRIEQTSQVSDAA--HGYSBRAIDMSNVTLSRDLHAMAEAMENY	2848
Oy	2987	HDINAKKKKEEL 2998	
Db	2849	HNIMAKKKGLLEI 2860	
RESULT 2			
US-09-538-092-979			
Sequence 979, Application US/09538092			
Patent No. 6753314			
GENERAL INFORMATION:			
APPLICANT: Glot, Iolc			
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same			
FILE REFERENCE: 15966-542			
CURRENT APPLICATION NUMBER: US/09/538,092			
CURRENT FILING DATE: 2000-03-29			
PRIOR APPLICATION NUMBER: 60/127,352			
PRIOR FILING DATE: 1999-04-01			
PRIOR APPLICATION NUMBER: 60/178,965			
PRIOR FILING DATE: 2000-02-01			
NUMBER OF SEQ ID NOS: 1387			
SOFTWARE: CuratPseqFormatter Version 0.9			
SEQ ID NO 979			
LENGTH: 5032			
TYPE: PRT			
ORGANISM: Homo sapiens			
FEATURE:			
NAME/KEY: misc_feature			
LOCATION: (0)...(0)			
OTHER INFORMATION: Polypeptide Accession Number P21817			
US-09-538-092-979			

Query Match	40.9%	Score 6442.5	DB 2	Length 5032
Best Local Similarity	44.3%	Pred. No. 0		
Matches 1377	Conservative 517	Mismatches 891	Indels 321	Gaps 66

QY	1	MAABAGSABEDDUYSPLRTBEMVCLSTAT----	GEVCCLAABEFGNRHGLENIAD-KN	55
Db	1	MGBAEG-----EDVQFPLRTDDEVVLQCSAVYAKQOLCLAA	BGFNRCLCEFTPSNAON	56
QY	56	IPPDLSOCVFYIBOALSVBALQELV----	TAASETEKGKSGHRTLLYGNAILLRHNSD	112
Db	57	VPBDLAICTFLEBLSVRLAQEMLANTVEGVESSQ--	GGGHRTLLYGHAILLRHNSR	114
QY	113	MYLACLASTSSQ-DKLAFDVGLQOHSQGEACWMTLLHPAS	KORSSEGEKVRVGDDLLIVSVA	171
Db	115	MYLSCLTTSRSMTDKLAFLVDGLQDANGEA	CMWTHMPASKORSSEGEKVRVGDDLLIVSVS	174
QY	172	TERYIHTTKENEVSIYVNASFHYTHMSVQPYGTGIS	RSRKTYGVYVGGDVLRFPHFG-DECL	230
Db	175	SERYIHTSTAGBELQVAVSFMQITLMMNNPI----	CSRCB-BEYFVYGAVHLRFHGHMBCL	230
QY	231	TIPSTWTDGONIVVVEGGSVMSOARSIMTELAFRT	MAGGFNTWHPMRIRITTGARY	290
Db	231	TI-SPAUSDORRLVYIEGGAVCTHANSIMLEPLRIS	SGSHLRKMGQPLRKYRVITTGQY	289
QY	291	LGVDONELVYVSBREATTASCAFCRLROEKDQOVL	EDKOLEVIGAPIIKYGDSTVIVQ	350
Db	290	LATBEDGLVVVDASKAMHTKATSPCRISK-EKDVA	PKRDVEGAGPREIKYGSLSFCVQ	348
QY	351	HSETEGLWTSYKSETKXKGVKVBKQALTHEBGM	DGLDPSQSQSEESTAYIRKCS	410
Db	349	HVASGLMTVYAPPKALRILG-VLKKKAMLHQEB	MDALSLTCCQOEBESQAAIMHSTN	407
QY	411	SLTFKFNGLTLOENRHS--MFPASVNTGEMMC	LEDLNYFAQOPDEMEHEKONKF	468
Db	408	GLYNOFISLDSFGSKPRGSGPPAGTALPI	GVILSLDOLLITYPEPSEDIQHEBKOSKL	467
QY	469	PALNRQDLFOEBGLIIMLEAIDKINITYSQGL	AGFLAGFLADGESQSWEMISGYLYOLLA	528
Db	468	RSIARRQSLFOEBGLSMVNLCDIRLNYTTAAH	PAER-ABEBAEBSKEIVNLLYELLA	526
QY	529	AIKGNHTNCAQOPANSRNLMTFSRLGS-QAS	GEQMLDYLYACLDSPALNMRDEH	587
Db	527	SLIRGNRNCALF--STWLDWLVSXKDLRL	ERAS---SGILEVLYCYLIEBPEVAILIOENH	581
QY	588	IKVIIISLEKKGROPKYDVLCSLCVNGGVA	VRSNONNICUYLLPGKULLQTLVHDVS	647
Db	582	IKSIISLDRKGRNKKVLDVCSLCVCGAVRS	QODLITENLLPGRLELQTNILINYT	641
QY	648	SVRPNIPIVGRVESAIVYKMYFEVYMDIRK-T	THMMPHRIIGNANTTGVYVPGGSEKW	706
Db	642	SIRPIPIFGRAEGTTOYSKMYFEVWVDE	VTPEFLTAQATHLAVGMLTBGTYPYGAGGWM	701
QY	707	GGNGVGDLLYSYGPDDAYLWSGKRTPVNR	THABEPPYIRKQDVIICALDLTPVILNPFN	766
Db	702	GGNGVGDDLSYSGFDGLHMTGHAHPV--	TSPQGHLLAPEDVIVSCCIDLSVPSISFRIN	759
QY	767	GVRVTGASTNTRLBEMFFPVYSKCSKSCR	FLGGHQRLLAYVAPBEGSPLVESILLPOI	826
Db	760	GCPVGVGESRNLDELFFPVVVSFSA	GVYVRFLLGGRHGEKFFLPPEGAPCHEAVALPER	819
QY	827	LSLBCPFYGNLSKRA--IAGPPLVQDDTA	FVPTPVDTLOITLTPYVQIQRDLAKENHE	884
Db	820	LHLEPIKRYRREBGRPHLVGPRSKLST	ITDVPVCPDVQVLYLPRHLERIRKLAENHE	879
QY	885	MMANMKIBAGMYGDQREDAHKRIHCPV	FERLPPAEKRYDIOAVOTLTKTILALGYIS	944
Db	880	LMALTRIBQWYTGVPDRDNKRHLHCLVD	FHSLPEPEBNYIMQMSGELTKTILALGCHVG	939
QY	945	I--DPPPARIRNVALPNEPFWQNSGYKAP	LDLSAVTLTPMDELYOULANTNINWABE	1002
Db	940	MADEFAEDNLKKTXYLP-KTYMMSNGYKAP	LDLSHVRJLTPQOTTLVYRLAENGHWARD	998
QY	1003	RLOQSWTGLNBDSPMHSRPHLVPPKVD	ADAIKXANRDTAAEYVTLTVGYMLDPPRGE	1062
Db	999	RVGQSMHSISAVODIYARANNRPLV	FRLLDEATKSNRSDCOARVTLGTYGNIEBPQOE	1058
QY	1063	QHEALLLEASKOKOAD-FRTYRAEKRYAV	SSGKMYFEFEILLTAGDMRVGAHADMAPGM	1121

Db	1059	PS-----QVENQRCORVARI	FRAEKSYTVQSGHWFEFAVTTG	ERVGMARPELR	PROVE	1113											
Qy	1122	LGODENSMAPDGINEKXY	SGNTESGKQMAVGVFLDIDT	ISFSLNGELMDAL	1187												
Db	1114	LGADELAVYFNHGRGORMH	L-SEPRGPMQBDVVGCMID	TENTNIIPTLLNGEVLMSDS	1172												
Qy	1182	GGETTADVO-GDNFPAC	TLTGQVQCARLTYQDQVNTL	KCYTTGLOJSEYEFCCNMNRD	1244												
Db	1173	GSETAFRELEIGDGF	LPCVSLGPGVGHNLQDQVSS	LSLFPAICGLOJSEFFALNMORP	1233												
Qy	1241	VTHMYTKDORIENTDEM	IDTRIDVRIEAGSDTEPC	LKISHTFETWEK-ANNEFELLS	1299												
Db	1233	VTTWFSKGLPQEPBV-	PLEHPRHYEVRVDTG	VTDPCLRLTHRTGSONSLVEMFL	FLTLS	1291											
Qy	1300	LPYICNBTIDEAKAR	RWEIKDROOILMKEAVE	QMPAHIDQIMRSGFTM	IKGLHY	1355											
Db	1292	LPVOFHQRCTA-----		GATPLAPGL-----		1314											
Qy	1360	EDNQEELPSKMKLR	PSRPRRGSMTRGV	IONNNLPQGVNGHNR	T-----SEEMAKY	1416											
Db	1315	-----OPPADARAA	APDPYENLR-----	RSAGWSEAKENKE		1349											
Qy	1417	DL---GAQGLTP	DDKKDGRSPFFKRSK	GESSDRAKSRKTPDP	FSDEVERGCA	1473											
Db	1350	GTAKSGAPGTF-----		QAGRARA-PAENEDAT-----	TEKKKRGF	1387											
Qy	1474	KRPNOIKVSOANRY	NGMNAFPSRTNL	YGSQVGLNMAITP	QDKOMTSTLSAOSATEV	1533											
Db	1388	LFXAKKV-----	AMTQPP-----	ATPLLR-----	LPHDVPAD	1417											
Qy	1534	GNEIDAEGL	LINEFYGVRIYP	QDOPRTHVYIGW	VTQYHLSHDPNQS	KVTSVIT	1593										
Db	1418	NRD--DEP	LLTNTTYYISVR	FAQOBPSCVMA	GVNTPDYHODMS	FDLSKRVVTVMG	1475										
Qy	1594	DDYDRVENVNQRS	CVMPADLELYNE	MAEATAKASQMG	IFGCSVDSTGS	VSFTCEGK	1653										
Db	1476	DEQGVNHS	LKSNCTYMWGDF---	VEBQOGR	ISHDVIYIGCLVD	ATGLMTPTANGK	1532										
Qy	1654	DTSFKNEPETK	LPRALFVEATSK	ELLQIELGRATS	LPLSAVLP	PTSDKHVLPQEPBR	1713										
Db	1533	BSNTFEQV	EPNTKLEPAFV	LPETHQNV	QFELGKQKIMPL	PSAMFGSRKJAPQCBPR	1592										
Qy	1714	LKVQGLKPHQ	MARVNOQLQYHAL	KLSDRIGSM	LCBVAQSM	LAIHREBRCDILEPT	1773										
Db	1593	LEMQMLPVS	SRMKNHFLQVET	RAGRLGWA	VOQCEPRL	MMALHPEENRCDIITLS	1652										
Qy	1774	EMDKL	LSFHSHTLTYAAL	CYOSNR	RAHALCTHV	DQOLUYALIOSQMS	GPLROGFYDL	1833									
Db	1653	ERLD	QRFHSHTLRL	YRAVCALGN	NRVAHALCS	HNDOQLH	HALEDANH	PEPLAAGTYDL	1712								
Qy	1834	LIALH	LESHATMEA	CKNEFVILP	GLBELKALYEED---	DMGSLRS	LQ---TESVRP	1884									
Db	1713	LISIH	LEBACSR	SRMSEYIV	LPE	TRATILFP	GRSTENG	PHRGLPGVYTSLRP	1772								
Qy	1885	QMKMTD-----	LABSITE	SNLSYSP	PLPELEVAR	EFMQALAB	VENQVAND	PIVGS	1937								
Db	1773	PHHFP	PCFVAALP	PAGA	AEAPARLS	PAIPEAL	RDKLRMG	IGAVNR	DGCHADPVGAS	1832							
Qy	1938	NENTL	PLPIK	YVDRLL	LVGM	REDEVE	KLIMTNPETW-----	DPSFD	KEGDHRK-	1989							
Db	1833	VEFO	VPLK	VLSTLL	NGIF	GEDE	VYKOLMK	IEPEV	TEEBEEBDEBEEBDEBEEBKE	1892							
Qy	1990	-----															
Db	1893	EDBE	TABQ	KEDE	KEB	BEAAB	GEKEB	GLG	LLQMKL	PSVYKQ	OMCHILE	FPDQGLQ	1952				
Qy	2019	RVEAL	ILIA	PAH	DFVD	LQ	DTOL	RRY-TEI	KOSDL	PSA	VAAKT	REPCRP	PREON	NAIISFK	2077		
Db	1953	RVES	ILAA	FAE	RYVD	KLQ	ANORS	RYOLIK	AKASMT	AAE	ARTR	REFR	SPPO	QIM	MLLOFK	2012	
Qy	2078	HL	EBED	KNC	CGGEL	IL	ARNMB	FHDT	LAHNS	LHAL	GP	DDAA	ENQ	EP	AKG	AGKLYNI	2137

Db 2013 --DGDDEDDCLPPEINQDLDLDFHODDLAHGCIQ-----DGESEEBEERTLGSRLMSL 2065

Qy 2138 INTVY-----ELBEEAKAIEBPCKTPEEKFRKVLQITVNAAESQIETPKLVNMF 2190

Db 2066 LEKRLVYKKEKEEKEEERSAESKPSRIQE-----LVSHVNVRAQEDFVQSPETVDMF 2120

Qy 2191 SLVROYDAVEELIRALEKTYVINAQKRLDVAEMVWGLSOTRALLPVQMSQEEELMRK 2250

Db 2121 SLNRQYDGLDEHLRALPRAYTISPSSEVDWMSLIECIGQIRSLITVQMGQESNLWIOS 2180

Qy 2251 LMKLVNHTFPQHPDLIRVLIRVHNWVAVMNNTLTGRRAQASDAQSPSSQPVABDSKEKD 2310

Db 2181 IGMINKNVFQHNLRALGMHTVIEVMVNLG-----GGSKE-IR 2223

Qy 2311 SHEWVACRFLCYCTGTGRONQAMFDHEDFLIENSNILISPSLIGSTPLDVAVSSLM 2370

Db 2224 PPKWVTSCECRFLCYFCRISRONQSMFDHLSYLLENGIGL--GMQGSTPLDVAASVI 2280

Qy 2371 ENTLEALALREHYLEKLAIVLSRGLQSNSELVKGPDLGMPDVEBERVLDLPRFCWV 2430

Db 2281 DNNEILALALQDLEKAVSYLAGGLQSCPLVAKGVPDIMGKPCGGERVLDLPRFV 2340

Qy 2431 NGSEVENANVIRLLIRPECTGPRALGE-GEGLTAVIDANMSRIA-----DR 2481

Db 2341 NGSEVENANVYVLLIRKPCRCPRALRGSGSLTALIEAIRISDPDPRDDEGIRDR 2400

Qy 2482 RKLREMEQSGDVNSHPLPSDEDEYIDTGAALNFYCTLVLDLGRCAPDAGVIALGN 2541

Db 2401 RR-----SHFG-----EPPRENNVHLGHAIMSFYALITDLGRCADEMHLQNGK 2447

Qy 2542 ESLEBARALISVPLEDQGVLSRFLTNPPAGEB-----RPSDMPESGLIPEHKQSVG 2597

Db 2448 EALTKRILNLSVLEPDLVGITSL--PLQIPLTGKDALVQPK--MSASVPPHKAQSMVL 2503

Qy 2598 FLERVYGIETQELFEYKLEBEAFPLDLSRAATMLDRNDGCSDMALSMNRVIGNSILPLLIK 2657

Db 2504 FLDRVYGIENQDPLHTVLDVGFPRDMRAASLDITATFTTBMLAVNRYICLAVLPITK 2563

Qy 2658 HAYVYNEAENVASILDATHTTYRLSLKRMPLTKGOREAVSDPLVALTSAMQPSMLKLR 2717

Db 2564 CAPLFACTERRAIVWDSMLHTVYRLSRGRSLTGAQRVIDEDCLMSLCRYIRPWLQHLRL 2623

Qy 2718 KLTVDKSLSEYTTVALRLTLTYERCAKTYGSTGAGQCAFSGASDBEKKLTMMLSNIF 2777

Db 2624 RLVDVDPLINEFAMPKRLTNHYERWKTY--CLPTGMANFQVTSBEHLTKRLFEGIF 2682

Qy 2778 DLSLKMDEYBELFGKALPCLTALGICALPRYSLSKYVDSEFYGEQOAGLD--NPOYDQ 2836

Db 2683 DSLAHKKYQDELYRKMNPCLCALAGALPRY-----VDASYSKAKKATVDAEGNDFR 2737

Qy 2837 PINTSSVALNNDINTVYQKFSBYHDWAMSRKIENGWYGEGMSDQKTHPLRKYNNL 2896

Db 2738 PVETLANVYIPEKIDSFINKPAEYTHEKPAFDKIQNNWSYGENIDEELTKHPMLRPXYTFS 2797

Qy 2897 DYERKEREKEVRSIKALLAIGNSVESHSEVDIENNRSSMRROSKSGGRPELYTDSATP 2956

Db 2798 EKQKEIYRWIKESLAKAMIAEWITIE-----KAREGEKTEKKTKTAKISQSAQT 2847

Qy 2957 FD-----YNPHVDMTNLTLSRQNNAAERLDANADIAWKKKEEL 2998

Db 2848 YDREGINPOPDPDLSAVTISRELQMAEQLAENYHNTWGRKKQOEL 2893

RESULT 3

US-09-424-783-4

Sequence 4, Application US/09424783

Patent No. 678608

GENERAL INFORMATION:

APPLICANT: Hakamata, Yaeuhiro

APPLICANT: Nishimura, Seichiro

APPLICANT: Barsomian, Edward Leon

TITLE OF INVENTION: Human Type 3 Ryanodine Receptor Protein

TITLE OF INVENTION: and DNA Molecules Coding Thereof

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FILE REFERENCE: 0652.2000000
CURRENT APPLICATION NUMBER: us/09/424,783
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: PCT/EP98/02926
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: DE 197 22 317.6
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 5037
TYPE: PRT
ORGANISM: Oryctolagus cuniculus
US-09-424-783-4

Query Match      40.9%; Score 6439; DB 2; Length 5037;
Best Local Similarity 44.1%; Pred. No. 0;
Matches 1364; Conservative 529; Mismatches 902; Indels 296; Gaps 63;

Qy      5 EGGAEEODDVSFRTEDMVCISCTAT----GGRVCLAAEGFGRNRHCPLENIAD-KNIPD 59
      3 DGEAGE-DEVOFLRTDEVLQCSATVLAKEQLKCLAAEGFGRNLCLEFESNAQNVPP 61
Qy      60 LSGCVFVLEQALSVRALQELV--TAAGSETGKGTSGHRTLLYGNAILLRHLSMDYLA 116
      62 LAICFTLEQSLSVRALQELMANTVBAVSSQ--GGGHRTLLYGHAILLRHLSRMYLS 119
Qy      117 CLTSSSSQ-DKLAFDVCLQHSQSGACWTLHPASKRSRSGEKRVDDLLIVSVATERY 175
      120 CLTSSSSMTDKLAFDVLQBDATGEACMTMHKRSRSGEKRVDDLLIVSVSERY 179
Qy      176 LHTEKNEVASIVNASFVTHMSVOPVGTG;SRMKYGVYVFGSDVLRFFHG-DECLTIPS 234
      180 LHSTSGELQVDSFQWITLMMNP----ICSCSESYVTGSHVLRPHGMDCLTI-S 234
Qy      235 TWTKDQGNIVYVYEGGSVMSQASLMLRLARTKMAAGFIMVYHPIRIITGRYLVGN 294
      235 AASDDQRLVYVYEGGAVCTHASSLMLRLRLISMWSGSHLRMGQPLAIRVTTGRVYALT 294
Qy      295 DONELYVSRBEATYASCACLRQEKDQKQVLEDKLAVIYGAITIKYGSIVYVQHSRT 354
      295 EDGLVVDVAKHTKATKSPCFRYSK-EKLDTPAKRVEGMPREIKYGSISLCPVQIVAS 353
Qy      355 GLWLSKYSEYETKKKGKGVKEKQALHBEGRKMDGLPFRSOREBSRTAVIRKCSLPT 414
      354 GLWLTAAAPPKALRLG-VLKKAALHQBGMDDALVTRCOQBSQAAAHVISTALYN 412
Qy      415 KFTNGLETTQENRHSWFPA--SVNLGEMVWCLEDLINYPADQDEDEHEKSKKPPALR 472
      413 QFIKGLDPSFGKRGSGPPAGPALPIEAVILSLQDLGYFEPREBELQHEKSKLARSLR 472
Qy      473 NRQDLFOEGEGLMLILEAIDKINVTISQGLAGLAGDESGQWEMISGLYQOLLAIIK 532
      473 NRQSLFOEGEGLMLIVLNCIDRLINVTYTAAPFAEY-AGEBAESKKEIVNLLEYLMSLIR 531
Qy      533 GNHTNCQAFANSRNLMLFRLGS-QASGEGTGLDVTHCVLIDSPALMMMDDEHMKVI 591
      532 GNANCLP--STNLDVNVSKLDRLEAS--SGILEVLYCVLIESPVLNIQENHKS1 586
Qy      592 ISLLEKHGRDPKVLVDVCSLCVNGGVAVRSQNNICVLLPGKULLQOTLVHDSVVR 651
      587 ISLDDKGRHKKVLDVCSLCVNGGVAVRSQNNITENLPRGRLLQOTLVINVTISIRP 646
Qy      652 NIFVGVGSAVTRKMYFEVYTMHIK-TTHMPLHRIGMANTTGYVPIYGGGKKGKGG 710
      647 NIFVGRAGESTOYKMYFEVVDVDEVPFLTAQATHLRVWALTEGYSPYGGGGKGGNG 706
Qy      711 VGDDLYGVGFGAALVMSGGRKTPVNRTHABEPIRKDDVIGCALDLVPIINPFNVRY 770
      707 VGDDLYGVGFGALVMTGHVAPV--TSQGHLLAPEDVVSCLDLSVPSISFINCPV 764
Qy      771 TGSFTNLSGMPFVVISCSKSLSCRFLLGEGHRLRYAAPEGYSLVESLIPQOIIISL 830

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Qy      889 NKIEAGMTGDQREDLHKIHPCLVPERLEPAEKRYDIQALVQTLKTIIALGYISL-D 946
      885 TRIQGMVYGPVADNKKRLHPCLVNFHSLEPERRNVLQWSGRTLKTIIALGCHVMADE 944
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      945 KADNLRKTKLP-KTYMSNGYKPARLDLSHVLTPAQTLTVRLLENGNVAVARVQAQ 1003
Qy      1007 GMTYGLNEDSDMRSFHLVLPYKADAIRKANSDTASVTRTLTVYGYMDPPTGEQHEA 1066
      1004 GMSYSAVODIPARRNPLVYRLIDEATKSNDSLSQAVRTLLGIGYNIPEPDQES-- 1061
Qy      1067 LLLASQKQAD-FRTYRAEKYAVSSGKYFEFEILTAGPMEVGNAAHMDAGMMLGOD 1125
      1062 ---QVENQSRWDRVRLFRABKSYTVQSGRYFEFEAVTTGEKVGVARPELRDVELGAD 1118
Qy      1126 ENSMAFDGYNEEYVSGNTESFGKQAVGVGVFPLDKTISFSLNGELLDALGERT 1185
      1119 ELAVYFNGHGRQWHLG-SEPFGRPMQSGGVGCMIDLENTIIFTLNGEVLMSDSGET 1177
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Qy      1484 QANQRYNQMARPSTNLVGSQVGLMAYTPQDKQNTSTLAQSATETV-GNEIPIAAC 1542
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      1724 CSRNRSMLSYIVPLPBTBALITLPPGRKGNARRGLRGVGVTTSLRPHHFSPCFV 1783

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2752 KKKKEEL 2758

RESULT 5
us-09-424-783-2
Sequence 2, Application US/09424783
Patent No. 6780608
GENERAL INFORMATION:
APPLICANT: Hakamata, Yasuhiro
APPLICANT: Nishimura, Seiichihiro
APPLICANT: Barounian, Edward Leon
TITLE OF INVENTION: Human Type 3 Ryanodine Receptor Protein
FILE REFERENCE: 0652.200000
CURRENT APPLICATION NUMBER: US/09/424,783
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: PCT/EP98/02926
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: DE 197 22 317.6
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 4866
TYPE: PRP
ORGANISM: Homo sapiens
US-09-424-783-2

Query Match 40.3%; Score 6354; DB 2; Length 4866;
Beet Local Similarity 43.2%; Pred. No. 0;
Matches 1325; Conservative 508; Mismatches 848; Indels 388; Gaps 52;

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Db 2348 SYSEPMAGNFCPDHAPVFLDRYVYGKDQTFLLHLEFVGPLPRLRASALDVTSLST 2407
QY 2637 SDMALSMNRYIGNSILPLIKHAYFYNEAENYASILDATLHTVYRLSKRMULTKGQREAV 2696
Db 2408 TRALLALNRYIGSAVLPILTRCAPLFGTEHCTSLIDSTLQITVYRLSKRSITKAQORDY 2467
QY 2697 SDPLVALTSAMQPSMMLKILRKLYDVVSLSEYTYVALPLTLHYRCAKYGGSTGAGG 2756
Db 2468 BECLLAIICNHLRPSMLQOLLRLVFDVPQLINECKMPLKLTNHRHQCKY-CLEPSWG 2526
QY 2757 AFGASDESKRLTMMLFSNIFPDSLMDYEPFLFGKALPCLALGALPPDYSLSKNYD 2816
Db 2527 STGLAVEBELHLETKLFWGILDSLSKXYDPDLFRALCLSLAGALPDPY-----LDS 2581
QY 2817 EFGY--KEQAGDLNDPOYDPOEINTSSVALNNDLNTIYQKSEHYHDAWASKIENGW 2874
Db 2582 RITATLEKQISVDAOG-NPDPRKINTMNFSLPEKLEYIYTKVAEHSMDKMACKSQSGWK 2640
QY 2875 YEGMSDSQKTPRLKPYTMADYERKRYKEPRESLKALLAIGVSEHSE-----VDIP 2929
Db 2641 YGISLDEANVYTHPLRPFYLTKEKEKIYRWPARESLKTMLAGWVTEKTEGELVQOR 2700
QY 2930 SNRRSMBRSQSGGRPREIVTDSATPPDYNPAPVMTNLTLSRBQNNALRADNAHDI 2989
Db 2701 ENEKLSVSOAQN-----SYSPAPDLDSNVLSKRELQGVVAAENYHNI 2747
QY 2990 WAKKKEEL 2998
Db 2748 WAKKKEEL 2756

RESULT 6
US-08-114-555A-8
; Sequence 8, Application US/08114555A
; Patent No. 5854392
; GENERAL INFORMATION:
; APPLICANT: Manly, Susan P.
; APPLICANT: Kozlowski, Michael R.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF beta-APP-C100
; TITLE OF INVENTION: RECEPTOR (C100-R)
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/114,555A
; FILING DATE: 30-AUG-1993

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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
;   NAME: Coruzzi, Laura A.
;   REGISTRATION NUMBER: 30,742
;   REFERENCE/DOCKET NUMBER: 6013-115
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (212) 790-9090
;     TELEFAX: (212) 869-8864/9741
;   TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 240 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: unknown
;   MOLECULE TYPE: protein
;   US-08-114-555A-8

Query Match
Best Local Similarity 34.7%; Score 336.5; DB 1; Length 240;
Pred. No. 7.1e-21;
Matches 82; Conservative 37; Mismatches 70; Indels 47; Gaps 4;

QY 1879 TESVRPQMKTD-----IASITEISNLSPYPLEVAREFVMOALAEAVTNQVNR 1931
DB 5 TTSLRPHHFSPPCFVALPAGVAAPARLSPAIFLEALRDKALMLGEAVDGGQHR 64
QY 1932 DPGVGSNENLFLPLIKLVDRLLVGMARDVDYKLLIMTNPETW-----DPSFDK 1981
DB 65 DPGGGSVEFQFVPLKLVSTLWMGIFGDEVDYKQILKMIPEVFTSEEESEEESEEE 124
QY 1982 ECKDEHRK-----GLHMKMAGATLQMCYLLQHN 2012
DB 125 EEDEBEKEDEEEBEKEDEAEKEEBAPEGEKEDLEEGLLQMKLPESVXLQMCNLLFYC 184
QY 2013 DQLRRHVAIIAFAHDFVGDLOTQDRLRYTEIKQS-DLPSAAVAKTREFRCPPR 2067
DB 185 DQELQHRVSLAFAFARYVDKIQANQSRVYALLMRAFTWSAETARTREFRSPQ 240

RESULT 7
US-08-559-397A-14
; Sequence 14, Application US/08559397A
; Patent No. 6083713
; GENERAL INFORMATION:
;   APPLICANT: Manly, Susan P.
;   APPLICANT: Kozlowski, Michael R.
;   APPLICANT: Neve, Rachael L.
;   TITLE OF INVENTION: CLONING AND EXPRESSION OF
;   TITLE OF INVENTION: BETA APP-C100 RECEPTOR (C100-R)
;   NUMBER OF SEQUENCES: 35
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Pennie & Edmonds
;     STREET: 1155 Avenue of the Americas
;     CITY: New York
;     STATE: NY
;     COUNTRY: USA
;     ZIP: 10036/2711
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FASTSEQ Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/559,397A
;     FILING DATE: 15-NOV-1995
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Coruzzi, Laura A.
;     REGISTRATION NUMBER: 30,742
;     REFERENCE/DOCKET NUMBER: 6013-115
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 212-790-9090
;       TELEFAX: 212-869-8864
```

```

;   TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 14:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 240 amino acids
;       TYPE: amino acid
;       STRANDEDNESS:
;       TOPOLOGY: unknown
;   MOLECULE TYPE: peptide
;   US-08-559-397A-14

Query Match
Best Local Similarity 34.7%; Score 336.5; DB 2; Length 240;
Pred. No. 7.1e-21;
Matches 82; Conservative 37; Mismatches 70; Indels 47; Gaps 4;

QY 1879 TESVRPQMKTD-----IASITEISNLSPYPLEVAREFVMOALAEAVTNQVNR 1931
DB 5 TTSLRPHHFSPPCFVALPAGVAAPARLSPAIFLEALRDKALMLGEAVDGGQHR 64
QY 1932 DPGVGSNENLFLPLIKLVDRLLVGMARDVDYKLLIMTNPETW-----DPSFDK 1981
DB 65 DPGGGSVEFQFVPLKLVSTLWMGIFGDEVDYKQILKMIPEVFTSEEESEEESEEE 124
QY 1982 ECKDEHRK-----GLHMKMAGATLQMCYLLQHN 2012
DB 125 EEDEBEKEDEEEBEKEDEAEKEEBAPEGEKEDLEEGLLQMKLPESVXLQMCNLLFYC 184
QY 2013 DQLRRHVAIIAFAHDFVGDLOTQDRLRYTEIKQS-DLPSAAVAKTREFRCPPR 2067
DB 185 DQELQHRVSLAFAFARYVDKIQANQSRVYALLMRAFTWSAETARTREFRSPQ 240

RESULT 8
US-08-114-555A-6
; Sequence 6, Application US/08114555A
; Patent No. 5854392
; GENERAL INFORMATION:
;   APPLICANT: Manly, Susan P.
;   APPLICANT: Kozlowski, Michael R.
;   APPLICANT: Neve, Rachael L.
;   TITLE OF INVENTION: CLONING AND EXPRESSION OF beta-APP-C100
;   TITLE OF INVENTION: RECEPTOR (C100-R)
;   NUMBER OF SEQUENCES: 18
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: PENNIE & EDMONDS
;     STREET: 1155 Avenue of the Americas
;     CITY: New York
;     STATE: New York
;     COUNTRY: U.S.A.
;     ZIP: 10036-2711
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/114,555A
;     FILING DATE: 30-AUG-1993
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Coruzzi, Laura A.
;     REGISTRATION NUMBER: 30,742
;     REFERENCE/DOCKET NUMBER: 6013-115
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (212) 790-9090
;       TELEFAX: (212) 869-8864/9741
;     TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 240 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: unknown
;   MOLECULE TYPE: protein
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Db 410 TITONERRF-----VTKLEBDIFVADVANNQGEVLVITKPN-----BEROK 454
Qy 477 LFOEGILNL---ILBAIDKINITSQGLAGFL-AGDESGQSMENISGLYOLLAAIIK 532
Db 455 IAREQVITLAVQFELKAPFEK--AGEGSLRLBEDLDGDKYAPYKMLRCLCYVL-----507
Qy 533 GHTNCAQFANSNRLMWLFSRLSQASGEGTGM--DVLCVLIDSPALNM-MRDEHIK 589
Db 508 -RHSQODYRNQGEYIAKNFCVMQSQI---GYDILADDTITALLHNRRKILLEKITAKEIE 563
Qy 590 VIISLEKHGRDPKVDVLCSLCVGNGVAVRSONNICDYL--PGK-NILLQALVDHS 647
Db 564 TFSVSLRRN-REPRFLDVLSDLCVSNTPALPVQELCKEMLSPGNADILIQTKVVSQA 622
Qy 648 S--VRPNIFVGRGSAVYRKAYFEVTMDHIEKTIHMMPLIRIG 689
Db 623 DNPMESSILSDDIDDEEVLWYIDSKKEPHGKAIIRLHAQEAKEG 666

RESULT 11
PCT-US96-01735-1
Sequence 1, Application PC/TUS9601735
GENERAL INFORMATION:
APPLICANT: Maika, Andrew R.
TITLE OF INVENTION: HUMAN T CELL INOSITOL 1,4,5,-TRISPHOSPHATE
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01735
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/386,039
FILING DATE: 09-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kole, Lisa B
REGISTRATION NUMBER: 35,225
REFERENCE/DOCKET NUMBER: A30042 - 165/30555
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2628
TELEFAX: 212-765-2519
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2713 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURES:
PCT-US96-01735-1

Query Match 1.8%; Score 289; DB 4; Length 2713;
Best Local Similarity 23.2%; Pred. No. 1.3e-14;
Matches 176; Conservative 106; Mismatches 306; Indels 172; Gaps 37;

Qy 15 SFLRTEDWVCLSCATATGERVCLAAEGFGRNRCFL- NIADKNIP- DLSQCFVI-----67
Db 7 SFLHTCD-ICSLYABEGSTNGFISTGLVDRCVQGETBDLNNPKKFRDCLFJLCPMNR 65
Qy 68 -----EQALSVALLOELVYAAASEFGKSGSHRTLL-----YGNAILR 107
Db 66 YSAQKQFWAAKPRGANSTTDVAVLNKLHHAADLEK-KQNETERKLLGTVIQGNVQLL 124
Qy 108 HNSDMYTLAC-LSTSSQDKLAFDVLQOHSQEGACMTWILPASKORSSEGEKRVGDDIL 166
Db 125 HLSKNMVLTVNRRRLPALLEKNMRYTLDE-AGNBSGMFYIQFPYKRSIGDSVVIDKXV 183
Qy 167 LVSATERYLHTTKE-----NEVSIVNASPHYTHMSVQPYGTSIMKTYV---GYV 214
Db 184 LNPVNAQPLHAASHQVLVDNPNCEVNSVNCN---TSWKI-----VLFMKSDNKKDIL 234
Qy 215 PGSDVLPFPHGDE-CLTIPSTWTDGCGNIVYBEG---SWSQABSLMLELAR-TRK 268
Db 235 KGGDVVRLPHAQERFLTCDEHRKK--QHVELRTTGRQSAVSATSKALMEVEVVDHP 291
Qy 269 MAGFPLNMYHPRIRHITTRGYLVN-----DQNELYLVREBATTA 310
Db 292 CRGAGAYMNSLRFPHKILATGHILAAEVDPDEEBECLEFPQSVDPDQD---ASRSRLRYA 347
Qy 311 SCAPCLRQEK-----DDQKQVLEDKOLEVYIADRIKYGDSVTIVQSHSETGLMIS 359
Db 348 -----QEKVYVSLVSVPEGNDISSIFELDPTTLRGDSLVRNRYVALRHLCITVTVV- 399
Qy 360 YKSYETKKKGKGVKVEKQAILH-----BEGMDQG-----LDFSSQBEEST 402
Db 400 ---HSTNIPIDKEEKQVMLKIGTSPVKEDKARGIVPSPAEVRDLDFAND-----A 449
Qy 403 ARVIRKCSLFTFKINGLETLOENRRHSMFPAVNIAGEVMCLBDILINYPADDEDMENE 462
Db 450 SKVL---GSIAKLEKG--TITONERS-----VTKLEBDLV-YFVVGCTNSGQD 493
Qy 463 EKQNP-RALNRQDLFOEGILNLILEAIDKINITSQGL-FLAGLAGDESGQSMEMIS 520
Db 494 VLEAVFSKPNRRQKLMREONILKQIFKLQAPFTDCCGPMRLREILDQDQHAAPRHIC 553
Qy 521 GVLQOLLAIIKGNHTNCAQFANSNRLMWLFSRLSQASGEGTGMVDVLCVLIDSPAL 580
Db 554 RLCTVLRHSQODYRNQGEYIA--KQFGMQKQIGDVLA---DITALLHNRRKLL 606
Qy 581 NMRDEH-----IKYISLEKHGRDPKVDVLCSLCVGNGVAVRSONNICDYLIPGN 635
Db 607 ----EKHTAIEDIFVSLVRKN-REPRFLDVLSDLCVSNKSIPTVQELCKAVLNPTN 661
Qy 636 --LILQTLV-----DHVSVRPNI FVGRVGSAYRKW 667
Db 662 ADILLETCLVLSRPFEGVSGTGENALBAGEDEBEVWLFW 701

RESULT 12
US-09-385-222A-4
Sequence 4, Application US/09385222A
Patent No. 6465211
GENERAL INFORMATION:
APPLICANT: RIKEN;
APPLICANT: Katsuhiko Mikoshiba
TITLE OF INVENTION: High affinity IP3 binding polypeptide
FILE REFERENCE: PH-657US
CURRENT APPLICATION NUMBER: US/09/385,222A
CURRENT FILING DATE: 1999-08-26
PRIOR APPLICATION NUMBER: JP98/242207
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 2749
TYPE: PRT
ORGANISM: Mus musculus
US-09-385-222A-4

Query Match 1.8%; Score 279; DB 2; Length 2749;
 Best Local Similarity 23.2%; Pred. No. 1e-13;
 Matches 167; Conservative 100; Mismatches 306; Indels 148; Gaps 34;

```

QY 15 SFLRTEDMVCSTATGGERVCLAAEGFGRHCFLE-NIADKRI PP-DLSQCYFVIT----- 67
DB 7 SFLHIGD-ICSLYAEGSTNGFISTGLVDRCVGPBAGDILNPPKPKFDCIFKICPMNR 65
QY 68 -----EQALSVRALOEIVTAAGSEFGKSGSHRTLL-----YGNAILLR 107
DB 66 YSAQKQFWKAAPGANSTTDAVLLNKLHHAADLEK-KQNETNRKILGTVIGYVIGIQL 124
QY 108 HUNSDMYTLAC-LSTSSODKLAFDVGLQOHSQGBACMTLHPASKORSEGEKRVVGDLL 166
DB 125 HLKSNKYLTVNKRLLPALLEKMMRVTLDE-AGNEGSMFYIQPFYKLSIGDSVIGDKV 183
QY 167 LVSVAETERYLHTTK-----NEVSIYNASFWHTMSVQPYGIGISMRYV-----GYV 214
DB 184 IMPVNAQOPFLHASSHQLVDNPGCNBYNSVNCN---TSMKI-----VLFMKMSDNKDIL 234
QY 215 PGGDVLRPFHGGDE-CLTIPSTWTKOGGONIVYBEG-----SWSQARSLMRLTLAR-TK 268
DB 235 KGGDVVRLFLHAEQKFLTCDEHRKK---QHVLRITTRGQSATSATSISKALMEVEVQHP 291
QY 269 WAGGFINTWHPMRIRHITTYGRYLVN-----DONELIVSREBATT 310
DB 292 CGGAGGYNNSLFRFHLATGHYLAABVDPDFEECELEFPQSVDPD-----ASRSLRNA 347
QY 311 SCAPFLCROEK-----DDQKQVLEDKLEVIAGPIIKYGDSVTIVQSEGLMIS 359
DB 348 -----DEKMYVSLVSVEGNDISSIFELDPTTLRGDSLVRNSYVLRHLCTNTWV- 399
QY 360 YKSYETKKKGVGKVEKQAILH-----BEGKMDGDLDSRQSEBSRTARVIRKSSLE 413
DB 400 -----HSTNIPIDKEBKPYMLKIGTSPLEKEDK-EAFALVPVSPAEVRDLDPANDASKYL 453
QY 414 TKFINGLE--TLQENRRHSMFPFASVNLGEMVCLDLINYPAPQDEMDHEBEKONKF-RA 470
DB 454 GSIAKLEKGTITTONERS-----VTKLLELV-YFTYGGNSQDVLVVFESKP 502
QY 471 LNRQDLPOEGILNLLEAIKINIVTSQG-FLAGFLAGDESQGSWEMISGYLQLLAA 529
DB 503 NNRQKLMREONILKQIFLCLAPFDGDPRLRLBELGDQRLHAFRHLICLCLRVLH 562
QY 530 IIKGHTNCAQFANSRLMLFSLGSGQASGEGTGLDVLAHCVLIDSPALNMGRDH-- 587
DB 563 SQQDYRKQOEYLA--KQGFQMKQIGYDVLA-----DTITALLHNNRKL-----EKHYT 611
QY 588 ---IKVITSLKKGHPKVLVDVLCGLCVNGVAVASSQNNICDYLPGKN--LILQTL 642
DB 612 MAEITPVSILVRKN-REPRDLTLDLCSVMKNSIVTQELIKAVLFTNADILLETKL 670
QY 643 V 643
DB 671 V 671

```

RESULT 13
 US-09-385-222A-2
 ; Sequence 2, Application US/09385222A
 ; Patent No. 6465211
 ; GENERAL INFORMATION:
 ; APPLICANT: RIKEN;
 ; APPLICANT: Katsuhiko Mikoshiba
 ; TITLE OF INVENTION: High affinity IP3 binding polypeptide
 ; FILE REFERENCE: PH-657US
 ; CURRENT APPLICATION NUMBER: US/09/385,222A
 ; PRIOR FILING DATE: 1999-08-26
 ; PRIOR APPLICATION NUMBER: JP98/242207
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2
 ; LENGTH: 604
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-385-222A-2

Query Match 1.4%; Score 222; DB 2; Length 604;
 Best Local Similarity 23.4%; Pred. No. 6.6e-10;
 Matches 131; Conservative 71; Mismatches 231; Indels 128; Gaps 27;

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QY 15 SFLRTEDMVCSTATGGERVCLAAEGFGRHCFLE-NIADKRI PP-DLSQCYFVIT----- 67
DB 7 SFLHIGD-ICSLYAEGSTNGFISTGLVDRCVGPBAGDILNPPKPKFDCIFKICPMNR 65
QY 68 -----EQALSVRALOEIVTAAGSEFGKSGSHRTLL-----YGNAILLR 107
DB 66 YSAQKQFWKAAPGANSTTDAVLLNKLHHAADLEK-KQNETNRKILGTVIGYVIGIQL 124
QY 108 HUNSDMYTLAC-LSTSSODKLAFDVGLQOHSQGBACMTLHPASKORSEGEKRVVGDLL 166
DB 125 HLKSNKYLTVNKRLLPALLEKMMRVTLDE-AGNEGSMFYIQPFYKLSIGDSVIGDKV 183
QY 167 LVSVAETERYLHTTK-----NEVSIYNASFWHTMSVQPYGIGISMRYV-----GYV 214
DB 184 IMPVNAQOPFLHASSHQLVDNPGCNBYNSVNCN---TSMKI-----VLFMKMSDNKDIL 234
QY 215 PGGDVLRPFHGGDE-CLTIPSTWTKOGGONIVYBEG-----SWSQARSLMRLTLAR-TK 268
DB 235 KGGDVVRLFLHAEQKFLTCDEHRKK---QHVLRITTRGQSATSATSISKALMEVEVQHP 291
QY 269 WAGGFINTWHPMRIRHITTYGRYLVN-----DONELIVSREBATT 310
DB 292 CGGAGGYNNSLFRFHLATGHYLAABVDPDFEECELEFPQSVDPD-----ASRSLRNA 347
QY 311 SCAPFLCROEK-----DDQKQVLEDKLEVIAGPIIKYGDSVTIVQSEGLMIS 359
DB 348 -----DEKMYVSLVSVEGNDISSIFELDPTTLRGDSLVRNSYVLRHLCTNTWV- 399
QY 360 YKSYETKKKGVGKVEKQAILH-----BEGKMDGDLDSRQSEBSRTARVIRKSSLE 413
DB 400 -----HSTNIPIDKEBKPYMLKIGTSPLEKEDK-EAFALVPVSPAEVRDLDPANDASKYL 453
QY 414 TKFINGLE--TLQENRRHSMFPFASVNLGEMVCLDLINYPAPQDEMDHEBEKONKF-RA 470
DB 454 GSIAKLEKGTITTONERS-----VTKLLELV-YFTYGGNSQDVLVVFESKP 502
QY 471 LNRQDLPOEGILNLLEAI 491
DB 503 NNRQKLMREONILKQIFL 523

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RESULT 14
 US-09-949-016-6507
 ; Sequence 6507, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6507
 ; LENGTH: 3259
 ; TYPE: PRT


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Oy 2820 GKEQAGLDNPQIDPQPIINTSSVALNDIATIVO-KSEHYNH-----DAMSRLKENGW 2874
Db 2514 GLRSHMDLNS---ENAKIDAEELIQYRDLNQVITIKSOOKQLLEVLQONKELENKCA 2570
Oy 2875 -YGEWMSDSQTHPEPL-KPYMMLNDYKERYKPEPRESLKALLA-----IG 2918
Db 2571 KLEELTKSESEANEDLRSFNALQEKDLSKE--TESLKYISISLITQVTLQEGEGLIG 2628
Oy 2919 WSEHSEVDIPSN-----RSSMR-----QSKSGRPPEIVTDSATPPDY 2955
Db 2629 --LVHAQLKVEEYHRLSALFSSSQKIALEBELVCSQKEAAKVGEIDKLKELKH 2686
Oy 2960 NPHVDWNTLISREMNMAERLMDNADIMAKKGEELVY 3000
Db 2687 LHHDAGL---WRNETETAERIVALELADLVEMQKLMVY 2723

RESULT 15
US-09-150-867-1
Sequence 1, Application US/09150867
Patent No. 6645748
GENERAL INFORMATION:
APPLICANT: Wood, Kenneth W.
APPLICANT: Sakowicz, Roman
APPLICANT: Goldstein, Lawrence S.B.
APPLICANT: Cleveland, Don W.
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Plus End-Directed Microtubule Motor Required for
FILE REFERENCE: 18557C-000110US
CURRENT APPLICATION NUMBER: US/09/150,867
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: US 60/058,645
EARLIER FILING DATE: 1997-09-11
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2954
TYPE: PRT
ORGANISM: Xenopus sp.
FEATURE:
OTHER INFORMATION: Xenopus centromere-associated protein-B (XCENP-B)
OTHER INFORMATION: member of the kinesin superfamily of microtubule
OTHER INFORMATION: motor proteins
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (1)..(472)
OTHER INFORMATION: kinesin like motor domain
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (473)..(2752)
OTHER INFORMATION: rod domain
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (2753)..(2954)
OTHER INFORMATION: tail domain
US-09-150-867-1

Query Match 1.3%, Score 197.5, DB 2, Length 2954,
Best Local Similarity 17.3%, Pred. No. 2,1e-06,
Matches 452, Conservative 425, Mismatches 983, Indels 757, Gaps 119,

Oy 296 QNELLYVREBEATTASCAFC-----LREQKDDQGVLEDDHLYVIGAP---II 340
Db 530 ENQLQVLRKDSGDMAVECKKASPEKEITSLQOOLQSKKEEKELVQSFELKIALEBQLSV 589
Oy 341 KYGDSVIVQHSSETGLMLSYKSYETKKKGVGKVEEKAALIHBEG-----KMDGL 390
Db 590 KAKULVMTNRSREHSINAEVGTDAEKE-----VVRKEMSVLDSDGYMASNSDLQSDVDGK 645
Oy 391 DFGSQQEESTRTARYIRKCSLLTFYKINGLETLDENRHSN---FFASVNLGEMVQCLE 446

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Db	646	RLSSHDECIERRMRLTQKTVLDEEFIFENLANKSENDKQSSBODFMESIQLCEALMA--	703
Qy	447	DLINYPAPQPEDEMSHREKONKFRALRRQDLFOEEGILNILEAKIDKINITYTSQGLAF	506
Db	704	-----BKANAIBELALMRNFD-----NILEN-----	726
Qy	507	LAGESSQSWEMTISGYVYOLLALITKGNHTNCAOFANSRLNMLPSRLSQASGEETGML	566
Db	727	-----ETLKRBIADLERISIKENQETN-----EFELERKETOKEHBAOL	764
Qy	567	DVLHCV-----LIDSPALMMMDENIKVILISLEKH-----	598
Db	765	--IHEISLKLVENAMMYONTBEDJETTKLKEQOIALERKADNLQKKVRNFDL	822
Qy	599	-----GRDPKVLVDLCSL--CVGNVAVRSSONNICDLTPKGNLLQTLAVDVHVSVRPN	652
Db	823	SVMSGDEKICEBELFOJKQSLSDAENVTRDAQKCSF--LNSBNLELKEKMD-----TSN	876
Qy	653	IFVGRVGSAAVRRKMYEVTMDHIEKTTMMPHLRIGMANNTGGVYPRGGGEKGNQVG	712
Db	877	WYNQEKRAASLFEKQLETERKSNYKMEADQKELQSAF--NEINVL-----NG--	922
Qy	713	DDLAYSFPDQAYILMSGGRKTP--VNTTHABEPIYRGDVIQGLDITVPIINPMQVR	769
Db	923	-----LAG--KVPRDLISVBLE--KVSPFSQLEALEREKALKEAVEVT	964
Qy	770	VTGSPFTNPNLEGMFPF--VISC-----SSKLSCRFLL--GSEHGRLRYAAEGYPLVEST	821
Db	965	CLASY-----KELPRNEVCIKNQJISKABEIMLQKQBHSMSIISKE-----IMQE	1013
Qy	822	LPOQILSEBCFYFGNLSKALAGPPLVODTFAVPTPVDLTQTLTPYYEQIRDKLAEN	881
Db	1014	QSEQLQL-----TBEVHTQSKV--QOTBEQYLEM--KKKMD	1048
Qy	882	IHEMMANKIEAGMYGDQREDL-----KHHCINLVFEERLP	919
Db	1049	LFEKYTIINKSEA-----EDLIREKENIKGTWESVEVKIADTKHELEETIRDKQL-L	1099
Qy	920	AERKYDIQLVQTLKTLLAGYYISLDKPRAPRIRNVLPNEPMSQNGYRAPLD--LSA	977
Db	1100	HEKKYFPQ-AMQITFFPTPL-----SDBLPFSKL-----VEGNSQDPIELNDVNL	1144
Qy	978	VTLTPKMDLVDOLAENTHNLWAKERIQQSGWTYGLNEDSPMHSPLVPRKYDDA--IKK	1036
Db	1145	IATATERNNIMVCLETERNSL--KEY-----IDLNTQLOSLQASIEKSDLOK	1191
Qy	1037	ANPDTABEYRTL-----LUVGYMLDPTPG--EQHEALLLESKQAKODFRYYRAE--KRYAV	1090
Db	1192	PKQDLERGEVYKLLMEMLKNGHITDSQLSIEKQLENLEVTKEQO---TLQSEMKYITI	1247
Qy	1091	SSGKMYPEFELLTGAPRYVGMAHADNMAPGMMLGODENSMAPFDGNEEKVYSGNTESPQKQ	1150
Db	1248	ERNELQTNFEDIKRAHNSLKQDLSSENIEGSIETPODELRPAAOBELRERKQO---VDSRQO	1304
Qy	1151	W-----AVGDVVGVPLDLIDKTIISFLNGE-----LMDALGSEYTF-----	1187
Db	1305	LLDSCVGISPRNHDVAVNQEKVSIGEVNSLOSEMLRGEDELQTSCKALVSELELRAHV	1364
Qy	1188	ADVQGNFVACITLGVQKARLTYGQDVNLKTYTTCGLOEGEYBPCVMKRDVTHMYTK	1247
Db	1365	KSVGEVLELITTKKLNGLKEBILKSGESEVYLK-----SMLENLKEDNNKLEQOAEVSSK	1419
Qy	1248	D-----OPIFENTDEMIDTRIDV--TRI PASDPTPRCLAK-SHNTFETMEKAMMEFL--R	1297
Db	1420	ENQPSLEBVSSGSKLVD--BIVULKAQULKAABER--LEIKNDYFELVOTANTYNLVEGK	1475
Qy	1298	LSLPVICHENFIDEAEKARRMVBK-----DEQOILMKEAVEAQMPAH-----IDQIMR	1346
Db	1476	LEFPLQADNH-EBSIDRSEMEIKVGEKLEBNQULERLOEKLELSNKLEILQKEME	1534
Qy	1347	SGFTMDIKGLAHVEDNOBELPSSKMRKLPBRPRKSGMTRGVITQVYNNIOPQOVNGMR	1406
Db	1535	TSVILKQ-----DLQOKLESILSENIILKE-----NIDTTLKHSIDTQA-----QLOK	1577

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QY 1407 STSEANAK-YDLGAQGLTPDDKKDKGRSPFKFRSGESSDPRANSKTPDPSDT 1465
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QY 1466 EVSEERARRPNQIKXSQANQRYNGMARRPTNLYGSGVGLMAMAPTPQDKMNTSTL 1555
Db 1617 LLLTEELHQKTEQEKILH-----EKNELOAQVELK-----CEVEHLMKMEIE 1660
QY 1526 AOSATETVGENEIFDAE--CLKLINEFYGVARIYPGDPPTHVYIGMTTYOYHLHKSDFNOS 1583
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QY 1584 KTVXSIVITDDYDRVENVNROSQYVRADELVEYMAEATKAGASQGFICGSVDYST 1643
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QY 1644 GSVSFTGEGDTSKFKMEBETKLPRAIPEVATSKELQ--TELGRATSPLSAVLP 1701
Db 1744 SOHRLQCEIHELKMSLK-DKESAL-----ETLKESEQKVINLQMEMEVMLEMBELKN 1795
QY 1702 SDKHVIRPQPPRLKVQ-----CLKPHQMAVFNQSLQVHALKJSDIRGMSMLCEDA 1752
Db 1796 SQRTVINE--ROLODULDAESVEMSIETODDLRKAQBALQOQDKVQELTSQSVQEK 1852
QY 1753 VSMIALHIPEEDRCIDILEPMDKLLSFHSHTLTLYAALCYOSNYRAHAALCTHYDQK 1812
Db 1853 ISLL-----ENQ 1859
QY 1813 LLYAISOVMNGPLROGFYDULLIALHESHATMEACKNEFVIRPELPEALVEEPMGH 1872
Db 1860 MLYNVATVKEITLBERDLNOSKOHLPSEIETLSLKEKF----- 1900
QY 1873 SLRSLQTESVYPQKMTDIAESIETISNLSPYFPLEVAREFVQALAEAVETNOVNRD 1932
Db 1901 ALFOAEDKADARKTIDITEKISNT-----BEQLLOQATNLKET--LYERE 1945
QY 1933 PVGGSNENLFLPIKLVDRL---LVGM--RDEDEKLLIMTNPETWDPSPDKGKD 1985
Db 1946 SLIQCEQLALNTEHLEETLKSQDLALGMEQERDEANAKVIALTEKMS-----SLBE 1998
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Db 1999 QINENVTTLKEGGEK--ETFYLQRPKQO-----SSSQMEELRE--SL 2038
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QY 2206 ALEKTVYINAKTLDVAEMVVGLSQIRALLPVQ-----MSQEEBELMRKRL 2251
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QY 2252 WKLVNNHTPEQ--HPDLIRVLAVHE---NVMAVMNMTLGR-----RAOQS-- 2292
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QY 2391 LSRGLOQNSELY-EKGYPDLGMDPVGERYLDPLRFCWVNGSEVEENANL--VIRILI 2447
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QY 2448 RRECCLOPALRGSGEGLIKAIYDA-----NKMSEIADRRK-----LREMEQGD 2492
Db 2479 KR-----LKAIVOSKIQREITVYINQBEAQLQEKKEQNKELMRMEHHG- 2522
QY 2493 VNFSHPLPESDEDEDYIDTGAALINFYCTLV-----LGRCAPDAGVIALGKNESLRAR- 2547
Db 2523 ---PSASVMEEN-----ARLIGILKTYQDESCKLQSRITMLNENLNVKODAMKGE 2572
QY 2548 --AILSLVPLEDLQVLS---LRFTL---NNPAGE--ERPKSDPESGLIPGHQSVGL 2597
Db 2573 KVALIODKLISRNAEALINMQVKLTFRKODNLOAMKEIENLOKMWAKGAVP--YKEEIDN 2631
QY 2598 FLERYVIGIEFQELFYKLEBAFPLDRAATMLDRNG 2634
Db 2632 LKTRVYKIEWEKIKYSKATDQELAYLXSC-LEDKEEG 2667

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 Job time : 95 secs

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OM protein - protein search, using sw model

Run on: April 14, 2006, 01:44:08 ; Search time 42 Seconds
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Title: US-10-668-767-128_COPY_1_3000

Perfect score: 15748

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Published Applications: AA.New:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6440.5	40.9	4868	7	US-11-044-111-24 Sequence 24, Appl
2	2983	18.9	3375	7	US-11-044-111-23 Sequence 23, Appl
3	2709.5	17.2	1056	7	US-11-044-111-22 Sequence 22, Appl
4	643	4.1	237	7	US-11-044-111-11 Sequence 11, Appl
5	623.5	4.0	240	7	US-11-044-111-10 Sequence 10, Appl
6	623.5	4.0	240	7	US-11-044-111-9 Sequence 9, Appl
7	614	3.9	237	7	US-11-044-111-12 Sequence 12, Appl
8	603	3.8	239	7	US-11-044-111-5 Sequence 5, Appl
9	603	3.8	229	7	US-11-044-111-25 Sequence 25, Appl
10	576.5	3.7	212	7	US-11-044-111-6 Sequence 6, Appl
11	576.5	3.7	212	7	US-11-044-111-26 Sequence 26, Appl
12	285	1.8	2671	6	US-10-876-787-6 Sequence 70, Appl
13	199	1.3	2668	7	US-11-124-368A-215 Sequence 215, Appl
14	198.5	1.3	2665	7	US-11-124-368A-214 Sequence 214, Appl
15	187.5	1.2	1249	6	US-10-506-454-486 Sequence 486, Appl
16	186	1.2	576	7	US-11-240-769-70 Sequence 70, Appl
17	186	1.2	5024	6	US-10-793-626-2964 Sequence 2964, Appl
18	183.5	1.2	2228	6	US-10-511-096-2 Sequence 2, Appl
19	183.5	1.2	2230	6	US-10-511-096-4 Sequence 4, Appl
20	183.5	1.2	2250	6	US-10-511-096-6 Sequence 6, Appl
21	183.5	1.2	2252	6	US-10-511-096-8 Sequence 8, Appl
22	172	1.1	5406	6	US-10-995-561-774 Sequence 774, Appl
23	166.5	1.1	1976	7	US-11-069-834-54 Sequence 54, Appl
24	164.5	1.0	3803	6	US-10-995-561-773 Sequence 773, Appl
25	164.5	1.0	3960	6	US-10-995-561-771 Sequence 771, Appl

26	164.5	1.0	5335	6	US-10-995-561-777 Sequence 777, Appl
27	164.5	1.0	5415	6	US-10-995-561-779 Sequence 779, Appl
28	164.5	1.0	5464	6	US-10-995-561-775 Sequence 775, Appl
29	163	1.0	2101	6	US-10-857-780-23 Sequence 23, Appl
30	160.5	1.0	2304	6	US-10-330-773-310 Sequence 310, Appl
31	159.5	1.0	1976	7	US-11-069-834-52 Sequence 52, Appl
32	158.5	1.0	5335	6	US-10-995-561-776 Sequence 776, Appl
33	158	1.0	1960	7	US-11-069-834-48 Sequence 48, Appl
34	157.5	1.0	630	7	US-11-196-400-5 Sequence 169, Appl
35	157.5	1.0	1404	6	US-10-878-556A-169 Sequence 169, Appl
36	151.5	1.0	1960	6	US-10-530-171-17 Sequence 17, Appl
37	151.5	1.0	1960	7	US-11-069-834-50 Sequence 50, Appl
38	151.5	1.0	8746	7	US-11-098-686-10232 Sequence 10232, A
39	150.5	1.0	2348	6	US-10-450-224A-2 Sequence 2, Appl
40	150.5	1.0	4384	6	US-10-821-234-1120 Sequence 1120, Ap
41	149	0.9	1562	7	US-11-052-554A-211 Sequence 211, Appl
42	149	0.9	1992	7	US-11-069-834-58 Sequence 58, Appl
43	146	0.9	1786	7	US-11-196-400-3 Sequence 3, Appl
44	145.5	0.9	957	7	US-11-051-720-1438 Sequence 1438, Ap
45	145	0.9	860	7	US-11-019-711-59 Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-11-044-111-24
; Sequence 24, Application US/11044111
; Publication No. US20050272362A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Wen
; APPLICANT: Strasbourg, Gale
; APPLICANT: Linz, John
; TITLE OR INVENTION: Genetic Test for PSE-Susceptible Turkeys
; FILE REFERENCE: MSU-09308
; CURRENT APPLICATION NUMBER: US/11/044,111
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 4868
; TYPE: PRT
; ORGANISM: Meleagris gallopavo
; US-11-044-111-24

Query Match	40.9%	Score 6440.5;	DB 7;	Length 4868;
Best Local Similarity	43.7%	Pred. No. 0;		
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QY 415 KPIINGLETLOENRRHSMFASVNIAGEMVWMLBDLINVFAOPDEDMHEEKONKFRALNR 474
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QY 475 QDLFOEEGLNLILBAIDKINVTTSOGFLAGLAGBSGQWEMISGYLYQILAAITKAN 534
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QY 1428 KKDQKGRSPFKFRKSGRGSSESDRAKSRKSKTDPDSDTVSPERGARRPNPOIKVSOANO 1487

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Db 1326 ----- 1327
QY 1548 EYFYGVRIYPGQDPHNHYVYGMWTTQYHLSKDPNOSKTKYSVITTDYDRVENVNRQS 1607
Db 1328 TYFYSRLIFAGODPPSVMGWMTPDYHFFYSEFPDINKCTVVTYTLDEGRGVHESYKRN 1387
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QY 1963 VEKLIIMNPEWTWDSFPXEGDEHR-----KGLIHM 1994
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QY 2167 LIQITVNNABESQIETPKLIREMFSLVROQDAVGLIRALEKTYVINAKTLDVAEMV 2226
Db 1963 ISQIMVRSQEDQIODEPLVAVIMTYLLRQVDSIELLOALRKAYTISAGSKYDITINLLA 2022
QY 2227 GLSQIRALLPVQMSQEBEELMRKRLMKNHTFPQHPDLIRLVHVENVMAVMNNTLGR 2286
Db 2023 ALGQIRSLISVAMGKEBELIMINGLIDIMNNKVFYQHPLMRVLQMHENVDVMVNLG- 2081
QY 2287 RAQASDAQPSQPAEBSKEXKOTISHENVVACCRFLCTFCRTGRONOKAMPHPRLLEN 2346
Db 2082 -----GDKQIYFPKNVASCRCFLCYFCRISRONQKAMFPHLSYLLLEN 2124
QY 2347 SNILSRPSLNGSTPLDVAVSSLMEMENTALALREHYLEKIAVLYVNSGLONSLEIVEK 2406
Db 2125 SSVGLAFPSMGSTPLDVAASVMDNNEIALALEBPDLDKVTYTLAAGLQRCPLILAKG 2184
QY 2407 YPDIGMDPEVGERYLDLRFQVWNGSVEEENANLVIRLLIRREPCLGAPALRG-GEGLT 2465
Db 2185 YPDIGMNPIDEGERYLSFLRFVAVVNSEVENASVVKLLIRRPFCFGBELRGEGBGGL 2244
QY 2466 KAIYDANKMSFRIADRRLREMEQEGDVNFSHPLPESDEDEDYIDTGAAIANFYTLVDL 2525


```
Db      177 AS---SGILEVLYCVLIESPEVNIIOENHIKSIISLDDGGRNKKVLDVLCSLCVNGV 233
QY      618 AVRS 621
        |||||
Db      234 AVRS 237

RESULT 8
US-11-044-111-5
; Sequence 5, Application US/11044111
; Publication No. US20050272362A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Wen
; APPLICANT: Strasbourg, Gale
; APPLICANT: Linz, John
; TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys
; FILE REFERENCE: MSU-09308
; CURRENT APPLICATION NUMBER: US/11/044,111
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 239
; TYPE: PRF
; ORGANISM: Meleagris gallopavo
US-11-044-111-5

Query Match      3.8%; Score 603; DB 7; Length 239;
Best Local Similarity 50.6%; Pred. No. 5.4e-36;
Matches 124; Conservative 50; Mismatches 63; Indels 8; Gaps 5;

QY      379 IHHBGMDDGLDPSRSGEESRTARVIRKCSLFTKFTINGLETL--QENRRHSMFPASVN 437
        |||||
        1 IHHBGMDDGLDPSRSGEESRTARVIRKCSLFTKFTINGLETL--QENRRHSMFPASVN 60
        |||||
QY      438 LGEVMWCLBDLINYPAPDEDMHEBKONKFRALRRNODLFOEGILNLTLEAIDKINVT 497
        : : : : | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
        : : : : | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
        1 IAAVILSLDLIAYFPAFPTTELQHEQRQNRSLRRRQDLFOEGMISLVNCTIDRLNVY 120
        : : : : | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
        498 TSQGLAGFLAGDESGOSWEMISGYLYOLLAIIKGNHTNCAOFANSNRLNMLFSRLGS- 556
        : : : : | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
        121 STRAHFAEF-AGEBAAMAKKEIVNLLYELLASIRGNRTNCALF--STNLDWLVSJLDRL 177
        : : : : | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      557 QASGEGTMLDVLYHCTVLIISPALNMRDEHIVITISLEKGRDPKVDVLCSLCVNGV 616
        : : : : | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
        : : : : | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
        178 EAS---SGILEVLYCVLIESPEVNIIOENHIKSIISLDDGGRNKKVLDVLCSLCVNA 234
        : : : : | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      617 VAVRS 621
        |||||
Db      235 VAVRS 239

RESULT 9
US-11-044-111-25
; Sequence 25, Application US/11044111
; Publication No. US20050272362A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Wen
; APPLICANT: Strasbourg, Gale
; APPLICANT: Linz, John
; TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys
; FILE REFERENCE: MSU-09308
; CURRENT APPLICATION NUMBER: US/11/044,111
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
; LENGTH: 239
; TYPE: PRF
; ORGANISM: Meleagris gallopavo
US-11-044-111-25

Query Match      3.8%; Score 603; DB 7; Length 239;
```

```
Best Local Similarity 50.6%; Pred. No. 5.4e-36;
Matches 124; Conservative 50; Mismatches 63; Indels 8; Gaps 5;

QY      379 IHHBGMDDGLDPSRSGEESRTARVIRKCSLFTKFTINGLETL--QENRRHSMFPASVN 437
        |||||
        1 IHHBGMDDGLDPSRSGEESRTARVIRKCSLFTKFTINGLETL--QENRRHSMFPASVN 60
        |||||
QY      438 LGEVMWCLBDLINYPAPDEDMHEBKONKFRALRRNODLFOEGILNLTLEAIDKINVT 497
        : : : : | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
        : : : : | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
        61 IAAVILSLDLIAYFPAFPTTELQHEQRQNRSLRRRQDLFOEGMISLVNCTIDRLNVY 120
        : : : : | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
        498 TSQGLAGFLAGDESGOSWEMISGYLYOLLAIIKGNHTNCAOFANSNRLNMLFSRLGS- 556
        : : : : | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
        121 STRAHFAEF-AGEBAAMAKKEIVNLLYELLASIRGNRTNCALF--STNLDWLVSJLDRL 177
        : : : : | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      557 QASGEGTMLDVLYHCTVLIISPALNMRDEHIVITISLEKGRDPKVDVLCSLCVNGV 616
        : : : : | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
        : : : : | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
        178 EAS---SGILEVLYCVLIESPEVNIIOENHIKSIISLDDGGRNKKVLDVLCSLCVNA 234
        : : : : | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      617 VAVRS 621
        |||||
Db      235 VAVRS 239

RESULT 10
US-11-044-111-6
; Sequence 6, Application US/11044111
; Publication No. US20050272362A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Wen
; APPLICANT: Strasbourg, Gale
; APPLICANT: Linz, John
; TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys
; FILE REFERENCE: MSU-09308
; CURRENT APPLICATION NUMBER: US/11/044,111
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 212
; TYPE: PRF
; ORGANISM: Meleagris gallopavo
US-11-044-111-6

Query Match      3.7%; Score 576.5; DB 7; Length 212;
Best Local Similarity 49.2%; Pred. No. 3.7e-34;
Matches 120; Conservative 43; Mismatches 48; Indels 33; Gaps 5;

QY      379 IHHBGMDDGLDPSRSGEESRTARVIRKCSLFTKFTINGLETL--QENRRHSMFPASVN 438
        |||||
        1 IHHBGMDDGLDPSRSGEESRTARVIRKCSLFTKFTINGLETL--QENRRHSMFPASVN 40
        |||||
QY      439 GEMWVCLBDLINYPAPDEDMHEBKONKFRALRRNODLFOEGILNLTLEAIDKINVT 498
        : : : : | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
        41 -----LRDLIAYFPAFPTTELQHEQRQNRSLRRRQDLFOEGMISLVNCTIDRLNVY 94
        : : : : | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      499 SQGLAGFLAGDESGOSWEMISGYLYOLLAIIKGNHTNCAOFANSNRLNMLFSRLGS-Q 557
        : : : : | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
        95 STRAHFAEF-AGEBAAMAKKEIVNLLYELLASIRGNRTNCALF--STNLDWLVSJLDRL 151
        : : : : | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      558 ASGEGTMLDVLYHCTVLIISPALNMRDEHIVITISLEKGRDPKVDVLCSLCVNGV 617
        : : : : | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
        : : : : | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
        152 AS---SGILEVLYCVLIESPEVNIIOENHIKSIISLDDGGRNKKVLDVLCSLCVNAV 208
        : : : : | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      618 AVRS 621
        |||||
Db      209 AVRS 212

RESULT 11
US-11-044-111-26
; Sequence 26, Application US/11044111
; Publication No. US20050272362A1
```

```

1 GENERAL INFORMATION:
2 APPLICANT: Chiang, Wen
3 APPLICANT: Strausburg, Gale
4 APPLICANT: Linz, John
5 TITLE OF INVENTION: Genetic Test for PGR-Susceptible Turkeys
6 FILE REFERENCE: MSU-09308
7 CURRENT APPLICATION NUMBER: US/11/044,111
8 CURRENT FILING DATE: 2005-01-27
9 NUMBER OF SEQ ID NOS: 27
10 SOFTWARE: PatentIn version 3.3
11 SEQ ID NO: 26
12 LENGTH: 212
13 TYPE: prt
14 ORGANISM: Meleagris gallopavo
15 US-11-044-111-26

```

Query Match	3.7%	Score	576.5	DB 7	Length	212
Best Local Similarity	49.2%	Pred. NO.	3.7e-34			
Matches 120, Conservative	43	Mismatches	48		Indels	33
					Gaps	5

```

QY      379  ILIHGGKKDDGADPFRSGOEBSERTARVRKSGSLPTKPTNGLETJQENRBRHBMFPASVNL 438
Db      1  ILHGGKMDLALSRSOGESQAAMMISTYGLYGSFTR----- 40

QY      439  GEMWVCTEDLIFYPAOPDMEHSEKONKFPALNRNODLPQEGILANTILAAIDKINITYT 498
Db      41  -----LBDLIAFPRAPTBLEQHORNRRLRELRRODLPQEGMISLVANCIDRLNAYS 94

QY      499  SGGFLAGRLADDESGQSWEMISGVLYOALLAIKKNNHNNCAQFASNNLNLVFSRLGS-Q 557
Db      95  TAAHFAER-AGEEAAANAKKEIVNLVIELLASSLRKNNTCALF--STINDLVYSQDLRLE 151

QY      558  ASGEGTGLDVLHCYLIDSPRALNNMRDEHIKVIISLEKRGDRPKVLDVLCSLCVGNGV 617
Db      152  AS---SGILRVLYCVLIESPRLVNTIIQENHIKSIISLDDKGRNKKVLDVLCSLCVCANV 208

QY      618  AVRS 621
Db      209  AVRS 212

```

RESULT 12
US-10-876-787-6
Sequence 6, Application US/10876787
Publication No. US20050287535A1
GENERAL INFORMATION:
APPLICANT: McGraw, Kevin P.
TITLE OF INVENTION: BIOMARKERS FOR WOUND HEALING
FILE REFERENCE: 1443.156US1
CURRENT APPLICATION NUMBER: US/10/876,787
CURRENT FILING DATE: 2004-06-24
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 2671
TYPE: PRT
ORGANISM: Homo sapiens
US-10-876-787-6

```

Query Match 1.8%; Score 285; DB 6; Length 2611;
Similarity 18.0%; Pred. No. 5,36-11;
Beet Local 431; Conservative 314; Mismatches 829; Indels 820; Gaps 101
Oy 31 GERVCLAEGFNGN-----RACPENIND--KNIPDLSQCVFV----- 67
Db 11 GDIVSLYREGSNGRISTGLVDDCCVVRPAAGDLDNPPKRRDCLFKVCPMKRYSAQK 70
Oy 68 -----EQALSVRALQELVTAASGETKGSGHR-----TLVGNAILRLHNSD 112
Db 71 YMKAKQTQKDEKINDVVLQKLGPAAGMEQKQNTENKXHGVDVKKGSVIGLHMKSN 130
Oy 113 MYLAC-ISTSSQDADPAVDGIQGHSGEACMTWLPASPASKORSEGEKRVGDGLILVSA 171

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Db	131	KYLIVNKRRLPRLLEKNA	MRYTLDA--	TGNESWLFIO	FWTLRSAGD	VVVVGDKITL	LPVN	189
Qy	172	TERYLHTTKE-----	NEVSIYNASFW	HTHMSVOP	YGTGISRMY	YGVYFGD	YLRFF	223
Db	190	AGQPLHASNVEL	SDNACKEVNSV	CNCL---	TSWKINFL	FMQFRDHL	BEV--	244
Qy	224	HGGEBCLTIP	BTWKDGO-----	NIVYEGSVM	SQABSLM	LELA--	RKMA	277
Db	245	HAOEKPL---	TCDEYXKQ	QVFLRTLL	RSASATS	SNMLME	VEVNHDP	301
Qy	278	HPMBIRHIT	TGRYGVNDONEL	YVUSRE	EAFTTAS	CACSLRQ	EOKDOQ	337
Db	302	GLYFPHL	ATGNVLA--	BNPST---	KGDASD	PLAAGMG	QGRGRNA	357
Qy	338	PIIKYG-----	-----	DSYIVOH	SETGLW-----	-----	-----	357
Db	358	P-----	HGNDIASL	FELDP	TLQKTD	SFVPRNS	SVYRLRL	414
Qy	358	LSYASYTKK	KGAVKEB	KOAILHE	EKGMDG	DFSQSE	BSRTAV	417
Db	415	LMGTCTPK-----	EDKEFAL	VSVPSE	IRDLR	PANDASS	LSMAVE	465
Qy	418	NGLETLQ	RNRHSMF	PASVNL	GEMV	MLCE	LDLINV	477
Db	466	-----	QNDRRF-----	-----	YQLLE	BDLV	FEFVSVP	508
Qy	478	FOEGLI	MLLEA	DKIN	VITS	OGFLA	FLA-----	532
Db	509	MREONIL	KQV--	GLXKY	PPRE	KGG--	EGPLV	565
Qy	533	GNHTNCA	OPANSR	NFLNL	FLSHLS	QASGE	GTMLD	588
Db	566	DYRKN	OEHLA--	KQFGM	SOIG	YDILAE-----	DTITAL	614
Qy	589	KVILS	LEKGR	BP	KYL	DVLC	SYGVNG	642
Db	615	VETVSL	VRKN--	REPR	LDY	LSDC	VSNHAI	673
Qy	643	-----	-----	VHSSV	VR	NI	FEVGRV-----	669
Db	674	KEMASH	HYLSI	EYSE	BEW	MLTW	DKNNH	733
Qy	670	E-----	-----	VTMD	HIKT-----	-----	THMPL	689
Db	734	KL	FARMC	LD	ROYLA	IDEI	SOQL	793
Qy	690	-----	-----	WANT	GV	PY	YGGE	713
Db	794	VT	PVKAR	LM	TEI	PTAIT	TDYD	847
Qy	714	-----	-----	DLYSY	GF	DFG-----	AYLW	726
Db	848	AV	PEAN	BK	KL	TE	EVUS	907
Qy	727	SG	GRKT-----	-----	-----	-----	-----	750
Db	908	PG	KNVR	RS	IS	IGV	GHMST	963
Qy	751	G	ALD	LV--	P	IN	MFG	776
Db	964	V	MT	KL	IL	BL	QILAL	1022
Qy	777	FN	LEG	M-----	FP	VS	SCS	825
Db	1023	M	N	R	I	G	B	1076
Qy	826	I	L	S	E	P	C	885
Db	1077	L	L-----	FG	H	S	Q	1126
Qy	886	W	A	N	K	-----	-----	932

Db 1127 WDDKSGSGEVEAGTAKDKEKRPTEBEGFLH-----DPGSKSE--NYOI 1171
Qy 933 LKTIILALGYISLDKBPARIIRVRLPNEPFMOGNGKYPAPLDLSAVTLTPKMDLVDOLA 992
Db 1172 VAGILE-----RLNKGCGVGEOMRKQOQLLKMDHAKMDLLOLPY-DKGDARKMELL 1225
Qy 993 ENTHNIMABERIIQCGWTYGLNEDSDMHSRPHLVPRKVDALIKKANDTASFTVTLVY 1052
Db 1226 RYTHOF-----LOKFCAGNPGNOLALHKHLFLTGLLEA-----ELMQHIFLN 1270
Qy 1053 GYMLDPRTGE-----QHEALLLEASKO--KQADF--RYTBAEKYAVSSGKMYPEFELLTG 1105
Db 1271 NYOLGSEISEPVLOQHVLHATHGRVVOYLDPLHTVYIKAGSKY-VKCCDMTWELTITNG 1329
Qy 1106 PWRVGAHADMAFGMMLGODENSMAFDGYNEEK--VYSGNTESFGQMAVGVVGFJDL 1163
Db 1330 DDVVVPRYNDKASLHNL--DMKKAARDGVBDHSPLMY-----HISL 1368
Qy 1164 IKTTSIFSLSLNGBLMDALGSETTFADVOGDNFPYA-----CTLGCGOKARLITYG 1212
Db 1369 VD-----LLAACAGSKNVYTEIKCTSLVPLEDVVSVVTHEDCITEV--KMAVY 1414
Qy 1213 QDVNTLKYFTTGLGDEY-----EPFCVNMKEDVHTWYTKQDPIENTDEMIDTPI 1263
Db 1415 NFNVNCYVDTEVEWKEIYTSNHIWTLFENFTLDMARVCS--KREKRVADPTLEKYVLSV 1471
Qy 1264 DVTRIPAGSDTP-----PCIKLSH-----NTFET 1287
Db 1472 VLDITNAFFSPSESENSTLQTHQPVVOLLOSTTRLLSCPMLOQHKSVEACIRTLAM 1531
Qy 1288 MEKANWEPLRLSLPVICNEPIDEAE-----KARRYVE--- 1320
Db 1532 VAKGRAILLPMDLAHISMSLSSGASCAAAQGNASSYKATTPAPRVTPTANQMYKNI 1591
Qy 1321 IKDROQIL-----MEAVEAQMPAHID-----QIMSFGTMNDIKL 1357
Db 1592 IKLODITLALBERLPLVDAELSVLVDVLMPELLFLGSEAYQCSGSGFLSKLQ-- 1649
Qy 1358 HYED--NOEELPSSKMKRLPSRPPRK-----GSMTRGVITQNYNNLPOGOVNMHST 1408
Db 1650 HTKDLMESEBKCIKYLRLTQOMLVKTKYGDGRNOLRMGLONY--LQ-----NRKST 1701
Qy 1409 SEAEAKYDLAGOGLTPD-----DKDKKGRSFP-----KFRSKGSESD 1449
Db 1702 SRGDLP--DPIGTGLDPMWSAIAATQCRLDKEGATLVCDLITSTNKEKIFQESIGLAIH 1759
Qy 1450 RAKSKSKTPDPDPSDEVSPERGARRPNQIKVSOANQRYNGMNAKPSKTNLYGSOVGN 1509
Db 1760 LLDGNTETIQSFHNLMMSDKSER--FPKV-----LHRRKRAQOETK--STVAVN 1807
Qy 1510 M-----ATPTQDRKQMTTSTLAOSATEVGNELFDAECLALINEFYGVRIYFGQDPTHVY 1565
Db 1808 NMDLSQPHEDREPVPTTKGRVASFISIGS-----SSRYSLGPRBLRGHREVS-- 1855
Qy 1566 IGMVTTQYHLHSKDNQSKVYKSSVITDDYDR--VVENVNROSQYVWRADDELVNEVM 1621
Db 1856 -----ERVOSEMGTSVLIWPIILRFLOLLCENHRDLQNFIR----- 1893
Qy 1622 AATAKAGASQMGFIGGSVDTSTGVSFTGEGKOTSKFKGPEPTKLPALFVEANSKELL 1681
Db 1894 -----CONNTKNYNLVC-----TLQVL 1911
Qy 1682 QIELGRSATSLPLSAVLPTSDKRVIPQFPRLKVOCLRP--HOMARVPNOSLOVH-- 1735
Db 1912 DIMCGSTTGGLGLIGIYNBDVNGVLIQTLLETITEXCOGPFCHENQCIYTHSNGDIT 1971
Qy 1736 ALKLSDIRGWSMLCEDAVSMALALHPEDRCIDILEPIEMDKLASHSTLTLYAALCYQ 1795
Db 1972 ALIINDI--SPICK-----YMDLVYLQKDNASKILLAL--ME 2005
Qy 1796 SNYRAAHA--LCTHDQKOLVAIISOQVMS-----GPLRQGYDILLALHESHAT 1844
Db 2006 SHRDESEMERILISLAPOBELVDTIKKAYIQEERENSEVSPREVGHNITVIALQLSRH-- 2063

Qy 1845 TWEACKNEFVPLGELKALYEEPMG--HSLSLQTESVROPWKMTDIAESITE 1897
Db 2064 -----NQLOJHLMPVKRIQEEBAEGISMSLNNKQLSQMLKSSAPAQEER 2111

RESULT 13
US-11-124-368A-215
; Sequence 215, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: C1001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 215
; LENGTH: 2668
; TYPE: PRF
; ORGANISM: Homo sapiens
US-11-124-368A-215

Query Match 1.3%; Score 199; DB 7; Length 2668;
Best Local Similarity 17.1%; Pred. No. 9,6e-05;
Matches 354; Conservative 340; Mismatches 780; Indels 602; Gaps 81;

Qy 1235 VNMKRDVHTWTKQDPIENTDEMIDTRIDVTRIPAGSPTPCLKISHTEPTEKANE 1294
Db 455 INLREIDESVCSSESDVPSNT--LDTLSLEIMNPA-----TGLNQENIE 497
Qy 1295 FLRLSPVLCNEFID-----BAEKARWVEIKDROQILMKEAVEAOMPAHIDQIMSQPT 1350
Db 498 SELNSLRADYNDVUDYEQLRTEKEMELKIKERKNDLDEFALERTKTK--DOEMOLHIE 555
Qy 1351 NMDIKGL-----HYEDNOEELPSSKMKRLPSRPPRKSGMTRGVITQNYNNLPOGOVNM 1404
Db 556 ISNLKLVGHARVYNQDLENEL--SSKVELRKEKDOIKKLQYIDSQKLENTIKMDLSYSL 614
Qy 1405 HRSTSEAEAKYDLAGOGLTPDCKDKXGRSFPKFRSKRGSSDRAKSKSKTPDPSPD 1464
Db 615 BSIBDPKQKQTLFPAETVALDAKRES-----AFLRSENLELKEMKELATTYKQEMND 668
Qy 1465 TEVSPERGARRPNQIKVSOANQRYNGMNAKPSKTNLYGSOVGLNMAVTPDQKQMTTST 1524
Db 669 IQ-----LQSOQ-----EAKKMQVD- 685
Qy 1525 IAOASATEVGNELFDAECLALINEFYGVRIYFGQDPTHVYI--GMVTTQYHLHSKD 1579
Db 686 -----LKEKLOSAFNEITKLTSLDGKVPKOLLGNLBLEGKITDLOKELAKE 732
Qy 1580 FNQSKVTKSSVITDDYDRVENVNR-----QSCMVVA--DELYNEVMAETIAG 1628
Db 733 VEENALREBEVITLSELKSLPSEVERLRKEIQDKSEBLHIIYSEKDKLFSBIVHK--ES 789
Qy 1629 ASQGNF--IGCSVD-----TSTGVSFTGEGKOTSKFKPMPEPTKLPALFVFA 1675
Db 790 RVQGLLEBIGTKDOLATQOSYKSTQDFQNFKTLHNDFEQKYVNVLEN-----ER 842
Qy 1676 TSKELIQI-----ELGRSATSLPLSAVLPTSDKRV-----IPQFPRL----- 1714
Db 843 NMQELIVNSKEAQKFDSSIGALKTELSTYKGLQEKTRVEQGRNLNMEQLKEKLENRDST 902
Qy 1715 -----KIQ-----CLKPQMARVPNQSQVHALKU--SDIRGMS 1746

Db 903 LGTVEREKTLYTEKLOOTLEEVKTLTQEKODLQLO-----ESLOIBRDQKSDI----- 952
 Qy 1747 MLCEDAVSMALAHIPREDRICIDILBPIEMDKLSFSPHTLTVAALCYOSNYAAH----- 1802
 Db 953 ---HDTVM---NIDPOBLRALBESIKQ-----HOETINTLKSXISEVSNLMEEN 1000
 Qy 1803 -----ALCTHDOKQLLYAIOGOYNSGPRQO-----FYDLT-----IALHUE 1840
 Db 1001 TGETKOBFOQIOWGIDKKODLBKANTQTLTADYKDNBEIIRQOKRISLIGEKNELOQME 1060
 Qy 1841 SHATTMACKN-----EPYIP-----LGPBK-----ALYEBDMGHS-- 1873
 Db 1061 SVIAEKEOKLTDKENIEMTIENOEIBRLIGDELKQOBIVAQKXNAIKCEBELRTCD 1120
 Qy 1874 -----LRSLOTEBVRPOMKMTDIAESTITEISNYSPPFLVABEFVMA 1918
 Db 1121 RLAEVEBKLEKSOLOEKQOOLINVOEEMSEKQKINIEIN----- 1163
 Qy 1919 LAEAVETNOVHNDPVGGSNENLFLPLIKLVDRLLVGMARDDEVEKLTMTNP-----ET 1974
 Db 1164 -----KNELKNE-----LTLBHEMTERBELAQKLNENYEVNSITKRYKAK 1207
 Qy 1975 WDSPEKQKDERKGLHMKKAEKALOKCYLLQHLNDIQLHRYEALIAFPAHDVGL 2034
 Db 1208 LOKSPETE--RDHLRGYIREIEATGLQTEBELKIAH---IHLKHOETI----- 1251
 Qy 2035 QTDOLAREYTEIKOSDPSAVALAKTREFRCPRRQONALISFGLHSEEDKENCPCGELL 2094
 Db 1252 --DELRRSVSEKTAQIINTODEKS-----HTKQOEBLTVLHESQELIPNKEVSETO 1302
 Qy 2095 ARKNEFH-----DTLMAHVSIALQEPDAENOEPEAKGAFGLYNIINTVKEL 2144
 Db 1303 ETMNEBELLEBOSTTKOSTTLARIEMERLANKPQESQEBIK--SLTERDMLKTIKKA 1360
 Qy 2145 ---EEBAKAIPEPPKTPPEEKFRKVLQTLVNAABESQIETPKVREN-----PSL 2192
 Db 1361 LEVXHQDLKEHIRETLAKIOESQSKO---EQSLNMEKON--ETTKIVSEKHOECPKPSDAL 1416
 Qy 2193 LVROYDAVEBLRALKTYVYNAKTLVDVAMVNGLSQIRALLPVQMSQEEBELMKRLM 2252
 Db 1417 LRIEIMLQ--LSKRLQESH---DEKMSVAKERKODLQRLQEV---QESQOLKENTIK 1466
 Qy 2253 KLVNNH-----TFQHPDLIRVLVHENVNAVMNTLGRRAQSD--AQPSQ 2299
 Db 1467 EIVAKHLETBEELKVAHCKKQBEBTINELRVNLSEKREIETIQOLBAINKLOKQK 1526
 Qy 2300 PV-----AEDSKKOTSHENVAVACRFLCYFCRTGRON-- 2332
 Db 1527 EYIEKEEOPNIKOISEVQEKVNELKOPKEHRKANDSALQISEKMLELTRLQESQEBIQ 1586
 Qy 2333 ---OKAFPHDFPLENSNILLSPSLRGSTPLDVAYSSL----- 2369
 Db 1587 IMIKEREMKRVQALQIERDQKENTKEIVAK--MKSQEKEXYQPLKMTAVNETOEKMC 1644
 Qy 2370 -----MENTELALALBHYLEKIAVYLSRCGLQSNSELVKGYPD 2409
 Db 1645 EIEHLKEQETQCLANIENTENIRLTQILHLENLEMRSTYTERDRLSVEHLK----- 1699
 Qy 2410 LGMDPVGSRYLDFLPCVWVNGESVEBANL--VIRLLIRPECLGPARLGRGEGALLKAI 2468
 Db 1700 ---VERDQKENTLRETTIRLLKDLKQEBELKIVMHLKEHOETIDKLRGIYSBKTNEL 1754
 Qy 2469 VDAKMSERLADRKARMEQEGDVNPSHLPESDEDEDTOTGAALINPYCTLVOLLGR 2528
 Db 1755 SINQKOLEHNSNDLKKQDLKIOBELRIAH--MHLKQOQETIDKLRGIVS---BKTKLSN 1809
 Qy 2529 CAPDAGVIALGKNESLPAAIILSLVLEBDQVLSLRFTLNNPAAGEERPKSDMPSGLI 2588
 Db 1810 MQDULE---NSNAKQOKYI-----QELKANHQULITLKQDVNETQKXSEMQLK 1858
 Qy 2589 PGHKQGVGLFLERVYGIETQSLFYKLEBAFLPDLBAATMLDNDGCSDMALSMNRYIG 2648
 Db 1859 QIKDQSLTYSKLEIENLNLAKLKHENLEB-----MKSVMKERDNLRRVETLKLBRD-- 1910

Qy 2649 NSILPILLIKHAYFVNEANVYASILDATHTVYRLSKRMILTKGQREAVSDFLVLT--SAM 2707
 Db 1911 ---QKESLOETARB-----LBIOELKTAARLSEKHKTVDKLRKIEBKTI 1956
 Qy 2708 QPSMLIKLIRKLTVDV--SKLSEYTVALLRLTL-----HYERCAKTYSGTAG 2754
 Db 1957 QISDIOKDLKSDKDELOKKIQLOELQKELQILRYGEDVNNSHKKINEMEQLOKQF----- 2010
 Qy 2755 QCAFASDSEBKRLTM-----MLFSNIPDSIMQDVEPBLFGALPCLTIALGALPP 2806
 Db 2011 -----BAQVLSMQSVYRMDNFOLTKLHESL--EIRVAERDELRIKESL-- 2055
 Qy 2807 DYSLSKNYDDEFYX--KEQAAAGLDLNPQYD-----QPINTSSVALNDLNTIYOK 2855
 Db 2056 ---KQEMDQFATLREMIARDRONHQYKPEKRLISDQOHLTESLREKCSRIKELKR 2110
 Qy 2856 FSS--HYH-----DAMASKIENGWYGGWSDOKTHPLKPYNN--LNDYB 2899
 Db 2111 YSEMDHYECLNRLSLDEKEIEFQKELSMRYVLSYVTKIKEQHESINFFEMDFIDEVE 2170
 Qy 2900 KERYKEPVASLKALALIGMSVH--SEVDIPSNSSMRBQSKSGRPREIYTSATPR 2957
 Db 2171 KQ-----KELLI---KIQHLOQDCDVPREIRDLKLNQMDLHIEILKD---F 2213
 Qy 2958 DYNPHFVDMTN-----LTLSEMONMAERLADNADH 2989
 Db 2214 SESEFPSITTEPQOVLNKRKEMTQFLBEWLTNTRFDI 2249

 RESULT 14
 US-11-124-368A-214
 ; Sequence 214, Application US/11124368A
 ; Publication No. US20050287559A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Michele Cargill
 ; APPLICANT: James J. Devlin
 ; APPLICANT: May Luke
 ; TITLE OF INVENTION: Genetic Polymorphisms Associated with
 ; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
 ; FILE REFERENCE: CL001524
 ; CURRENT APPLICATION NUMBER: US/11/124,368A
 ; PRIOR FILING DATE: 2005-05-09
 ; PRIOR APPLICATION NUMBER: US 60/568,845
 ; PRIOR FILING DATE: 2004-05-07
 ; PRIOR APPLICATION NUMBER: US 60/625,936
 ; NUMBER OF SEQ ID NOS: 2112
 ; SOFTWARE: FaestSeq for Windows Version 4.0
 ; SEQ ID NO 214
 ; LENGTH: 2665
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-11-124-368A-214

 Query Match 1.3%; Score 198.5; DB 7; Length 2665;
 Best Local Similarity 16.9%; Pred. No. 0.0001;
 Matches 369; Conservative 359; Mismatches 777; Indels 675; Gaps 86;

 Qy 1235 VNMKRDVTMYTKDQPIFENTDEMDTRIDVTRIPASDTPCLKISHNFTMEKANE 1294
 Db 455 INMLREIDSVCSESVFNT---LDTLSBIENPA-----TKLNGENT 497
 Qy 1295 FLRLSLPVICHNFID---EAKKARWVEIKDRQOILMKEAVEAQMPAHIQIMSGRT 1350
 Db 498 SRINSLRADYDNLVLDYEQLRTEKEMELKLRKNDLDFELALERTKPK--DOEMQLIHE 555
 Qy 1351 MNDIKGL-----HYEDNOEBLPSKMKRLPSRPPKSGMTGVTQNTQNNILOPGVNGA 1404
 Db 556 ISHLKMLVGHAYYNODLLENL--SSRYELLREKEDQIKGLQEIYSQKLENIMKDLSTYL 614
 Qy 1405 HNSTSENAKYDLGAQGLTPDQKDKGRGSRPFKFRSRKGSSSDRAKSRKSTPDPFD 1464

Db 615 ESTEDKOKQOTLPDAETVALDAKRES-----AFRSENLKKEKMKELATTYKQKEND 668
Qy 1465 TEVSPERGARRPNDOIKVSONORVNGMAPSRNTLYGSOVGLANMATPDOKKQNTST 1524
Db 669 IQ-----LYGSQL-----EAKKQVQD- 685
Qy 1525 LQASATETWQNEIFDAECLKLINEYGVARIYQDQPTHYI-----GWTTQYHLSKD 1579
Db 686 -----LEKELQSAFNEITKLTSLIDGKVPKODLCLNLEBKJTDLOKELNKE 732
Qy 1580 FNOBKTKSVIITDDYDRVENVNR-----OSCVWVRA--DELYNVAEATANG 1628
Db 733 VEENELAREVILLSELKSLPSEVERUKREIQDKSEBHIITSEBKQALPSEVHK--ES 789
Qy 1629 ASQGMF--IGCSVD-----TSTGSVSFTCBGKQTSFPAKMEPTKLPALFVFA 1675
Db 790 RVQGLLEBIEIGKTDLATTOGNSYKSTDFQNFKTLHMBEQKXVLEEN-----ER 842
Qy 1676 TSKEIILQI-----ELGRATSLPLSAVLPISDKAV-----IPQPPRL----- 1714
Db 843 MNOEIVNLKSKAQKPPSSIGALKTBELSYKTOELQEBKREVOERLNMEOQLKEQERDST 902
Qy 1715 -----KVO-----CLKPHQMARVNSQLQVHALKL--SDIRGMS 1746
Db 903 LQTVEREKTLITEKLOOTLEBVVTLTQEBKODLKQLO-----ESLQIERDQKSDI----- 952
Qy 1747 MLCEDAVSMALAHIPREDCIDILBPIENDKLSFHSHTLTUVAALCYOSNYRAAH----- 1802
Db 953 ---HDTVNN--NIDQEOELRNALLESKQ-----HQETINTLKXISSEVSNNLMEN 1000
Qy 1803 -----ALCTHVQKOLVAIQSOVNSGPIKQO-----FYDIL-----IALHIE 1840
Db 1001 TGETKDFQOKRWGIDKQDLEAKNTQTLTADVKDNEIIEQQRKPSLLOEKNELOQME 1060
Qy 1841 SHATTWEACQN-----BEVYIP-----LGPBLK-----ALYEBPDGMS-- 1873
Db 1061 SYIAEKOQLTKLKENIEMTIENTQEBRLIGDBLKQOEIVAOEKHAKLKSGEISRTD 1120
Qy 1874 -----LRSLOTESVPRQMKNTDIASITEISNLYSPYPLVAREFVMOA 1918
Db 1121 RLAEVEBKLEKSKSQOQKQOQLNAVQEMSEMOKKINEBUL----- 1163
Qy 1919 LAEAVETNOVNRDPVGGSNENULFPLIKVDBLLVGMREDVEXKILMTP-----ET 1974
Db 1164 -----KNEIKNKE-----LTLEMETERLELAQKLNENVEVNSITKERKVLKE 1207
Qy 1975 WPSFDKEGDEHRKGLHMQVABGAKLQMCYLLQHLNDIOLRHRVEALITAFADHPVDL 2034
Db 1208 LQKSEFTE--RQHLKGIYREIATGILQTEBELKIAN--IHLKEHQETI----- 1251
Qy 2035 QTDOLRRYTEIKQSDLPsAVAAKKTREPCRPPEQNNALSPKULEEBDEKENCPCGEELI 2094
Db 1252 ---DELRRSVSEKTAQIINTQDEKS-----HTKQOEIPVLHBEQELLPPVKEVSEIQ 1302
Qy 2095 AMNNEFH-----DTLMAVSLHALQEPDAAENQEPKAFGGLNINTVKEI 2144
Db 1303 ETMNEBELLTBOSTTKDSTTLKRIEMERILNKEKFOESQEBIK--SLTERDNLKTIKXA 1360
Qy 2145 -----EEBAKATEEPKKTPEEKFRKVLQIOTIVNMAESQIETPKLVREM-----FSL 2192
Db 1361 LEVKHDQLKHEHIRETLAKIQESQSKO--EQLANKKON--ETTKIVSEMEQPKPRDSAL 1416
Qy 2193 LVROYDAVAGELIRALEKTVIVINAKTLDVAEMVVGLSQIRALLPYQMSQEBEELMKRLM 2252
Db 1417 LRIETEMG-LKRLQESH-----DEMKSYAKKEDDLQRIQVYL-----QSESDQLKENIK 1466
Qy 2253 KLVNNH-----TFQHPDLIRVLRVHENVMAVMNTLGRRAQASD-AQPSQ 2299
Db 1467 EIVAKHLETEBELKVAHCLAKQOEBTINELRVNLSEKETEISTIQOJEAINDKIQNKIQ 1526
Qy 2300 PY-----AEDSKEKQTSHEMVVAVACCFKCYFCRTGRON-- 2332
Db 1527 EYEBKEBOPNIKOISEVQEKVNEKQFKEHRRAKOSALQSISSKMLELTNRLQESQEBEQ 1586

Qy 2333 -----QKMFHDFELENSNILLRPSLRGSTPLDVAVSYL----- 2369
Db 1587 IMIKEKEMKRVQELQIBRDQKENTKEIYAK--MKESQEKBYQFLKATVAVNETQEKMC 1644
Qy 2370 -----MENTELALAREHYLEKIAVYLSRCLQSONSELVEKGYD 2409
Db 1645 EIEHLKEQFETQKLNLENIETENIRLTQILHNLBEMRSVTKERDRLRVEETLK----- 1699
Qy 2410 LQMDPVEGERYLDLFRFCVWVNGESVEEVANLVIRLLIRPRPCGLPAGGEGGLLKAVI 2469
Db 1700 -----VERQKLENIRETITRLEKQEBLK--IYMHLEKHEBTIDKAGIYSEKTNES 1752
Qy 2470 DANKSERIADRRKLREMEQEDVNSHPLEPSDEDEDYIDTGAALNFYCTLVLDLGRK 2529
Db 1753 NMQKOLEHNDALKAQDLKIQELRIAH--MHLEKQOEITDKRGIVS--EKTDLKSNM 1807
Qy 2530 ARDA-----GVYALGN-----ESLRARAILASLV----- 2554
Db 1808 QKDLNSNAKQOEKIQELKANEHOLITLKQDVNETOKKVSSEBOLKQIKQDLSLSKLE 1867
Qy 2555 -----PLBDLQVL-----SLRFTLNNPAAGERPKSDMP 2584
Db 1866 TENALAQKLENLEBMSVMEKRDNLRAVESTLKLERDQLKESLQETPAEDLEIQOEK 1927
Qy 2585 SG--LIPGHKQSVGLFERVYGIETQ-----ELFYKU--LEBAFLPDLRAAT 2627
Db 1928 TABMLSEKHEVTVDKREKISEKTIQISDIQDLKSKOELQKIQELQKQELQLRVKE 1987
Qy 2628 MLDPRDGCESDMALSMRYTIGNSILPPLIKAHYFNEAVNYSILD----- 2673
Db 1988 DVNMSHKIKINEMOQKQFOEAQNLMSQVMDNFQLTQKGLHSLBIEIRIVAKERDELARI 2047
Qy 2674 -----ATLHTVRLSKNMLTKQREAVSDFLVALTSAMQPSM-----LLK-- 2714
Db 2048 KESLMEKRDQFIATREMIARQNHQVKEPKRLSDQGHITSELRKCSRIKELIKY 2107
Qy 2715 -----LRLKLTVDVSKLSYTTVALRLTYHBRCAKYVSGTAGAGAFASGDEBK 2766
Db 2108 SEMDHYEBCLNLSIDLEKIEIFRHRIMKCL-----KYVLS-----YVTYKIEBQ 2151
Qy 2767 RLTYMLPSPNIPDLSKMDYEPPLFGKALPCLAI-----GCLPFP-----DYSLSKYVDE 2817
Db 2152 HESINKFE--MDFIDEVKEQKEL-----LIKIHLQODCCVPFREILDLKLNQMDIH 2202
Qy 2818 FYKQQAAGDLDNPQYDPOPIVTSVALNNDINTIYOKFSBEYHDAMASRKILENGVYGB 2877
Db 2203 I---EELKDPSESEF--PSITTEFOYLSNRKEMTQFLBEMILNTRFDIEKJNG----- 2252
Qy 2878 GMSDSQKTHPLKPYNMLNDEKERYKEPVRESLK-----ALLAIGMSVSEHVDIPS-- 2930
Db 2253 ---IQKENDRI--COVNNFPNNRIIAMIWSTEFEBRSATISKEM-----EQLKSLK 2300
Qy 2931 -----NNRSMRQSSGGRPREIYVDSATFPPIYNNHPVD--KTNLTLS--REMQNNAS 2980
Db 2301 EKNEKLPKRYQTLKTSLSASQO-----VNPPTQDNKNPHVTSRAVQTLTEKIRELENSLH 2355
Qy 2981 RLADNADHIWAK--KKKEEL 2998
Db 2356 EAKESAMKESKITIMQKEL 2375

RESULT 15
US-10-506-454-486
; Sequence 486, Application US/10506454
; Publication No. US20060068386A1
; GENERAL INFORMATION:
; APPLICANT: Slesarev, Alexi I
; APPLICANT: Mezhevaeva, Katja V
; APPLICANT: Polushin, Nikolai N
; APPLICANT: Shcherbinina, Olga V
; APPLICANT: Shakhova, Vera V
; APPLICANT: Malykh, Andrei G

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OM protein - protein search, using sw model

Run on: April 14, 2006, 01:28:13 ; Search time 313 seconds
(without alignments)
4211.298 Million cell updates/sec

Title: US-10-668-767-128_COPY_1_3000
Sequence: 1 MEAEBCGASBODVSLRTR.....RLADNAHIMAKKKEELVT 3000

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20048:*
8: geneseqp20058:*
9: geneseqp20068:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15748	100.0	5128	8 ADM68884	Adm68884 Heliothis
2	15693.5	99.7	5134	8 ADM68886	Adm68886 Heliothis
3	15655.5	99.4	5142	8 ADM68900	Adm68900 Heliothis
4	15550.5	98.7	5140	8 ADM68758	Adm68758 Heliothis
5	15475	98.3	5102	8 ADM68902	Adm68902 Heliothis
6	12738	80.9	5127	8 ADM68764	Adm68764 Peregrinu
7	12516.5	79.5	5137	8 ADM68878	Adm68878 Drosophi
8	12489.5	79.3	5113	8 ADM68877	Adm68877 Drosophi
9	12465.5	79.1	5127	8 ADM68876	Adm68876 Drosophi
10	12460.5	79.0	5109	8 ADM68766	Adm68766 Drosophi
11	12445	78.6	5104	8 ADM68762	Adm68762 Periplane
12	12384	78.3	5107	4 ABBS5257	Abbs5257 Drosophi
13	12354	78.3	5112	8 ADM68881	Adm68881 Drosophi
14	12338	78.3	5126	8 ADM68880	Adm68880 Drosophi
15	12338	78.3	5126	8 ADM68812	Adm68812 Drosophi
16	12327	78.3	5101	8 ADM68760	Adm68760 Myzus per
17	12311	78.2	5112	8 ADM68882	Adm68882 Drosophi
18	12295	78.1	5126	8 ADM68879	Adm68879 Drosophi
19	12178.5	77.3	4868	8 ADM68813	Adm68813 Mosquito
20	7210	45.8	5071	8 ADM68814	Adm68814 Nematode
21	6986.5	44.4	5317	8 ADM68815	Adm68815 Sea urchi
22	6828	43.0	5107	8 ADM6817	Adm6817 Bacteri
23	6778	43.0	4968	8 ADM6817	Adm6817 Rabbit ry
24	6769	43.0	4767	4 ABBI1532	Abbi1532 Human rya

25	6769	43.0	4967	8 ADM68818	Adm68818 Human rya
26	6758	42.9	4967	8 ADM68816	Adm68816 Mouse rya
27	6566.5	41.7	3647	7 ADJ70630	Adj70630 Human hea
28	6445.5	40.9	5035	2 AAR25450	Aar25450 MH mutant
29	6443	40.9	5038	8 ADQ18491	Adq18491 Human sof
30	6443	40.9	5038	9 ADY19486	Ady19486 PRO polyP
31	6443	40.9	5081	4 ABG04969	Abg04969 Novel hum
32	6442.5	40.9	5032	7 ADJ68220	Adj68220 Human hea
33	6440	40.9	5081	4 ABBI1480	Abbi1480 Human rya
34	6411.5	40.7	5072	2 AAR11510	Aar11510 Ryanodine
35	6370.5	40.5	4771	4 AAU02939	Aau02939 Angiotens
36	6356	40.4	4899	4 ABG12314	Abg12314 Novel hum
37	6356	40.4	4899	7 ADF60293	Adf60293 Human con
38	6356	40.4	4934	4 ABG23346	Abg23346 Novel hum
39	6354	40.3	4866	2 AAU77410	Aau77410 Human rya
40	6293	40.0	4987	2 AAR10834	Aar10834 Ryanodin
41	4416	28.0	2000	9 ADY15562	Ady15562 PRO polyP
42	942	6.0	374	4 AAB70482	Aab70482 Ryanodine
43	722.5	4.6	616	4 ABG23345	Abg23345 Novel hum
44	712	4.5	1232	4 ABG03701	Abg03701 Novel hum
45	698.5	4.4	599	4 ABG23343	Abg23343 Novel hum

ALIGNMENTS

RESULT 1	AD68884	AD68884 strand; protein; 5128 AA.
XX	AD68884	
XX	AD68884	
AC	AD68884	
XX	AD68884	
DT	17-JUN-2004	(first entry)
XX		
DE	Heliothis virescens ryanodine receptor protein SEQ ID NO:128.	
XX		
KW	ryanodine receptor; insect ion channel; insecticide; pesticide;	
KM	calcium balance disruption; receptor calcium release mechanism.	
XX		
OS	Heliothis virescens.	
XX		
PN	W02004027042-A2.	
XX		
PD	01-APR-2004.	
XX		
PF	23-SEP-2003; 2003WO-US029834.	
XX		
PR	23-SEP-2002; 2002US-0412795P.	
PR	18-NOV-2002; 2002US-0427324P.	
XX		
PA	(DUPO) DU POINT DE MEMOIRS & CO E I.	
XX		
PI	Casper T, Cordova D, Gutteridge S, Rauh JJ, Smith RM, Wu L,	
PI	Tao Y;	
XX		
DR	WPI: 2004-295411/27.	
DR	N-PSDB; ADM68883.	
XX		
PT	New isolated nucleotide fragment encoding a ryanodine receptor, useful	
PT	for isolating other pest ryanodine receptors and in developing screens to	
PT	identify insecticidally active compounds.	
XX		
PS	Claim 15; SEQ ID NO 128; 687bp; English.	
XX		
CC	The present invention describes an isolated nucleotide fragment (I)	
CC	comprising: (a) a nucleic acid sequence encoding a ryanodine receptor	
CC	having an amino acid sequence identity of at least 80% when compared to a	
CC	polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,	
CC	128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a	
CC	nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.	
CC	1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant	
CC	construct comprising (I) operably linked to at least one regulatory	
CC	sequence; (2) a transformed host cell comprising the recombinant	

CC construct; (3) a method to isolate (1) encoding ryanodine receptors and
CC related polypeptides; (4) an isolated polypeptide having ryanodine
CC receptor activity; (5) a method for evaluating at least one compound for
CC its ability to modulate calcium homeostasis; (6) a method for evaluating
CC at least one compound which modulates ryanodine receptor activity; (7) an
CC isolated nucleic acid fragment encoding an insect ion channel comprising
CC at least two fully defined polypeptide sequences selected from SEQ ID
CC Nos. 63-119 provided that the polypeptide sequences is not SEQ ID No. 56,
CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC insect ion channel; (9) a method for expressing an isolated nucleic acid
CC fragment encoding a toxic insect ion channel; and (10) recombinant
CC construct comprising in the 5' to 3' direction a promoter operably linked
CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC The isolated nucleotide fragment (1) encoding a ryanodine receptor is
CC useful for the isolation of other pest ryanodine receptors and developing
CC screens to identify insecticidally active compounds. The nucleic acid
CC fragments are useful as pesticides, fragments of protein for antibody
CC production, fragments of protein for determination of the structure of
CC insecticide binding sites and in the identification of insecticides that
CC disrupt the calcium balance in cells through other messengers that
CC interact with the receptor calcium release mechanism. The present
CC sequence is used in the exemplification of the present invention.

XX Sequence 5128 AA;

Query Match 100.0%; Score 15748; DB 8; Length 5128;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAEAGASRQDVSLFRTEDMCLSTATGERVCLAAEFGNRHCFLENIADKNIPPL 60
DB 1 MAAEAGASRQDVSLFRTEDMCLSTATGERVCLAAEFGNRHCFLENIADKNIPPL 60
QY 61 SOCVFYEQALSVRALQELVTAAGSETGKGSGHRTLYGNAILLRHLSNDMYLA 120
DB 61 SOCVFYEQALSVRALQELVTAAGSETGKGSGHRTLYGNAILLRHLSNDMYLA 120
QY 121 SSSQDDKLAEPDVLQDSQSGACWTLHPASKQSRSEGEKVRVGDLLVSVATERYL 180
DB 121 SSSQDDKLAEPDVLQDSQSGACWTLHPASKQSRSEGEKVRVGDLLVSVATERYL 180
QY 121 SSSQDDKLAEPDVLQDSQSGACWTLHPASKQSRSEGEKVRVGDLLVSVATERYL 180
DB 121 SSSQDDKLAEPDVLQDSQSGACWTLHPASKQSRSEGEKVRVGDLLVSVATERYL 180
QY 181 ENEVSTVNASFHTTHMSVOPVGTGISMKVGVVFGDVLRFPHGDECLTIPSTTK 240
DB 181 ENEVSTVNASFHTTHMSVOPVGTGISMKVGVVFGDVLRFPHGDECLTIPSTTK 240
QY 181 ENEVSTVNASFHTTHMSVOPVGTGISMKVGVVFGDVLRFPHGDECLTIPSTTK 240
DB 181 ENEVSTVNASFHTTHMSVOPVGTGISMKVGVVFGDVLRFPHGDECLTIPSTTK 240
QY 241 GQRIVYVEGGSVNASRLWRLRLARTKAGGFINWYHPIRHITTGRTLYGVNDQ 300
DB 241 GQRIVYVEGGSVNASRLWRLRLARTKAGGFINWYHPIRHITTGRTLYGVNDQ 300
QY 241 GQRIVYVEGGSVNASRLWRLRLARTKAGGFINWYHPIRHITTGRTLYGVNDQ 300
DB 241 GQRIVYVEGGSVNASRLWRLRLARTKAGGFINWYHPIRHITTGRTLYGVNDQ 300
QY 301 LVSRBEATTASCAFCILRQEKDQKQVLEDKOLEVIGAPILIKYGDSTFVIV 360
DB 301 LVSRBEATTASCAFCILRQEKDQKQVLEDKOLEVIGAPILIKYGDSTFVIV 360
QY 301 LVSRBEATTASCAFCILRQEKDQKQVLEDKOLEVIGAPILIKYGDSTFVIV 360
DB 301 LVSRBEATTASCAFCILRQEKDQKQVLEDKOLEVIGAPILIKYGDSTFVIV 360
QY 361 KSVETKKGKGVKBEKQKQIHEBGKDDGLDFSRQSEBESRTARVIRKSGSL 420
DB 361 KSVETKKGKGVKBEKQKQIHEBGKDDGLDFSRQSEBESRTARVIRKSGSL 420
QY 361 KSVETKKGKGVKBEKQKQIHEBGKDDGLDFSRQSEBESRTARVIRKSGSL 420
DB 361 KSVETKKGKGVKBEKQKQIHEBGKDDGLDFSRQSEBESRTARVIRKSGSL 420
QY 421 ETLQENRRHSMFPFASVNLGEMWCLLEDILNYFAOPDEDMHEKQKFPALRR 480
DB 421 ETLQENRRHSMFPFASVNLGEMWCLLEDILNYFAOPDEDMHEKQKFPALRR 480
QY 421 ETLQENRRHSMFPFASVNLGEMWCLLEDILNYFAOPDEDMHEKQKFPALRR 480
DB 421 ETLQENRRHSMFPFASVNLGEMWCLLEDILNYFAOPDEDMHEKQKFPALRR 480
QY 481 EGIILNLILBAIDKINVTISQGLAGFLAGDESGQSEWEMISGYLYOLLA 540
DB 481 EGIILNLILBAIDKINVTISQGLAGFLAGDESGQSEWEMISGYLYOLLA 540
QY 481 EGIILNLILBAIDKINVTISQGLAGFLAGDESGQSEWEMISGYLYOLLA 540
DB 481 EGIILNLILBAIDKINVTISQGLAGFLAGDESGQSEWEMISGYLYOLLA 540
QY 541 FANSNRLNMLFSLRGSGASGEGTGM DLVHCVLIDSEALNMNRDEHIKYL 600
DB 541 FANSNRLNMLFSLRGSGASGEGTGM DLVHCVLIDSEALNMNRDEHIKYL 600
QY 541 FANSNRLNMLFSLRGSGASGEGTGM DLVHCVLIDSEALNMNRDEHIKYL 600
DB 541 FANSNRLNMLFSLRGSGASGEGTGM DLVHCVLIDSEALNMNRDEHIKYL 600
QY 601 DPEVLDVLCGLCVNGGVAVSSQNNICDYLLPGKLLLTQALVDVHVSVP 660
DB 601 DPEVLDVLCGLCVNGGVAVSSQNNICDYLLPGKLLLTQALVDVHVSVP 660

QY 661 SAVYRKWFEVMTMDIEKTHMPEHLRIGMANTTGYVPPGGGEKMGNGVDDLYSGF 720
DB 661 SAVYRKWFEVMTMDIEKTHMPEHLRIGMANTTGYVPPGGGEKMGNGVDDLYSGF 720
QY 721 DDAVYMSGGRKPPVNRTHAEEPYIRKGDVIGCALDLYPIINFMNGRVTSFTNF 780
DB 721 DDAVYMSGGRKPPVNRTHAEEPYIRKGDVIGCALDLYPIINFMNGRVTSFTNF 780
QY 781 GMFFPVISCSXLSGRFLGSGHGRLYAAPBGVSLPVESLLPQILSLPCFYGNLSK 840
DB 781 GMFFPVISCSXLSGRFLGSGHGRLYAAPBGVSLPVESLLPQILSLPCFYGNLSK 840
QY 841 RALAAPVVDOTAVVPPVPTLQITLPTVYEQIDKLAENHEMAMNKIAGMWTG 900
DB 841 RALAAPVVDOTAVVPPVPTLQITLPTVYEQIDKLAENHEMAMNKIAGMWTG 900
QY 901 REDLKHHPCLVPEFRLPPAEKRYDIOAVQTKTLLAGYISLDKPPARIRNRLPNE 960
DB 901 REDLKHHPCLVPEFRLPPAEKRYDIOAVQTKTLLAGYISLDKPPARIRNRLPNE 960
QY 961 PFMQNGKYPAPLDLSAVTLPPKMDLVQDLAENTHIMARERIOGWTYGLNEDSDMR 1020
DB 961 PFMQNGKYPAPLDLSAVTLPPKMDLVQDLAENTHIMARERIOGWTYGLNEDSDMR 1020
QY 1021 SPHLVYPRKDDAIKKANBDTASETVTLVYGYMLDPPTGHEHALLEASKQOAPDR 1080
DB 1021 SPHLVYPRKDDAIKKANBDTASETVTLVYGYMLDPPTGHEHALLEASKQOAPDR 1080
QY 1081 TYRAKNYAVSGKRYPEFEILTAGPMRVGNAAHMAAGMMLGQDENSMAFGVNEKY 1140
DB 1081 TYRAKNYAVSGKRYPEFEILTAGPMRVGNAAHMAAGMMLGQDENSMAFGVNEKY 1140
QY 1141 SNTESFGKQMAVGVDFDLIDKTSIFSINGELMDALGETTFADVQDNEVPACT 1200
DB 1141 SNTESFGKQMAVGVDFDLIDKTSIFSINGELMDALGETTFADVQDNEVPACT 1200
QY 1201 LGVGQKARLTYQDVNTLYFTTQGLQSGYEPFCYNNKRDVTHWYTKOPIFENT 1260
DB 1201 LGVGQKARLTYQDVNTLYFTTQGLQSGYEPFCYNNKRDVTHWYTKOPIFENT 1260
QY 1261 TRIDVTRIPAGSDTPPCIKISHNTEFMEKANWELSLPLVICHNEFIDSEKARWYE 1320
DB 1261 TRIDVTRIPAGSDTPPCIKISHNTEFMEKANWELSLPLVICHNEFIDSEKARWYE 1320
QY 1321 IKDROOILMKEAVEAQMBAHIDQIMRSGETMNDIKGLHYEDNOBELPSSKMR 1380
DB 1321 IKDROOILMKEAVEAQMBAHIDQIMRSGETMNDIKGLHYEDNOBELPSSKMR 1380
QY 1381 KGSMTRGVTIQNTNMLQPGQVNGHRSSEAMAKYDUGAQLTDDDKDKRGSPFKE 1440
DB 1381 KGSMTRGVTIQNTNMLQPGQVNGHRSSEAMAKYDUGAQLTDDDKDKRGSPFKE 1440
QY 1441 RSKRGESSDRAKRSKTPDPSPDTEVSPBEGARPNOIKYSQANORHNGMNA 1500
DB 1441 RSKRGESSDRAKRSKTPDPSPDTEVSPBEGARPNOIKYSQANORHNGMNA 1500
QY 1501 LYGSQVGLNMAPTDORQMTTSTLAQASATETVGNIEFDABCLKLINEFYGV 1560
DB 1501 LYGSQVGLNMAPTDORQMTTSTLAQASATETVGNIEFDABCLKLINEFYGV 1560
QY 1561 PTHVYIGWTTQYHLHSDPFNQS KTKTSVITDDYDVEVENVNRQS CMVPA 1620
DB 1561 PTHVYIGWTTQYHLHSDPFNQS KTKTSVITDDYDVEVENVNRQS CMVPA 1620
QY 1621 MAEATKAKASQGMFGSGVDNSTGSVSTCGKQKTSFPEKMEPEKLPALIVE 1680
DB 1621 MAEATKAKASQGMFGSGVDNSTGSVSTCGKQKTSFPEKMEPEKLPALIVE 1680
QY 1681 IQIELGRSATSLPLSAALVPTSDKAVIQPPRLKYQCLKPHQMARVNO 1740
DB 1681 IQIELGRSATSLPLSAALVPTSDKAVIQPPRLKYQCLKPHQMARVNO 1740
QY 1741 DIRGSMCLCEBAVSMALAHIPBEDRCIDLIEPIMDKLLSFHSHTLTLYAL 1800
DB 1741 DIRGSMCLCEBAVSMALAHIPBEDRCIDLIEPIMDKLLSFHSHTLTLYAL 1800

Db 1741 DINGMSLCEDAVSMALHTPEEDRCDILEPIEMDQLSPHSHTLTLYALCQSNYRA 1800
 Qy 1801 AAALCTHVQKQLLYAISOQYMSGPRLOGFYDLLIALHLSHATTMEACNBEFVPLGPE 1860
 Db 1801 AAALCTHVQKQLLYAISOQYMSGPRLOGFYDLLIALHLSHATTMEACNBEFVPLGPE 1860
 Qy 1861 LKALYEEPDWGHSLRSIQTESVPRQMKMTDIAESITISNLYSPPELEVAAREFVQALA 1920
 Db 1861 LKALYEEPDWGHSLRSIQTESVPRQMKMTDIAESITISNLYSPPELEVAAREFVQALA 1920
 Qy 1921 EAVETQVNHNDPVPVGSNENLFLPLITQVDRLLLVGMREDEVDKLLIMNPEIWPBSPD 1980
 Db 1921 EAVETQVNHNDPVPVGSNENLFLPLITQVDRLLLVGMREDEVDKLLIMNPEIWPBSPD 1980
 Qy 1981 KEGKDEHRKGLIMHKNMAGAKQWICYLLOHNDIQLHRVEATIAFAHDFVGLQTDQLR 2040
 Db 1981 KEGKDEHRKGLIMHKNMAGAKQWICYLLOHNDIQLHRVEATIAFAHDFVGLQTDQLR 2040
 Qy 2041 RYTEIKQSDLPAAVAAKTRBPRCPREQNNALISFGLHEEDKENCPCGEBELIARNEF 2100
 Db 2041 RYTEIKQSDLPAAVAAKTRBPRCPREQNNALISFGLHEEDKENCPCGEBELIARNEF 2100
 Qy 2101 HDPLMAHVSJLALQEPDPAENQEPKAPGAFGKLYNIIINTVKLEBEAKALIEBPCKTPE 2160
 Db 2101 HDPLMAHVSJLALQEPDPAENQEPKAPGAFGKLYNIIINTVKLEBEAKALIEBPCKTPE 2160
 Qy 2161 EKEFRKVLIOITVMAEBSQIETPKLVEMFSLVROYDAVGLIRALEKTVVNAKTKLD 2220
 Db 2161 EKEFRKVLIOITVMAEBSQIETPKLVEMFSLVROYDAVGLIRALEKTVVNAKTKLD 2220
 Qy 2221 VAEWVGLSQIRALLPVQMSQOESEBELMRKELMKLVNNTPEFPHDILIRVLRVHENVAW 2280
 Db 2221 VAEWVGLSQIRALLPVQMSQOESEBELMRKELMKLVNNTPEFPHDILIRVLRVHENVAW 2280
 Qy 2281 MNTLGRRAQASDAQSPSQAEDSKEDTSHENVAACCFPCYFCGTGQONQKAFDHF 2340
 Db 2281 MNTLGRRAQASDAQSPSQAEDSKEDTSHENVAACCFPCYFCGTGQONQKAFDHF 2340
 Qy 2341 DPLLENSNITLSRPSLRGSTPLDVAAGSLMENTELALREHLYBKAVLSRQGLQSN 2400
 Db 2341 DPLLENSNITLSRPSLRGSTPLDVAAGSLMENTELALREHLYBKAVLSRQGLQSN 2400
 Qy 2401 ELVEKGYPDLGMPDVEGERYLDPLRFCVWNGSVEBENAVIRLLIRREPCGAPLRGE 2460
 Db 2401 ELVEKGYPDLGMPDVEGERYLDPLRFCVWNGSVEBENAVIRLLIRREPCGAPLRGE 2460
 Qy 2461 GEGLLKALIVDANKSERIADRRKLRMEQEGDVNFSPHLPESDEDEYIDTGAIIINFYC 2520
 Db 2461 GEGLLKALIVDANKSERIADRRKLRMEQEGDVNFSPHLPESDEDEYIDTGAIIINFYC 2520
 Qy 2521 TVVDLGRCAPDAGVIALGKNSILRAAIIIRSLVPLEDOGVSLRPTLNPPAAGERPK 2580
 Db 2521 TVVDLGRCAPDAGVIALGKNSILRAAIIIRSLVPLEDOGVSLRPTLNPPAAGERPK 2580
 Qy 2581 SDMPSGILPQHKSQVGLFERVYGIETQELFYKLEBAFPLDRAATMLDRNDGCSDMA 2640
 Db 2581 SDMPSGILPQHKSQVGLFERVYGIETQELFYKLEBAFPLDRAATMLDRNDGCSDMA 2640
 Qy 2641 LSNMRYIGNSILPLLKHAIFYNEAENYASILDATHTTVYRLSKNMLTKGQEAVSDFL 2700
 Db 2641 LSNMRYIGNSILPLLKHAIFYNEAENYASILDATHTTVYRLSKNMLTKGQEAVSDFL 2700
 Qy 2701 VALTSAMPQSMILKLRKLTVDVSKSEYTTVALRLLTTHYECARKYGTGAGQAFGA 2760
 Db 2701 VALTSAMPQSMILKLRKLTVDVSKSEYTTVALRLLTTHYECARKYGTGAGQAFGA 2760
 Qy 2761 SPSDEKRLTMMLPFNSIPDSLSKMDYBPLFGKALPCLIAIGCALPPDYSLSKMYDDEBFY 2820
 Db 2761 SPSDEKRLTMMLPFNSIPDSLSKMDYBPLFGKALPCLIAIGCALPPDYSLSKMYDDEBFY 2820
 Qy 2821 KEOAGDLDNPQYDPOPINTSSVALNNDNTTVQKSEHYHDAMASRKIENGWYGEWGS 2880

Db 2821 KEOAGDLDNPQYDPOPINTSSVALNNDNTTVQKSEHYHDAMASRKIENGWYGEWGS 2880
 Qy 2881 DSQKTHPRLRKPYNMLNDYKERYKEPVRESLALALIGMSVHSEVDPIDSNRRSSNRQS 2940
 Db 2881 DSQKTHPRLRKPYNMLNDYKERYKEPVRESLALALIGMSVHSEVDPIDSNRRSSNRQS 2940
 Qy 2941 KSGGRPEIYVDSATFPDYNPHPVDMTNLTLSREMNNAERLADNAHDIWAKKKEELVT 3000
 Db 2941 KSGGRPEIYVDSATFPDYNPHPVDMTNLTLSREMNNAERLADNAHDIWAKKKEELVT 3000
 Db 2941 KSGGRPEIYVDSATFPDYNPHPVDMTNLTLSREMNNAERLADNAHDIWAKKKEELVT 3000
 RESULT 2
 ADM6886
 ID ADM6886 standard; protein; 5134 AA.
 XX
 AC ADM6886;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Heliothis virescens ryanodine receptor protein SEQ ID NO:130.
 XX
 DE ryanodine receptor; insect ion channel; insecticide; pesticide;
 KW calcium balance disruption; receptor calcium release mechanism.
 OS Heliothis virescens.
 OS
 PN MO2004027042-A2.
 PD 01-APR-2004.
 XX
 PF 23-SEP-2003; 2003MO-US029834.
 XX
 PR 23-SEP-2002; 2002US-0412795P.
 PR 18-NOV-2002; 2002US-0427324P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 XX
 PI Caspar T, Cordova D, Gutteridge S, Rauch J, Smith RM, Wu L;
 PI Tao Y;
 DR WPI, 2004-295411/27.
 DR N-PSDB; ADM68865.
 XX
 PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
 PT for isolating other pest ryanodine receptors and in developing screens to
 PT identify insecticidally active compounds.
 XX
 PS Claim 15; SEQ ID NO 130; 687bp; English.
 XX
 CC The present invention describes an isolated nucleotide fragment (1)
 CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
 CC having an amino acid sequence identity of at least 80% when compared to a
 CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
 CC 128, 130, 144, or 146; or (b) the complement of (a). (1) comprises a
 CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
 CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
 CC construct comprising (1) operably linked to at least one regulatory
 CC sequence; (2) a transformed host cell comprising the recombinant
 CC construct; (3) a method to isolate (1) encoding ryanodine receptors and
 CC related polypeptides; (4) an isolated polypeptide having ryanodine
 CC receptor activity; (5) a method for evaluating at least one compound for
 CC its ability to modulate calcium homeostasis; (6) a method for evaluating
 CC at least one compound which modulates ryanodine receptor activity; (7) an
 CC isolated nucleic acid fragment encoding an insect ion channel comprising
 CC at least two fully defined polypeptide sequences selected from SEQ ID
 CC NOS. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
 CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
 CC insect ion channel; (9) a method for expressing an isolated nucleic acid
 CC fragment encoding a toxic insect ion channel; and (10) recombinant
 CC construct comprising in the 5' to 3' direction a promoter operably linked
 CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
 CC The isolated nucleotide fragment (1) encoding a ryanodine receptor is
 CC useful for the isolation of other pest ryanodine receptors and developing

CC of screens to identify insecticidally active compounds. The nucleic acid
CC fragments are useful as pesticides, fragments of protein for antibody
CC production, fragments of protein for determination of the structure of
CC insecticide binding sites and in the identification of insecticides that
CC disrupt the calcium balance in cells through other messengers that
CC interact with the receptor calcium release mechanism. The present
CC sequence is used in the exemplification of the present invention.

XX Sequence 5134 AA;

Query Match 99.7%; Score 15693.5; DB 8; Length 5134;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2992; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 MABEAGASBQDDVSLFRTEDMVCSTATGEBVCIAAEGFGRHCFLENIADKNIPDL 60
DB 1 MABEAGASBQDDVSLFRTEDMVCSTATGEBVCIAAEGFGRHCFLENIADKNIPDL 60
QY 61 SQCVPIEQLSTRALQELVTAAAGSTGKGTSGHRTLYGNAILLRHLSMDMYLACLS 120
DB 61 SQCVPIEQLSTRALQELVTAAAGSTGKGTSGHRTLYGNAILLRHLSMDMYLACLS 120
QY 121 SSSQDLPAPVGLQOHSQGEACMWTLPASKORSEBKVAVGDDLIVSATERVYLTTK 180
DB 121 SSSQDLPAPVGLQOHSQGEACMWTLPASKORSEBKVAVGDDLIVSATERVYLTTK 180
QY 181 ENEVSIVNASFHTVHSVOPGTGTSRMKVYGVVFGDVLRFPHGDECLTIPSTWKD 240
DB 181 ENEVSIVNASFHTVHSVOPGTGTSRMKVYGVVFGDVLRFPHGDECLTIPSTWKD 240
QY 241 GQNIIVYEGSVNSQARSLRRLARTKAGGFINVHPRIHITTTGRTLYGNDONELY 300
DB 241 GQNIIVYEGSVNSQARSLRRLARTKAGGFINVHPRIHITTTGRTLYGNDONELY 300
QY 241 GQNIIVYEGSVNSQARSLRRLARTKAGGFINVHPRIHITTTGRTLYGNDONELY 300
DB 241 GQNIIVYEGSVNSQARSLRRLARTKAGGFINVHPRIHITTTGRTLYGNDONELY 300
QY 301 LVSRBEATTASCAFCRROEKDQOVLKEDLKVIGAPILIKYGDSTVIYVHSEGTMLSY 360
DB 301 LVSRBEATTASCAFCRROEKDQOVLKEDLKVIGAPILIKYGDSTVIYVHSEGTMLSY 360
QY 361 KSYETKKKGKGVKVEKQALIHBEKGKDDGLDFRSQSEBSRTARVIRKCSLTKEING 420
DB 361 KSYETKKKGKGVKVEKQALIHBEKGKDDGLDFRSQSEBSRTARVIRKCSLTKEING 420
QY 421 ETTQENRRISMFPASVNLGEMVCLBDLINVPAQDPEDMEHEKQKFPALRRQDLFQ 480
DB 421 ETTQENRRISMFPASVNLGEMVCLBDLINVPAQDPEDMEHEKQKFPALRRQDLFQ 480
QY 481 EGTILNLLBAIDKINVTTSQGLAGFLAGDESGQSWEMTSGVLYOHLAIIKGNHNCQ 540
DB 481 EGTILNLLBAIDKINVTTSQGLAGFLAGDESGQSWEMTSGVLYOHLAIIKGNHNCQ 540
QY 541 FANSNRLNMLFSRLGSAQSGEGTGMLDVLAICVLIDSPBALNMNRDHIKVIISLEKGR 600
DB 541 FANSNRLNMLFSRLGSAQSGEGTGMLDVLAICVLIDSPBALNMNRDHIKVIISLEKGR 600
QY 601 DPEYLDVLSLCTGVNGVAVASSQNNICDYLLPGKNTLLQTAIVDHYSVRENI FVRVGS 660
DB 601 DPEYLDVLSLCTGVNGVAVASSQNNICDYLLPGKNTLLQTAIVDHYSVRENI FVRVGS 660
QY 661 SAYARRKMYPEVTMDHI EKTTHMMPHLRIGMANTTGVVPYGGEGKKGNGVGDDLSYGF 720
DB 661 SAYARRKMYPEVTMDHI EKTTHMMPHLRIGMANTTGVVPYGGEGKKGNGVGDDLSYGF 720
QY 721 DGAIVLSGGRKTPVNEETHAEEPIRKGDVIGCALDITVPIINFMFGVAVTSGFTFMLE 780
DB 721 DGAIVLSGGRKTPVNEETHAEEPIRKGDVIGCALDITVPIINFMFGVAVTSGFTFMLE 780
QY 781 GMFFPVISCSKSLSCRFILGEGHGRLYAAPESYSPVLESILPQOILSLPCCYFENLSK 840
DB 781 GMFFPVISCSKSLSCRFILGEGHGRLYAAPESYSPVLESILPQOILSLPCCYFENLSK 840
QY 841 RALAGPVLVODDPAFVPTVDTLQITLPTVVEQIRKLAENIHEMAMNKIEAGMYGQ 900
DB 841 RALAGPVLVODDPAFVPTVDTLQITLPTVVEQIRKLAENIHEMAMNKIEAGMYGQ 900

QY 901 REDLKHICPLVFERLPPAEKRYDIOAVOTLTKTLLALGYTISLDKPPAIRNVLNE 960
DB 901 REDLKHICPLVFERLPPAEKRYDIOAVOTLTKTLLALGYTISLDKPPAIRNVLNE 960
QY 961 PPMQSNKVPAPLDISAATLPPQMDLVQDLAENHNIMARERIOQMTYGNEDSDMR 1020
DB 961 PPMQSNKVPAPLDISAATLPPQMDLVQDLAENHNIMARERIOQMTYGNEDSDMR 1020
QY 1021 SPHLVYPKVDPAIKKARNDTASETRTLVYGYMLDPEPTGEHALLLEASQKQADPR 1080
DB 1021 SPHLVYPKVDPAIKKARNDTASETRTLVYGYMLDPEPTGEHALLLEASQKQADPR 1080
QY 1081 TYRAEKNTAVSSGKKYFPEFEITTAGPMRVGMAHADMAFGMLGQDENSAFPGYNEKY 1140
DB 1081 TYRAEKNTAVSSGKKYFPEFEITTAGPMRVGMAHADMAFGMLGQDENSAFPGYNEKY 1140
QY 1141 SGNTESPGQMAVGVGVFLDLIDKTSISFSLNGELMDALGGETTPADVQDNPVACT 1200
DB 1141 SGNTESPGQMAVGVGVFLDLIDKTSISFSLNGELMDALGGETTPADVQDNPVACT 1200
QY 1201 LGVGQKARLTYGQDVNTLKYFTTCGLQEGYBEFCVNMKRDVTHMYTKQPIFENTDEMID 1260
DB 1201 LGVGQKARLTYGQDVNTLKYFTTCGLQEGYBEFCVNMKRDVTHMYTKQPIFENTDEMID 1260
QY 1261 TRIDVTRIPAGSDPPCKISHTNTEMEKANWEFLRLSLPYTCHNEFTIDEAKARWYE 1320
DB 1261 TRIDVTRIPAGSDPPCKISHTNTEMEKANWEFLRLSLPYTCHNEFTIDEAKARWYE 1320
QY 1321 IKDRQOILMKVEAWEQMAHIDQIMRSGFTMNDIGLHYEDNOBELPSSKMRLLSRPR 1380
DB 1321 IKDRQOILMKVEAWEQMAHIDQIMRSGFTMNDIGLHYEDNOBELPSSKMRLLSRPR 1380
QY 1381 KGSMTGVTYIQYNNILOPGQVNGMRSTSEAMAKYDGAQGLTPDDKDKRGRSPKFF 1440
DB 1381 KGSMTGVTYIQYNNILOPGQVNGMRSTSEAMAKYDGAQGLTPDDKDKRGRSPKFF 1440
QY 1441 RSKRGESSDRAKRSKTPDPSPDTEVS PERGARRPNQIKVSQANQRYNGNAPPSRTN 1500
DB 1441 RSKRGESSDRAKRSKTPDPSPDTEVS PERGARRPNQIKVSQANQRYNGNAPPSRTN 1500
QY 1501 LYGSQVGLNMATPPDORCOMTSTTLAGATENVGEITDAECLKLINEFVGVRITYPGD 1560
DB 1501 LYGSQVGLNMATPPDORCOMTSTTLAGATENVGEITDAECLKLINEFVGVRITYPGD 1560
QY 1561 PTHVYIGWTTQYHLSKDFNQSRYTKSSVITTDYDRVENVVNSQCYMRADELYNEV 1620
DB 1561 PTHVYIGWTTQYHLSKDFNQSRYTKSSVITTDYDRVENVVNSQCYMRADELYNEV 1620
QY 1621 MABATKAGASQGMFTGCSVDITSTGVSFTCBGKDTSPFKMEPEYKLPALIVEATSKEI 1680
DB 1621 MABATKAGASQGMFTGCSVDITSTGVSFTCBGKDTSPFKMEPEYKLPALIVEATSKEI 1680
QY 1681 LOIELGRSATSLPSAAVLPISDKHVIPOPPRLVQOCLKPHQMARVPQOSQVVALKLS 1740
DB 1681 LOIELGRSATSLPSAAVLPISDKHVIPOPPRLVQOCLKPHQMARVPQOSQVVALKLS 1740
QY 1741 DIRGSMCEADAVSMALHPIEEDRCIDILBPIBMDKLLSFHSHTLTYAALCYOSNYRA 1800
DB 1741 DIRGSMCEADAVSMALHPIEEDRCIDILBPIBMDKLLSFHSHTLTYAALCYOSNYRA 1800
QY 1801 AHALCTHYDQQLLYAIOQYVNSGFLRQGFYDILLALHLESHAATMEACKNEFVPLGPE 1860
DB 1801 AHALCTHYDQQLLYAIOQYVNSGFLRQGFYDILLALHLESHAATMEACKNEFVPLGPE 1860
QY 1861 LKALYEEBDMGSLASLQTESVRPQMKMTDIAESTTESNLNSYPFPLEVAREFMQALA 1920
DB 1861 LKALYEEBDMGSLASLQTESVRPQMKMTDIAESTTESNLNSYPFPLEVAREFMQALA 1920
QY 1921 EAVETNOYHNRDPVGSNENLFLPLIKLVDRLLLVGMKRDDEVEKLLINTNPETWDPSFD 1980
DB 1921 EAVETNOYHNRDPVGSNENLFLPLIKLVDRLLLVGMKRDDEVEKLLINTNPETWDPSFD 1980

QY 1981 KEGDEHRRKGLLNKMAEGAKLQNCYLLQHLNDIQLRHRYEALIAFAHDFVGLQDTQLR 2040
 DB 1981 KEGDEHRRKGLLNKMAEGAKLQNCYLLQHLNDIQLRHRYEALIAFAHDFVGLQDTQLR 2040
 QY 2041 RYTEIKQSDLPANVAACKTREFRCPREONNAIISFHLSEEDKENCPCCEBELLARNEF 2100
 DB 2041 RYTEIKQSDLPANVAACKTREFRCPREONNAIISFHLSEEDKENCPCCEBELLARNEF 2100
 QY 2101 HDTLMAHVSJLHLOEPDAENQEPBAKPGAFGKLXNTIINWKELEBKAIAIEBPCKTPE 2160
 DB 2101 HDTLMAHVSJLHLOEPDAENQEPBAKPGAFGKLXNTIINWKELEBKAIAIEBPCKTPE 2160
 QY 2161 EKFRKVLIGTIYVMAESQIETPKLVEMFSLVROQDAVGBELRALEKTYVINAKTKLD 2220
 DB 2161 EKFRKVLIGTIYVMAESQIETPKLVEMFSLVROQDAVGBELRALEKTYVINAKTKLD 2220
 QY 2221 VAEKMWGLSQIRALLPVQMSQEBEELMRKLMKLVNHTPFQHPDLIRVLRVHEMVAVM 2280
 DB 2221 VAEKMWGLSQIRALLPVQMSQEBEELMRKLMKLVNHTPFQHPDLIRVLRVHEMVAVM 2280
 QY 2281 NMTLGRRAQASDAPSSQPAVEDSKKOTSHENWVACRPLCYFCRGRONOKAMPDHF 2340
 DB 2281 NMTLGRRAQASDAPSSQPAVEDSKKOTSHENWVACRPLCYFCRGRONOKAMPDHF 2340
 QY 2341 DFLLENSNILLSRPSLRGSTPLDVAYSLSMENTELALREHYLEKIAVYLSSRCGLQSN 2400
 DB 2341 DFLLENSNILLSRPSLRGSTPLDVAYSLSMENTELALREHYLEKIAVYLSSRCGLQSN 2400
 QY 2401 ELVEKGYPDGMDPVEGERYLDLRFQVWNGESVEENANLVRLIRREPCIGPALRGE 2460
 DB 2401 ELVEKGYPDGMDPVEGERYLDLRFQVWNGESVEENANLVRLIRREPCIGPALRGE 2460
 QY 2461 GEGGLKAIYDANKMSERIADRRKLRMEQSGDNVPSPLRESDEDEYIDTGAALIFYC 2520
 DB 2461 GEGGLKAIYDANKMSERIADRRKLRMEQSGDNVPSPLRESDEDEYIDTGAALIFYC 2520
 QY 2521 TLVDLLGRCAPDAGVIALGKNESSLARAILRSIVPLEDLOGVLSLRETLNPAAGEBRPK 2580
 DB 2521 TLVDLLGRCAPDAGVIALGKNESSLARAILRSIVPLEDLOGVLSLRETLNPAAGEBRPK 2580
 QY 2581 SDMPSGILPGHKOSVGLFLERVYGIETQELPYKLEBAFLPDILRAATMLDRNDGCSBMA 2640
 DB 2581 SDMPSGILPGHKOSVGLFLERVYGIETQELPYKLEBAFLPDILRAATMLDRNDGCSBMA 2640
 QY 2641 LSNMRYTGNSTILPLITGHAFYNEBAENYASLLDATTHTVRLSKNMLTGOREAVSDFL 2700
 DB 2641 LSNMRYTGNSTILPLITGHAFYNEBAENYASLLDATTHTVRLSKNMLTGOREAVSDFL 2700
 QY 2701 VALTSAMQPSMLKTLRKLTVDSYKLSSETTVVALRLTLHYERCAKYYGSTGAGGAFGA 2760
 DB 2701 VALTSAMQPSMLKTLRKLTVDSYKLSSETTVVALRLTLHYERCAKYYGSTGAGGAFGA 2760
 QY 2761 SASDEKRLTMMLFNSIFDSLSKMDYEBELFGKALPCLIAIGCALPPDYSLSKNYDEFFY 2820
 DB 2761 SASDEKRLTMMLFNSIFDSLSKMDYEBELFGKALPCLIAIGCALPPDYSLSKNYDEFFY 2820
 QY 2821 KEQAAGLDNDPQYDPOPIINTSSVALNNDLNTIYQKSEBHHDMAASKINGWYGBGWS 2880
 DB 2821 KEQAAGLDNDPQYDPOPIINTSSVALNNDLNTIYQKSEBHHDMAASKINGWYGBGWS 2880
 QY 2881 DSOKTHRLKPYMNLNDYEKERYKEPVRESIKALLAIGMSEVSEVDIPENNSSMRROS 2940
 DB 2881 DSOKTHRLKPYMNLNDYEKERYKEPVRESIKALLAIGMSEVSEVDIPENNSSMRROS 2940
 QY 2941 KSGGRPEBIY-TDSATPFDYNPHFVDMTNTLTLSREMONMAERLADNADIMAKKCEELV 2999
 DB 2941 KSGGRPEBIYOTDSATPFDYNPHFVDMTNTLTLSREMONMAERLADNADIMAKKCEELV 2999
 QY 3000 T 3000
 DB 3001 T 3001

RESULT 3
 ADM68900
 ID ADM68900 standard; protein; 5142 AA.
 XX
 AC ADM68900;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Heliothis virescens ryanodine receptor protein SEQ ID NO:144.
 XX
 KW ryanodine receptor; insect ion channel; insecticide; pesticide;
 XX calcium balance disruption; receptor calcium release mechanism.
 OS Heliothis virescens.
 PN W02004027042-A2.
 XX
 PD 01-APR-2004.
 XX
 PF 23-SEP-2003; 2003WO-US029834.
 XX
 PR 23-SEP-2002; 2002US-0412795P.
 PR 18-NOV-2002; 2002US-0427324P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 XX
 PI Caspar T, Cordova D, Gutteridge S, Raun JU, Smith RM, Wu L;
 PI Tao Y;
 DR WPI; 2004-295411/27.
 DR N-PSDB; ADM68899.
 XX
 PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
 PT for isolating other pest ryanodine receptors and in developing screens to
 PT identify insecticidally active compounds.
 XX
 PS Claim 15; SEQ ID NO 144; 687bp; English.
 XX
 CC The present invention describes an isolated nucleotide fragment (I)
 CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
 CC having an amino acid sequence identity of at least 80% when compared to a
 CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
 CC 128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
 CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
 CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
 CC construct comprising (I) operably linked to at least one regulatory
 CC sequence; (2) a transformed host cell comprising the recombinant
 CC construct; (3) a method to isolate (I) encoding ryanodine receptors and
 CC related polypeptides; (4) an isolated polypeptide having ryanodine
 CC receptor activity; (5) a method for evaluating at least one compound for
 CC its ability to modulate calcium homeostasis; (6) a method for evaluating
 CC at least one compound which modulates ryanodine receptor activity; (7) an
 CC isolated nucleic acid fragment encoding an insect ion channel comprising
 CC at least two fully defined polypeptide sequences selected from SEQ ID
 CC NOS. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
 CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
 CC insect ion channel; (9) a method for expressing an isolated nucleic acid
 CC fragment encoding a toxic insect ion channel; and (10) recombinant
 CC construct comprising in the 5' to 3' direction a promoter operably linked
 CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
 CC The isolated nucleotide fragment (I) encoding a ryanodine receptor is
 CC useful for the isolation of other pest ryanodine receptors and developing
 CC of screens to identify insecticidally active compounds. The nucleic acid
 CC fragments are useful as pesticides; fragments of protein for antibody
 CC production; fragments of protein for determination of the structure of
 CC insecticide binding sites and in the identification of insecticides that
 CC disrupt the calcium balance in cells through other messengers that
 CC interact with the receptor calcium release mechanism. The present
 CC sequence is used in the exemplification of the present invention.
 XX
 SQ Sequence 5142 AA;
 Query Match 99.4%; Score 15655.5; DB 8; Length 5142;

Best Local Similarity 99.3%; Pred. No. 0;
Matches 2986; Conservative 5; Mismatches 7; Indels 9; Gaps 2;
QY 1 MAEAGSAGBODVBSFLRTEDMYCLSTATGERVCLAEGBGNRHFLENIAADKNIPDIL 60
Db 1 MAABEGSAGQDDVBSFLRTEDMYCLSTATGERVCLAEGBGNRHFLENIAADKNIPDIL 60
QY 61 SQCVFYIYBQALSTRALQELVYAAAGSET----GKGTGSGHRTLLYGNAILLRHNSDMYL 115
Db 61 SQCVFYIYBQALSTRALQELVYAAAGSETGKGTGSGHRTLLYGNAILLRHNSDMYL 120
QY 116 ACSTSSSDQKLAFDVGLQOHSQGBACMWTLLHPASKORSSEKRYRGDDLIIVSVATERY 175
Db 121 ACSTSSSDQKLAFDVGLQOHSQGBACMWTLLHPASKORSSEKRYRGDDLIIVSVATERY 180
QY 176 .LHTTKENEVSIIVNASFVHTMSVQPYGTGJSRMKRYGVYGGDVLRFPHGDECLTTPST 235
Db 181 LHTTKENEVSIIVNASFVHTMSVQPYGTGJSRMKRYGVYGGDVLRFPHGDECLTTPST 240
QY 236 WTKDGGONIVYVYGGSVMSQARSMLRLLELARTKAGGFIMVHPMRIRHITGRYLVND 295
Db 241 WTKDGGONIVYVYGGSVMSQARSMLRLLELARTKAGGFIMVHPMRIRHITGRYLVND 300
QY 296 QNELYIVSREATYATSCAFCLROBKDOQVLEDKOLEVIGAPIIKYGDSTVVOHSENG 355
Db 301 QNELYIVSREATYATSCAFCLROBKDOQVLEDKOLEVIGAPIIKYGDSTVVOHSENG 360
QY 356 LMLSYKSYETKKKGKGVKEBKQAILHEBGMDDGLDPSRSQEBESHTAIVIRKCSLFTK 415
Db 361 LMLSYKSYETKKKGKGVKEBKQAILHEBGMDDGLDPSRSQEBESHTAIVIRKCSLFTK 420
QY 416 FINGLETLOENRHSNMFASVNLGEMVCLIEDLINTPAODEMEHEBKONKFRALRNQ 475
Db 421 FINGLETLOENRHSNMFASVNLGEMVCLIEDLINTPAODEMEHEBKONKFRALRNQ 480
QY 476 DLEQEBGILNLTLEAIDKINVTISQGLAGFLAGDSGSGWEMISGYLYOLLAIIKGNH 535
Db 481 DLEQEBGILNLTLEAIVKINVTISQGLAGFLAGDSGSGWEMISGYLYOLLAIIKGNH 540
QY 536 TNCQAFANSRLNMLFSLRQSASGEGTGLDVLHCVLIDSPALNMBDEHIKVIISLL 595
Db 541 TNCQAFANSRLNMLFSLRQSASGEGTGLDVLHCVLIDSPALNMBDEHIKVIISLL 600
QY 596 EKXGRDPKVLIDVCSLCVGNAGVAVRSQNNICDYLPGKNLLQTLVNVHVSVPNNIV 655
Db 601 EKXGRDPKVLIDVCSLCVGNAGVAVRSQNNICDYLPGKNLLQTLVNVHVSVPNNIV 660
QY 656 GRVGSAAVYRKVFEVYTMHIEKTHMMPLRIGMANTGYVYVPGSGKMGNGVGDLL 715
Db 661 GRVGSAAVYRKVFEVYTMHIEKTHMMPLRIGMANTGYVYVPGSGKMGNGVGDLL 720
QY 716 YSYGPDGAYLMSGKRTPVNRTAEBPYIRKGDVIGCALDLTVPIINFMNGVRYTSGFT 775
Db 721 YSYGPDGAYLMSGKRTPVNRTAEBPYIRKGDVIGCALDLTVPIINFMNGVRYTSGFT 780
QY 776 NFNLEBGFPPVYISCSKSLGRPLGGBHGRLYAABEGISPLVESLILPQOILSLBPCFYF 835
Db 781 NFNLEBGFPPVYISCSKSLGRPLGGBHGRLYAABEGISPLVESLILPQOILSLBPCFYF 840
QY 836 GNLKRALGPRLYVODDTAFVTPVDTLQITLPTYVBOIRGDKAENIHMMANMKIEAM 895
Db 841 GNLKRALGPRLYVODDTAFVTPVDTLQITLPTYVBOIRGDKAENIHMMANMKIEAM 900
QY 896 MYGDQREDLHKIHPCLVPERLPPAEKRYDIQLAVOTLKTIIALGYISILDXRPAIRNV 955
Db 901 MYGDQREDLHKIHPCLVPERLPPAEKRYDIQLAVOTLKTIIALGYISILDXRPAIRNV 960
QY 956 RLDPNEPFMOSSNGYKPAPLDISAVTLTPKDELVDOIAENYTHIMWASERIQQCGWYGLND 1015
Db 961 RLDPNEPFMOSSNGYKPAPLDISAVTLTPKDELVDOIAENYTHIMWASERIQQCGWYGLND 1020
QY 1016 SDMHRSBPHVVPYKXVDAIKKANRDTASEVTTLVYGYMLDPPTGEOHEALLBASKOK 1075
Db 1075 SDMHRSBPHVVPYKXVDAIKKANRDTASEVTTLVYGYMLDPPTGEOHEALLBASKOK 1075

Db 1021 SDMHRSBPHVVPYKXVDAIKKANRDTASEVTTLVYGYMLDPPTGEOHEALLBASKOK 1080
QY 1076 QADFRITRAEKXVAVSSGKMYFEFELTAGPNRVGMADHADA PMGMLQGDENSMAFDGYN 1135
Db 1081 QADFRITRAEKXVAVSSGKMYFEFELTAGPNRVGMADHADA PMGMLQGDENSMAFDGYN 1140
QY 1136 EKKYVSGNTSFPGKQMAVGVFLDILDKTISLSNGELMDLNGSETTPADVOGDNF 1195
Db 1141 EKKYVSGNTSFPGKQMAVGVFLDILDKTISLSNGELMDLNGSETTPADVOGDNF 1200
QY 1196 VPACTIGVQKARLTYYGQDVNTLKYFTTCGLQEGEFPFCVNNKRVYTHYTDQPIFENT 1255
Db 1201 VPACTIGVQKARLTYYGQDVNTLKYFTTCGLQEGEFPFCVNNKRVYTHYTDQPIFENT 1260
QY 1256 DEMIDTRIDVTRIIPASGDTPECLKISHNTFETMERKAMNEFLRLSLPVICHNEFIDEAKA 1315
Db 1261 DEMIDTRIDVTRIIPASGDTPECLKISHNTFETMERKAMNEFLRLSLPVICHNEFIDEAKA 1320
QY 1316 RRVWEIKDROQILMEKAVBAQMPAHIDQIMSGFTMNDIKGLHYEDNOBELPSSKTKLP 1375
Db 1321 RRVWEIKDROQILMEKAVBAQMPAHIDQIMSGFTMNDIKGLHYEDNOBELPSSKTKLP 1380
QY 1376 SRPFRKGSWTRGVTIQYNNILOPGOVNGHRSISEAMAKYDLAGOGLTPDDKDKRGKS 1435
Db 1381 SRPFRKGSWTRGVTIQYNNILOPGOVNGHRSISEAMAKYDLAGOGLTPDDKDKRGKS 1440
QY 1436 PPKFRSRKGSSESDRAKRSKTPDPFSDEVSPEGRARRPNQIKVSAQANRYNGMAR 1495
Db 1441 PPKFRSRKGSSESDRAKRSKTPDPFSDEVSPEGRARRPNQIKVSAQANRYNGMAR 1500
QY 1496 PSTRNLVYSGQVGLN---MATTPDRKOMTSTLSQASITYGNEIFPAECLKLINEFY 1551
Db 1501 PSTRNLVYSGQVGLNMAQMAPTPDOKOMTSTLSQASITYGNEIFPAECLKLINEFY 1560
QY 1552 GVRIVPGDPPTHVYIGWTTQYHLHSKOPNOSKVTSSYIITDDYRVVENVROSCTVY 1611
Db 1561 GVRIVPGDPPTHVYIGWTTQYHLHSKOPNOSKVTSSYIITDDYRVVENVROSCTVY 1620
QY 1612 RADELINYMVAEATKAGSOGMFIGSVDTSIGSVFTCEGKDTSFKTMEBETYLFPAL 1671
Db 1621 RADELINYMVAEATKAGSOGMFIGSVDTSIGSVFTCEGKDTSFKTMEBETYLFPAL 1680
QY 1672 FYEATSKETLQIELGRSATSLPLSAVLPSTBDKHYIPQPPRLKVOCLKPHQMAVPPNS 1731
Db 1681 FYEATSKETLQIELGRSATSLPLSAVLPSTBDKHYIPQPPRLKVOCLKPHQMAVPPNS 1740
QY 1732 LOVHALKISDRIKGSMLCEDAVSMALAIPEBDRCIDLIEPTEMDKLSFSHSHTLYLA 1791
Db 1741 LOVHALKISDRIKGSMLCEDAVSMALAIPEBDRCIDLIEPTEMDKLSFSHSHTLYLA 1800
QY 1792 LCYGNSYRAAHALCTHVDOQKOLLVAIQSYMSGRLRQGFYDILLALHLSHAATTMEACKN 1851
Db 1801 LCYGNSYRAAHALCTHVDOQKOLLVAIQSYMSGRLRQGFYDILLALHLSHAATTMEACKN 1860
QY 1852 EFVITPLGEBELKALYEEBPMGHSLSRLQTESVRPQMKMTDIABSTIEISNLVSPPYPLBYA 1911
Db 1861 EFVITPLGEBELKALYEEBPMGHSLSRLQTESVRPQMKMTDIABSTIEISNLVSPPYPLBYA 1920
QY 1912 REFVQALAEAVETQVNRDPVGGSNENLFLPLKLDVRLLYVGMBSDEDEYKLLIMTN 1971
Db 1921 REFVQALAEAVETQVNRDPVGGSNENLFLPLKLDVRLLYVGMBSDEDEYKLLIMTN 1980
QY 1972 PETWDPSPDKGKDBHRKGLLHMKVABAGAKLQMCYLLQHLNDIQLRHVEAIIAFAHDFV 2031
Db 1981 PETWDPSPDKGKDBHRKGLLHMKVABAGAKLQMCYLLQHLNDIQLRHVEAIIAFAHDFV 2040
QY 2032 GDLQTDQRLRTYTEIQOSLPSAVAAKTRRERCPPREOMNAIISPKHLEEBDKEXCPGE 2091
Db 2041 GDLQTDQRLRTYTEIQOSLPSAVAAKTRRERCPPREOMNAIISPKHLEEBDKEXCPGE 2100
QY 2092 ELIARMBFHTLMAHVSLSHLQEPDAENQEPKAPKAPGGLYNIINTVLELEBEAKAI 2151
Db 2101 ELIARMBFHTLMAHVSLSHLQEPDAENQEPKAPKAPGGLYNIINTVLELEBEAKAI 2160

QY 116 ACISTSSODKALFDVGLQSHSGEACWTLHPASKORSSEKVRVGDLLIVSVATERY 175
DB 121 ACISTSSODKALFDVGLQSHSGEACWTLHPASKORSSEKVRVGDLLIVSVATERY 180
QY 176 LHTTKENEVSIVNASFHVTHMSVOPYGTGTSBKMYGVYVGGDVLPFGHGDCLTIPST 235
DB 181 LHTTKENEVSIVNASFHVTHMSVOPYGTGTSBKMYGVYVGGDVLPFGHGDCLTIPST 240
QY 236 WTKDQGNIVVYEGGSVMSQARSIMLRLARTKAGGFIWYHPMBIRHITTRYLGVND 295
DB 241 WTKDQGNIVVYEGGSVMSQARSIMLRLARTKAGGFIWYHPMBIRHITTRYLGVND 300
QY 296 QNELYVSRREATTASCAPCLROBKDOQVLEDBKOLEVYGAPITKXGDSVTYVQHSERG 355
DB 301 QNELYVSRREATTASCAPCLROBKDOQVLEDBKOLEVYGAPITKXGDSVTYVQHSERG 360
QY 356 LMLSYSEYETKKGVKVEEKOAILHEBGMDGLDPSRSOEESTARTIRKCSLFTK 415
DB 361 LMLSYSEYETKKGVKVEEKOAILHEBGMDGLDPSRSOEESTARTIRKCSLFTK 420
QY 416 FINGELTQENRHSNMFASVNLGBVMCLLEDLINYPAOPDEDEHEBEKONKFRALNRQ 475
DB 421 FINGELTQENRHSNMFASVNLGBVMCLLEDLINYPAOPDEDEHEBEKONKFRALNRQ 480
QY 476 DLFOEBGILMLJLEAIDKINVTISQGFPLAGLADBSGQSEMI SGTYLQOLAIIKGNH 535
DB 481 DLFOEBGILMLJLEAIDKINVTISQGFPLAGLADBSGQSEMI SGTYLQOLAIIKGNH 540
QY 536 TNCAGPANSRLMMLFSLGSOASGEGTGLDYLHCILIDSPALMMDEHITKVIISLL 595
DB 541 TNCAGPANSRLMMLFSLGSOASGEGTGLDYLHCILIDSPALMMDEHITKVIISLL 600
QY 596 EKHGRDPXYLDVLCSLCVNGVAVRSGONNICDYLPGKNTLLQTLVHVHVSVRNIEV 655
DB 601 EKHGRDPXYLDVLCSLCVNGVAVRSGONNICDYLPGKNTLLQTLVHVHVSVRNIEV 660
QY 656 GVEGSAVVRKMYFEVTHMHIKKTMMHPLRGANNTGYVYPCGGSEKNGNGVDUL 715
DB 661 GVEGSAVVRKMYFEVTHMHIKKTMMHPLRGANNTGYVYPCGGSEKNGNGVDUL 720
QY 716 YSYPFGAYLMSGGRKTPVNRTHAEBPYIRKGDVIGCALDLYPIINPFNGVRYTGSFT 775
DB 721 YSYPFGAYLMSGGRKTPVNRTHAEBPYIRKGDVIGCALDLYPIINPFNGVRYTGSFT 780
QY 776 NENLBMFPFVIVSCSSKLSRPLGSEHGRLYAABEGYSPLESILPQOIIISLBECFV 835
DB 781 NENLBMFPFVIVSCSSKLSRPLGSEHGRLYAABEGYSPLESILPQOIIISLBECFV 840
QY 836 GMLSKRALLGPRVODDTAFVPPVDTLOITLPTYEQIRDKLAENITHEMAMNKIEAGW 895
DB 841 GMLSKRALLGPRVODDTAFVPPVDTLOITLPTYEQIRDKLAENITHEMAMNKIEAGW 900
QY 896 MYGDORBEDLHKIHPCLVPERLPAPAKRYDIOLAVOGLTILALGYTISLDRPARIRV 955
DB 901 MYGDORBEDLHKIHPCLVPERLPAPAKRYDIOLAVOGLTILALGYTISLDRPARIRV 960
QY 956 RLPNEPFMOSNGYKPAJDLASVTLTPKXDELVDQLAENTHMLMARERIOQGMTYGLAND 1015
DB 961 RLPNEPFMOSNGYKPAJDLASVTLTPKXDELVDQLAENTHMLMARERIOQGMTYGLAND 1020
QY 1016 SDMHSSPHLVYPKDDAIKKAANDTASSETVTLVYGYMDLDPRTGEOHEALLLEASXOK 1075
DB 1021 SDMHSSPHLVYPKDDAIKKAANDTASSETVTLVYGYMDLDPRTGEOHEALLLEASXOK 1080
QY 1076 QADPRTYABKRYAVASSGKMYEPFELTAGPMRVGAHADMA PGWMLGQDENSMAFDGN 1135
DB 1081 QADPRTYABKRYAVASSGKMYEPFELTAGPMRVGAHADMA PGWMLGQDENSMAFDGN 1140
QY 1136 BEKYVSGNTESFGKQAVGDVGVFLDLIDKTIISFSLNGELMDLADGSETTFADYQGNF 1195
DB 1141 BEKYVSGNTESFGKQAVGDVGVFLDLIDKTIISFSLNGELMDLADGSETTFADYQGNF 1200
QY 1196 VPACTLGVGQKARLYTGQDVNTLKTFTTCGLOBGIEBPFCVNMKRDVTHMYTQOPIFENT 1255

DB 1201 VPACTLGVGQKARLYTGQDVNTLKTFTTCGLOBGIEBPFCVNMKRDVTHMYTQOPIFENT 1260
QY 1256 DEMIDTRIDVTRIPAGSDTRPCLKISHNTEFEMKAMFELSLSPVICNHSFIDEAEXA 1315
DB 1261 DEMIDTRIDVTRIPAGSDTRPCLKISHNTEFEMKAMFELSLSPVICNHSFIDEAEXA 1320
QY 1316 RRMWEIKORQOILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNOBELSPSKMRKL 1375
DB 1321 RRMWEIKORQOILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNOBELSPSKMRKL 1380
QY 1376 SRPFRKGSRTGVITQNTNNLOPGVNGHRSSTSEANAKTYLGAOGLTPDDKDKRGGS 1435
DB 1381 SRPFRKGSRTGVITQNTNNLOPGVNGHRSSTSEANAKTYLGAOGLTPDDKDKRGGS 1440
QY 1436 PRKFRFSKRGSSDDAKSRKSTPPFSDTEVSPERGARPNPQIKVSGANRYNGMNR 1495
DB 1441 PRKFRFSKRGSSDDAKSRKSTPPFSDTEVSPERGARPNPQIKVSGANRYNGMNR 1500
QY 1496 PSRTNLVGSQVGLN----MATPTODRKQMTTSTLQASATETVGNBIFDAECLKLINEFY 1551
DB 1501 PSRTNLVGSQVGLNNAQVATPTODRKQMTTSTLQASATETVGNBIFDAECLKLINEFY 1560
QY 1552 GVRITPGDPTMYIGMTTQYHLKSDPNQSKTSSYITDDYDRVVENNRQSCYV 1611
DB 1561 GVRITPGDPTMYIGMTTQYHLKSDPNQSKTSSYITDDYDRVVENNRQSCYV 1620
QY 1612 RADELYNEVMAEATKAGSQGWFICGSVDTSVGSFPCBEGDTPFKFPMBETKLPFAI 1671
DB 1621 RADELYNEVMAEATKAGSQGWFICGSVDTSVGSFPCBEGDTPFKFPMBETKLPFAI 1680
QY 1672 FVZATSKETLOIELGRASATSLPLSAAYLPTSDKAVIPQEPRLKYQCLKPHQMARVPNS 1731
DB 1681 FVZATSKETLOIELGRASATSLPLSAAYLPTSDKAVIPQEPRLKYQCLKPHQMARVPNS 1740
QY 1732 LQVHALKSIDIRGMSMLCEDAVSMALAHIPBEDRCIDILIEPHEMOKLSFHSHTITLYVA 1791
DB 1741 LQVHALKSIDIRGMSMLCEDAVSMALAHIPBEDRCIDILIEPHEMOKLSFHSHTITLYVA 1800
QY 1792 LQVSNYRAAHLCTHVQOKOLLYAIOQVNSGPRGOFYDILLALHLSHATTMEACN 1851
DB 1801 LQVSNYRAAHLCTHVQOKOLLYAIOQVNSGPRGOFYDILLALHLSHATTMEACN 1860
QY 1852 BEVILGPELXALYEPDMGHSLSLQTESVAPQWKTDIASITESNLSYRPLEEVA 1911
DB 1861 BEVILGPELXALYEPDMGHSLSLQTESVAPQWKTDIASITESNLSYRPLEEVA 1920
QY 1912 REFVQALAEAVETVQVHNRDPVGSNENLPLIKLYDRLLVGMKDEDEVEKLLIMTN 1971
DB 1921 REFVQALAEAVETVQVHNRDPVGSNENLPLIKLYDRLLVGMKDEDEVEKLLIMTN 1980
QY 1972 PETWPSFPGKGDHRKGLHMKMAEGAKIOMCYLLOHLNDIOLRHYEATIAFAHDPV 2031
DB 1981 PETWPSFPGKGDHRKGLHMKMAEGAKIOMCYLLOHLNDIOLRHYEATIAFAHDPV 2040
QY 2032 GDLQTDQRLRYTEIKQSDLPNSAVALKTRBRCPREQWNAISFKHLBEBDEXKPCGE 2091
DB 2041 GDLQTDQRLRYTEIKQSDLPNSAVALKTRBRCPREQWNAISFKHLBEBDEXKPCGE 2100
QY 2092 ELIARMEFHDITMAHVSILHALQEPDAENQEPKAPGAGLNYIINTYKELBEEAKAI 2151
DB 2101 ELIARMEFHDITMAHVSILHALQEPDAENQEPKAPGAGLNYIINTYKELBEEAKAI 2160
QY 2152 BEPPKCTPEEKPRKLYIOTIVNMAEBSQIETPKLYREHFSLLVROYDAVGBILIRALEKTY 2211
DB 2161 BEPPKCTPEEKPRKLYIOTIVNMAEBSQIETPKLYREHFSLLVROYDAVGBILIRALEKTY 2220
QY 2212 VINAKTKLDVABEMVGSQIRALLPVQMSOBBEELMRRLKLVNNHTFQHPDLIRYL 2271
DB 2221 VINAKTKLDVABEMVGSQIRALLPVQMSOBBEELMRRLKLVNNHTFQHPDLIRYL 2280
QY 2272 VHENVAMMNTLGRBAQSDAOPSSQPVABDSKXOTSHBMVYACCRFLCYFERTGRQ 2331

Db 2281 VHEWVAWVWNTLGRRAQAOADAPSSQPAVEDNKEKDTSEHWVAVACCRFLCYCRTCGRQ 2340
 QY 2332 NOKAMPDHPDLLENNSILLSPRLRGSTPLDVAVSSIMMENTELALREHYLEKIAVYL 2391
 Db 2341 NOKAMPDHPDLLENNSILLSPRLRGSTPLDVAVSSIMMENTELALREHYLEKIAVYL 2400
 QY 2392 SRCGLQSNSELVEKGYDGLGMDPVEGERYLDPLFCVWNGESVVENANLVIALLIRPE 2451
 Db 2401 SRCGLQSNSELVEKGYDGLGMDPVEGERYLDPLFCVWNGESVVENANLVIALLIRPE 2460
 QY 2452 CLGALNAGEEGGLKALVDANKSERIADRKLAEKMEQGVNNSHPLPESDEDEDYDT 2511
 Db 2461 CLGALNAGEEGGLKALVDANKSERIADRKLAEKMEQGVNNSHPLPESDEDEDYDT 2520
 QY 2512 GAALINFTCTLVLDLGRCAPDAGVYALGKNESLRARALRSLPVEDLQGLSLRFLANN 2571
 Db 2521 GAALINFTCTLVLDLGRCAPDAGVYALGKNESLRARALRSLPVEDLQGLSLRFLANN 2580
 QY 2572 PAAGEBRPKSDMPGSLIPGHKQSVGLFLERVYGIETDELFYKLLBEAFPLDRLAATMLDR 2631
 Db 2581 PAAGEBRPKSDMPGSLIPGHKQSVGLFLERVYGIETDELFYKLLBEAFPLDRLAATMLDR 2640
 QY 2632 NDGESDMALSMNRYIGNSILPLIKAYFYNEAENYASLIDATLHTVYRLSKRMITKG 2691
 Db 2641 NDGESDMALSMNRYIGNSILPLIKAYFYNEAENYASLIDATLHTVYRLSKRMITKG 2700
 QY 2692 QREAVSDPLVALTSAMQPSMLKLRLKLTIVVSKSEYTVVALRLTLHYERCAKYGST 2751
 Db 2701 QREAVSDPLVALTSAMQPSMLKLRLKLTIVVSKSEYTVVALRLTLHYERCAKYGST 2760
 QY 2752 GAGGAGGASDSDEKRLTMMLPSNIPDLSMDYEPBLFGKALPCLIAIGCALPPDYSL 2811
 Db 2761 GAGGAGGASDSDEKRLTMMLPSNIPDLSMDYEPBLFGKALPCLIAIGCALPPDYSL 2820
 QY 2812 KNTYDERYGEQAAGDLDNPQYDQPIINTSSVALANNDLNTVQKSEHYHDMAKRIEN 2871
 Db 2821 KNTYDERYGEQAAGDLDNPQYDQPIINTSSVALANNDLNTVQKSEHYHDMAKRIEN 2880
 QY 2872 GMVYGEQMSDSOKTHPRLKPYNNMNDYKERYKSEPVESLKAALAIQMSVSHSVDI 2931
 Db 2881 GMVYGEQMSDSOKTHPRLKPYNNMNDYKERYKSEPVESLKAALAIQMSVSHSVDI 2940
 QY 2932 NRSRMRQSKSGRPPRIVDSATPPDYNPHPVDMTLLTSRENNNAERLADNAHDIA 2991
 Db 2941 NRSRMRQSKSGRPPRIVDSATPPDYNPHPVDMTLLTSRENNNAERLADNAHDIA 3000
 QY 2992 KKKKEELVT 3000
 Db 3001 KKKKEELVT 3009

RESULT 5
 ADM68902
 ID ADM68902 standard; protein, 5100 AA.
 AC ADM68902;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Heliochla virescens ryanodine receptor protein SEQ ID NO:146.
 XX
 KM ryanodine receptor; insect ion channel; insecticide; peatcidic;
 XX
 KW calcium balance disruption; receptor calcium release mechanism.
 OS Heliochla virescens.
 XX
 MO2004027042-A2.
 XX
 PD 01-APR-2004.
 XX
 PP 23-SEP-2003; 2003WO-US029834.
 XX
 PR 23-SEP-2002; 2002US-0412795P.

PR 18-NOV-2002; 2002US-0427324P.
 PA
 XX (DUPO) DU PONT DE NEMOURS & CO E. I.
 PI
 PI Caspar T, Cordova D, Gutteridge S, Rauh JT, Smith RM, Wu L;
 PI Tao Y;
 XX
 DR WPI: 2004-295411/27.
 DR N-PSDB; ADM68901.
 PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
 PT for isolating other pest ryanodine receptors and in developing screens to
 PT identify insecticidally active compounds.
 PS
 XX Claim 15; SEQ ID NO 146; 687bp; English.
 CC
 CC The present invention describes an isolated nucleotide fragment (1)
 CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
 CC having an amino acid sequence identity of at least 80% when compared to a
 CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
 CC 128, 130, 144, or 146; or (b) the complement of (a). (1) comprises a
 CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
 CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
 CC construct comprising (1) operably linked to at least one regulatory
 CC sequence; (2) a transformed host cell comprising the recombinant
 CC construct; (3) a method to isolate (1) encoding ryanodine receptors and
 CC related polypeptides; (4) an isolated polypeptide having ryanodine
 CC receptor activity; (5) a method for evaluating at least one compound for
 CC its ability to modulate calcium homeostasis; (6) a method for evaluating
 CC at least one compound which modulates ryanodine receptor activity; (7) an
 CC isolated nucleic acid fragment encoding an insect ion channel comprising
 CC at least two fully defined polypeptide sequences selected from SEQ ID
 CC NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
 CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
 CC insect ion channel; (9) a method for expressing an isolated nucleic acid
 CC fragment encoding a toxic insect ion channel; and (10) recombinant
 CC construct comprising in the 5' to 3' direction a promoter operably linked
 CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
 CC The isolated nucleotide fragment (1) encoding a ryanodine receptor is
 CC useful for the isolation of other pest ryanodine receptors and developing
 CC of screens to identify insecticidally active compounds. The nucleic acid
 CC fragments are useful as pesticides, fragments of protein for antibody
 CC production, fragments of protein for determination of the structure of
 CC insecticide binding sites and in the identification of insecticides that
 CC disrupt the calcium balance in cells through other messengers that
 CC interact with the receptor calcium release mechanism. The present
 CC sequence is used in the exemplification of the present invention.
 CC
 XX
 SQ Sequence 5100 AA;
 Query Match 98.3%; Score 15475; DB 8; Length 5100;
 Best Local Similarity 98.4%; Pred. No. 0;
 Matches 2958; Conservative 4; Mismatches 5; Indels 38; Gaps 3;
 QY 1 MAEAGGASQDDVDFLRTEDMYCLSTATGERVCLAAGFGNRHCFLENIADKNIPDL 60
 Db 1 MAEAGGASQDDVDFLRTEDMYCLSTATGERVCLAAGFGNRHCFLENIADKNIPDL 60
 QY 61 SOCVFVEQALSVRALQELVTAAGSET----GKGTSGHRTLLYGNAILLRHNSDMYL 115
 Db 61 SOCVFVEQALSVRALQELVTAAGSETGKNTLKGKGTSGHRTLLYGNAILLRHNSDMYL 120
 QY 116 ACISTSSQDKAPVDGLQOHSGEACWMTLHPASRORSSEGEYRVGDDLLIVSVATERY 175
 Db 121 ACISTSSQDKAPVDGLQOHSGEACWMTLHPASRORSSEGEYRVGDDLLIVSVATERY 180
 QY 176 LHTTKENSVIVASFFVTHMSVQPYGTGSRMKYGVYGVGDLVRFHGGDECLTIPST 235
 Db 181 LHTTKENSVIVASFFVTHMSVQPYGTGSRMKYGVYGVGDLVRFHGGDECLTIPST 240
 QY 236 WTKDGGNIVIVYGGSVMSQARSLMRLELARTYMAAGFINWHPKIRHITTRRYGVND 295
 Db 241 WTKDGGNIVIVYGGSVMSQARSLMRLELARTYMAAGFINWHPKIRHITTRRYGVND 300

Qy 296 QNELYLVSREBATTASCAFCLEKQEKDQKQVLEBKDLJEVIGAPIIKYGDSTVIVQHSBTG 355
Db 301 QNELYLVSREBATTASCAFCLEKQEKDQKQVLEBKDLJEVIGAPIIKYGDSTVIVQHSBTG 360
Qy 356 LMLSYKYEYTKKKQGVVEEKQALIHBEKGMDGLDLSRSGEBSRTARVTRKSSLFTK 415
Db 361 LMLSYKYEYTKKKQGVVEEKQALIHBEKGMDGLDLSRSGEBSRTARVTRKSSLFTK 420
Qy 416 FINGLETLOENRRSMFFASVNLGEMVCLLEDLINFPAQPEDDEHEHEKQKFPALBNRQ 475
Db 421 FINGLETLOENRRSMFFASVNLGEMVCLLEDLINFPAQPEDDEHEHEKQKFPALBNRQ 480
Qy 476 DLFOEGILMLILEAIDKINVITSQGLAGFLAGDESQSWEMISGYLYOLAAIIGKNH 535
Db 481 DLFOEGILMLILEAIDKINVITSQGLAGFLAGDESQSWEMISGYLYOLAAIIGKNH 540
Qy 536 TNCQAFANSRNLMLFSLRQSQASGEGTMDLHCTULIDSPALNMMRDEHITVITSL 595
Db 541 TNCQAFANSRNLMLFSLRQSQASGEGTMDLHCTULIDSPALNMMRDEHITVITSL 600
Qy 596 EKGRDPRKVLDTCLCVNGVAVRSSQNNICDYLPGKNLLQTLALVDHVS SVRPNI FV 655
Db 601 EKGRDPRKVLDTCLCVNGVAVRSSQNNICDYLPGKNLLQTLALVDHVS SVRPNI FV 660
Qy 656 GRVGSAAVRRKWEYEVMTMDHI EKTTHMPLRIGMANTTGYVPYGGGEGKGGANGVDL 715
Db 661 GRVGSAAVRRKWEYEVMTMDHI EKTTHMPLRIGMANTTGYVPYGGGEGKGGANGVDL 720
Qy 716 YSYVFDQAYILMSGGRKTPVNRTHABEPIYIRKGVITGALDLTVPIINPMNGRVRVTSFT 775
Db 721 YSYVFDQAYILMSGGRKTPVNRTHABEPIYIRKGVITGALDLTVPIINPMNGRVRVTSFT 780
Qy 776 NFNLEGNFPVYISGSSKLSGCRFLGEGHGLRYAAPGYSPLVBSLLPOQILSLPECFYF 835
Db 781 NFNLEGNFPVYISGSSKLSGCRFLGEGHGLRYAAPGYSPLVBSLLPOQILSLPECFYF 840
Qy 836 GNLSKRALAGPVLVODDTAFVPTVPDITLQITLPTVYEQIRDKLAENIHEMMAMNKIBAGW 895
Db 841 GNLSKRALAGPVLVODDTAFVPTVPDITLQITLPTVYEQIRDKLAENIHEMMAMNKIBAGW 900
Qy 896 MYGQORBDLKHIEHCLVPERFLRPAEKRYDIOQLAVOTLKTILALGYIISIDKPPARIRNV 955
Db 901 MYGQORBDLKHIEHCLVPERFLRPAEKRYDIOQLAVOTLKTILALGYIISIDKPPARIRNV 960
Qy 956 RLPEBPMQNGYKAPLDLSAVTLTPKMDLVOLAEHTHNLARERIQQGWTYGLNED 1015
Db 961 RLPEBPMQNGYKAPLDLSAVTLTPKMDLVOLAEHTHNLARERIQQGWTYGLNED 1020
Qy 1016 SDMHRSPHLVPPKVDDAIKKANEDTASETVRLLVGYMLDPTGSEHALLLEASKOK 1075
Db 1021 SDMHRSPHLVPPKVDDAIKKANEDTASETVRLLVGYMLDPTGSEHALLLEASKOK 1080
Qy 1076 QADPRTRAKRYAVSSGKMYFEFEILTAGPMRGAMHADMAPMMLGODENSWAPDGYN 1135
Db 1081 QADPRTRAKRYAVSSGKMYFEFEILTAGPMRGAMHADMAPMMLGODENSWAPDGYN 1140
Qy 1136 EEEKYSGNTESFGKQMAVGVDFDLIDKITSFSLNGELMDALGSETTPADVOGDNF 1195
Db 1141 EEEKYSGNTESFGKQMAVGVDFDLIDKITSFSLNGELMDALGSETTPADVOGDNF 1200
Qy 1196 VPACTIGVGKARLITYGQDVNTLKYFTTCGLQSBGYEBFCVNMKRDVTHWYTKQOPIENT 1255
Db 1201 VPACTIGVGKARLITYGQDVNTLKYFTTCGLQSBGYEBFCVNMKRDVTHWYTKQOPIENT 1260
Qy 1256 DEMIDTIDVTIRIPAGSDTPPCLKISHTPTETMEKAMWFLRLSLPIYICNNEPIDEAKA 1315
Db 1261 DEMIDTIDVTIRIPAGSDTPPCLKISHTPTETMEKAMWFLRLSLPIYICNNEPIDEAKA 1320
Qy 1316 RRVWEIENDROOILMKAEVAQMPAHIDQIMRSGFTMDIKGLHYEDQOEELPSSKMKRLP 1375
Db 1321 RRVWEIENDROOILMKAEVAQMPAHIDQIMRSGFTMDIKGLHYEDQOEELPSSKMKRLP 1380

Qy 1376 SRPPRKGSTRTGYTQNTNNLQPGVNGHRSSTSEAMAKYDUGAQGLTPDDKDKRGRS 1435
Db 1381 SRPPRKGSTRTGYTQNTNNLQPGVNGHRSSTSEAMAKYDUGAQGLTPDDKDKRGRS 1428
Qy 1436 PFKFRPSKGESSDRAKSRKSTPDPSPDEVEPEEGARRBNQIYVSOANORVGNMNR 1495
Db 1429 PFKFRPSKGESSDRAKSRKSTPDPSPDEVEPEEGARRBNQIYVSOANORVGNMNR 1481
Qy 1496 PSRTNLYGSOVGLMMAPTQDRKQMTSTLAQSAETEIVGNEIPDAECLKLINEFYGVRI 1555
Db 1482 -----MPTPDQRQMTSTLAQSAETEIVGNEIPDAECLKLINEFYGVRI 1527
Qy 1556 YPGQDPHTVITIGVNTTQYHLSKDFNQSXYTKTSVITTDYDVRVENNRQSCYMRADE 1615
Db 1528 YPGQDPHTVITIGVNTTQYHLSKDFNQSXYTKTSVITTDYDVRVENNRQSCYMRADE 1587
Qy 1616 LYNEVMAEATKASQGMFTGCSVDSTGVSFTGCKDQSPFKMKPEPKLPALFVEA 1675
Db 1588 LYNEVMAEATKASQGMFTGCSVDSTGVSFTGCKDQSPFKMKPEPKLPALFVEA 1647
Qy 1676 TSKEIILQIBLGRSATSPLSAAYLPTSDEKAVIPEPPRLKVQCLAKPHQMARVENQSLQVH 1735
Db 1648 TSKEIILQIBLGRSATSPLSAAYLPTSDEKAVIPEPPRLKVQCLAKPHQMARVENQSLQVH 1707
Qy 1736 ALKLSDIKQSMYCEDAVSMALHIEBEDCIDLEPIEMDKLSFHSHTLTLYAALCYQ 1795
Db 1708 ALKLSDIKQSMYCEDAVSMALHIEBEDCIDLEPIEMDKLSFHSHTLTLYAALCYQ 1767
Qy 1796 SNYRAHALCTHVDQOLYALIOSOYMSGPLRGFPDILIALHESHAATTMEACKNBEV 1855
Db 1768 SNYRAHALCTHVDQOLYALIOSOYMSGPLRGFPDILIALHESHAATTMEACKNBEV 1827
Qy 1856 PLGPELKALYEEDDMGSHLSRQTESVVRPQMKTTDAESITBESNLVSYPFPLEVAREFV 1915
Db 1828 PLGPELKALYEEDDMGSHLSRQTESVVRPQMKTTDAESITBESNLVSYPFPLEVAREFV 1887
Qy 1916 MQALAEAVETNOYVNRDPVGGSNENLFLPLIKLVDRLLVGMNRDDEVECLIMTPEBT 1975
Db 1888 MQALAEAVETNOYVNRDPVGGSNENLFLPLIKLVDRLLVGMNRDDEVECLIMTPEBT 1947
Qy 1976 DPFDEKGEDEHKKGLHMKMAEGAKLQMCYLLQHLNDILOLRHVAITAFAPHPGDLQ 2035
Db 1948 DPFDEKGEDEHKKGLHMKMAEGAKLQMCYLLQHLNDILOLRHVAITAFAPHPGDLQ 2007
Qy 2036 TDQLRRTYTELKOSDLPASAATAKTRBFCPPREONNAIISFKILBEEKENCGEBELIA 2095
Db 2008 TDQLRRTYTELKOSDLPASAATAKTRBFCPPREONNAIISFKILBEEKENCGEBELIA 2067
Qy 2096 RNNEFHDITMAHVSILHALQEPDAENQEPBAKFGAGKLYNITNTYKLEBBAKAIIEBP 2155
Db 2068 RNNEFHDITMAHVSILHALQEPDAENQEPBAKFGAGKLYNITNTYKLEBBAKAIIEBP 2127
Qy 2156 KKTPEKPRKVLQITLVNNAESQIETPKLVNEMFSLROYOVAVEBLIRALEKTYVINA 2215
Db 2128 KKTPEKPRKVLQITLVNNAESQIETPKLVNEMFSLROYOVAVEBLIRALEKTYVINA 2187
Qy 2216 KTKLDVAEMVVGISQIRALLPYQMSQEBELMKRKLNNHTFPOHPLIRLVNHN 2275
Db 2188 KTKLDVAEMVVGISQIRALLPYQMSQEBELMKRKLNNHTFPOHPLIRLVNHN 2247
Qy 2276 VNAVMNNTIGRRQAQSDAQPSQPYAEDSKEDTSHENVVACRFLCYFCRTGRONOKA 2335
Db 2248 VNAVMNNTIGRRQAQSDAQPSQPYAEDSKEDTSHENVVACRFLCYFCRTGRONOKA 2307
Qy 2336 MPDHPFLSNSIILSRSLGSPDLVAYSSIMNTEALALRBYLLEKTAIVYISRCG 2395
Db 2308 MPDHPFLSNSIILSRSLGSPDLVAYSSIMNTEALALRBYLLEKTAIVYISRCG 2367
Qy 2396 LOSNSELVEKGYPDGLMDVEGERYLDPLRFQVYVNGESVBEVANIVIRLLIRPECLG 2455
Db 2368 LOSNSELVEKGYPDGLMDVEGERYLDPLRFQVYVNGESVBEVANIVIRLLIRPECLG 2427
Qy 2456 ALRGEGBGLLKALVDANKMSERIADRRKLREMEQBGDVNFSHPDLPSEDEDEYITDGAAL 2515

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DB 2428 ALRGESEGLKALVDANKSERIADRKLAEMEQEGVNSHPLPESDEDEDYIDGAAI 2487
QY 2516 LNFYCTLVLDLGRCAPDAGVIALGKNEISLARAALIRSLVLEBDIOGVLSLFTLNPAAG 2575
DB 2488 LNFYCTLVLDLGRCAPDAGVIALGKNEISLARAALIRSLVLEBDIOGVLSLFTLNPAAG 2547
QY 2576 EBRPKSDMPGSLPGHKQSVGLFLERYVGIETQELFYKLEBAFLPDRAATMLDRDGC 2635
DB 2548 EBRPKSDMPGSLPGHKQSVGLFLERYVGIETQELFYKLEBAFLPDRAATMLDRDGC 2607
QY 2636 ESMALSMNNRYIGNSILPLIKIAYFYNEAKENTASLIDATLHTYTRLSKRMATKQREA 2695
DB 2608 ESMALSMNNRYIGNSILPLIKIAYFYNEAKENTASLIDATLHTYTRLSKRMATKQREA 2667
QY 2696 VDFELVALTSAMQPSMLKILRLKLTVDVSKLSETTVALKLTLYHERCAKYGGTAGQ 2755
DB 2668 VDFELVALTSAMQPSMLKILRLKLTVDVSKLSETTVALKLTLYHERCAKYGGTAGQ 2727
QY 2756 GARGASDDEKRLTMMFLFSNIPDLSMDYEPFLFGALPCLIAIGCALPPDYSLSKNYD 2815
DB 2728 GARGASDDEKRLTMMFLFSNIPDLSMDYEPFLFGALPCLIAIGCALPPDYSLSKNYD 2787
QY 2816 DEFYKQQAAGLDNPDQDPIINTSSVALANDLNTIYOKFSHYHDMAWSRKIEGWTY 2875
DB 2788 DEFYKQQAAGLDNPDQDPIINTSSVALANDLNTIYOKFSHYHDMAWSRKIEGWTY 2847
QY 2876 GEMWSOSQTHPRPKPYNMLANDYKERYKAPVRESLKALLAIGMSVSHSVDPISNNRS 2935
DB 2848 GEMWSOSQTHPRPKPYNMLANDYKERYKAPVRESLKALLAIGMSVSHSVDPISNNRS 2907
QY 2936 MRQSGSGGRPEIYVDSATPPDYNPHPVMTNLTLSRENNMAERLADNAHDIWAKKK 2995
DB 2908 MRQSGSGGRPEIYVDSATPPDYNPHPVMTNLTLSRENNMAERLADNAHDIWAKKK 2867
QY 2996 EBLVT 3000
DB 2968 EBLVT 2972

RESULT 6
ADM68764
ID ADM68764 standard; protein; 5127 AA.
XX
AC ADM68764;
XX
DT 17-JUN-2004 (first entry)
XX
DE Peregrinus maidis ryanodine receptor protein SEQ ID NO:8.
XX
KW ryanodine receptor; insect ion channel; insecticide; pesticide;
XX calcium balance disruption; receptor calcium release mechanism.
XX
OS Unidentified.
XX
PN MO2004027042-A2.
XX
PD 01-APR-2004.
XX
PF 23-SEP-2003; 2003MO-US029834.
XX
PR 23-SEP-2002; 2002US-0412795P.
XX 18-NOV-2002; 2002US-0427324P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E. I.
XX
PI Caspar T, Cordova D, Gutteridge S, Rauh JJ, Smith RM, Wu L;
XX 750 Y.
XX
DR WPI, 2004-295411/27.
XX N-PSDB; ADM68763.
XX
PT New isolated nucleotide fragment encoding a ryanodine receptor, useful

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PT for isolating other pest ryanodine receptors and in developing screens to
PT identify insecticidally active compounds.
XX
XX Claim 15; SEQ ID NO 8; 687pp; English.
XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC construct comprising (I) operably linked to at least one regulatory
CC sequence; (2) a transformed host cell comprising the recombinant
CC construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC related polypeptides; (4) an isolated polypeptide having ryanodine
CC receptor activity; (5) a method for evaluating at least one compound for
CC its ability to modulate calcium homeostasis; (6) a method for evaluating
CC at least one compound which modulates ryanodine receptor activity; (7) an
CC isolated nucleic acid fragment encoding an insect ion channel comprising
CC at least two fully defined polypeptide sequences selected from SEQ ID
CC Nos. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC insect ion channel; (9) a method for expressing an isolated nucleic acid
CC fragment encoding a toxic insect ion channel; and (10) recombinant
CC construct comprising in the 5' to 3' direction a promoter operably linked
CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC useful for the isolation of other pest ryanodine receptors and developing
CC of screens to identify insecticidally active compounds. The nucleic acid
CC fragments are useful as pesticides, fragments of protein for antibody
CC production, fragments of protein for determination of the structure of
CC insecticide binding sites and in the identification of insecticides that
CC disrupt the calcium balance in cells through other messengers that
CC interact with the receptor calcium release mechanism. The present
CC sequence is used in the exemplification of the present invention.
XX
XX
SQ Sequence 5127 AA;
XX
Query Match 80.9%; Score 12738; DB 8; Length 5127;
Best Local Similarity 80.5%; Pred. No. 0;
Matches 2446; Conservative 236; Mismatches 278; Indels 78; Gaps 24;
QY 1 MABEGASBODDVSFRTEDMYCLSTCTAGERVCLAAEGFGRHGFLENIAADKNTPDL 60
DB 1 MADSEGG-SEQDDVSFLRTEDMYCLSTCTAGERVCLAAEGFGRHGFLENIAADKNTPDL 59
QY 61 SOCVPYIQLSVRALQELVTAAAGSFTGKTGSGHRTLLYGNAILLRHLSNDMYLACLST 120
DB 60 STCVPIEQALSVRALQELVTAAAGSEKGTGSGHRTLLYGNAILLRHQSDMYLACST 119
QY 121 SSSQDYKAPFVGIQHSQSGACWTLHPASKQSBSEKRVAGDILLVATRYLYHTTK 180
DB 120 SSSNDKXSPVGVLOHSSQSGACWTVHPASKQSBSEKRVAGDILLVATRYLYHTTK 179
QY 181 ENEVSTVNASFHTVHNSVOPVGTGTSRMKVGVVFGSDVLPFRPHGDECLTISTWTGK 240
DB 180 ENDLSTVNASFHTVHNSVOPVGTGTSRMKVGVVFGSDVLPFRPHGDECLTISTWTGK 239
QY 241 GONIIVYEGGSVNSQASRLRLRLARTKVAAGFINNTHPMRIHTTGRYLVGNDONELY 300
DB 240 GONIIVYEGGSVNSQASRLRLRLARTKVAAGFINNTHPMRIHTTGRYLVGNDONELY 299
QY 301 LVSRBEATTNASCAPCLRQEKQDKOYLEDKOLEVITGAPITIKYGDSTYIVHSHSTGLMSTY 360
DB 300 LIVRDEATTNLSAFCLRQEKQDKOYLEDKOLEVITGAPITIKYGDSTYIVHSHSTGLMSTY 359
QY 361 KSYETKKKGKGVKBEKQALIHESGKMDPGIDFSRQSEBSRTARVIRKQSLFTKFINGL 420
DB 360 KSYETKKKGKGVKBEKQALIHESGKMDPGIDFSRQSEBSRTARVIRKQSLFTKFINGL 419
QY 421 ETLQENRRHSMFPASVNLGEMVACLDELINYPADPDEMBEKKQKFRALRRNODLFOE 480

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Db 420 ETLQVNRBBSLFCATVNLNEMWCLBELLINYPAQPADMEHEKONFRALRRQDLFOR 479
Qy 481 EGIJLNLLEAIDICINVTSCGFLAGLAGDSQSGWEMISGYIYOLIAAIIKKNHTNCAQ 540
Db 480 EGIJNLLEAIDICINVTSCGFLVGS-LAGDESGQSMIIISGYIYOLIAAIIKKNHTNCAQ 538
Qy 541 PANSNRLNMLFSLRGSQASGBGTGMLDVHLCVLDISEALNMNRDEHIKVIISLEHGR 600
Db 539 PANSNRLNMLFSLRGSQASGBGTGMLDVHLCVLDISEALNMNRDEHIKVIISLEHGR 598
Qy 601 DPKVLDVLCGLCVNGVAVASSQNNICDYLLPGKNLLQTLAVDHVSSVAPNIFVSGVEG 660
Db 599 DPKVLDVLCGLCVNGVAVASSQNNICDPLPGKNLLPQTLVDHVASVAPNIFVGRVVG 658
Qy 661 SAVYRKMYFEVYMDHIEKTTMHMPHLRIGNANTTGYVPYPGGSEKMGNGVGDLYSYGR 720
Db 659 SAVYQKMYFEVYMDHIEQTLTHMPHLRIGNANTSGVVPYPGGSEKMGNGVGDLYSYGR 718
Qy 721 DGAYLMSGGRKTPVNTTHAEEPIYIRKGDVIGCALDLTPRIINFMFGVAVTGSFTNPNLE 780
Db 719 DGNLMTGGKRTCV-LPHATEPPIKKGADVIGVSLDLTPRIITPSFNGSPIRGCFRDFND 777
Qy 781 GMEFPYISGSSKLSCHFLGEGHGRLYAAPEGYSPLVESILPQOILISLEPCFYFGNLK 840
Db 778 GMEFPYISGSHKLSCHFLGEGHGRLYKVPPEBSPLVESILPQOYLSTIDPCFYFGNLK 837
Qy 841 RALAGPPLVODDTAFLVPTPVDTLQITLPTYVEQIRDKLAENIHEMANMKIEAGMYGDO 900
Db 838 CVLSGWTVEEDTAPFPTPVDTLKVSLPNYIESIRDKLAENIHEMANMKIEAGMYGEX 897
Qy 901 REDLHIFHCLVFEERLPAEKRYDIOLAVQTLKTLAIGUYISLKKPARLANNVLPME 960
Db 898 RDDRIRVHPLCLQFDLPRAEKRYDSOLAVQTLKTLAIGUYITMCKPBRKTIYLPME 957
Qy 961 PEMQSGYRPAPLDLAVTLTPKDELVQLAENTHNLMAERIIQOGWTYGLNEDSDMR 1020
Db 958 PEMQSGYRPAPLDLAISTPQMBELVQLAENTHNLMAKERIIQOGWTYGLNEDSDMR 1017
Qy 1021 SPHLVYPRVYDAIKKANRDTASETYRTLIVGYMLDPTGEQHALLEBASQKQADPR 1080
Db 1018 SPHLVYCVKDEAIKKANRDTASEYRTLIVGYMLDPTGEAHEALLABASRLQTHRR 1077
Qy 1081 TYRAENYAVSSGSKWFEERELLTAGBMRGMAHADMAPGMLGODENSNAFOCYNEKY 1140
Db 1078 TYRAENYAVTTGKWFEEBELLTAGBMRGMAHSDCPGSQLGNDYSNAFDFENKEY 1137
Qy 1141 SGNTSEFGQMAVGDVGVFLDLIDKTISSFLNGELLMALGGETTFADVOGDNFYAC 1200
Db 1138 LGTGSEFGQMGVGDVGVFLDLIDHTMGSFSLNGELLMALGGETTFADVOGSEFYAC 1197
Qy 1201 LGVGOVAKLLTYGQDVNTLKYPTTCGLQEGYBPCVNMKQDVTHMYTKQPIBENTDEMID 1260
Db 1198 LGVGOVAKLLTYGQDVNTLKYPTTCGLQEGYBPCVNMRAVTVYTKDHPFBENTDYAD 1257
Qy 1261 THIDVTRIRAGSDTPCLKISHHTPFTMEKAMNEPRLSLPYICNHEPIDEAKARWYE 1320
Db 1258 SHIDVTRIRAGSDTPCLKISHHTPFTMEKAMNEPRLSLPYICNHEPIDEAKARWYE 1317
Qy 1321 IDORQOILMKEAVEAQMPAHIDQIRSGFTMNDIKGLH--YEDN-----QBELPSK 1370
Db 1318 IIRQRHRLVEN-DOYTPAHMEOIMKSGMSGDIKGLHGRGSDVAEADMMQSGITPTTK 1376
Qy 1371 MK-RLESPRPKSGMTRGVTTIONYNLQPGQVNG-----MHRSTSEAMAKYDLQAGL 1423
Db 1377 SKMRGSRPBRKGSLSR-----NEDWPMINGLEQSKMRSTSELDLANNYNDLQF- 1427
Qy 1424 TDDDKDKDKGRSPKFRSKRGESSDRAASRKSCTDPSPDTEVSEBGRARPN-----P 1478
Db 1428 DKDDKK-KKGRSPFRFSRKRASNER--SKAKXSPBNMBAJRGQGRGQHHMMRTP 1484
Qy 1479 QIKVSOANORVYGMNAPRSTNLYGSOVLNMAATPQDRKQMTTSTLAOSATETVGNELF 1538
Db 1485 TYKVTAAPMKVLPPTI-PERSNM-----PKOMTGALSGSGIESVGNELF 1528

Qy 1539 DAECLKLINBYFYGVRIYEGQDPTHVYIGWVTOYHLSKDNFQSKVTSSVIIITDDYDR 1598
Db 1529 DGECLKLINBYFYGVRIYEGQDPTHVYGVVTVQYHFAPIEFQSKVRKYVTHLDEFSR 1588
Qy 1599 VVENVRQSCYMMRADELXNVEAENATKAGASGCMTIGCSVDNSTGSVSTCGSKOTSRK 1658
Db 1589 VNESVDRQSCYMMRSDELXNVEAENATKAGASGCMTIGCVDAATGYISTCGSKOTSRK 1648
Qy 1659 FKMEPEPKLPALFVATSKELIQLIBLSATSLSPTSAALFPTSDKVIYPOPEPKLVQC 1718
Db 1649 FKMEPEPKLPALFVATSKELIQLIBLSATSLSPTSAALFPTSDKVIYPOPEPKLVQC 1708
Qy 1719 LKPHQVARYPNOSLOVHALKLSDIRGWSMLCEDAVSMLALHIEEDRCIDILIEPMDKL 1778
Db 1709 LKPHQVARYPNOSLOVHALKLSDIRGWSMLCEDPMESMLALHIEEDRCIDILIEPMDKL 1768
Qy 1779 LSFHSHTLTYALACVQSNYRAAHLCSTVDQKQLYALQSQVMSGPLRQFPDILLALH 1838
Db 1769 LSFHSHTLTYALACVQSNYRAAHLCSTVDQKQLYALRSDMSGPLRQFPDILLALH 1828
Qy 1839 LBSHATMBACKNEFVIRPAGBELKALYEERPMGSHLSRQTESVPRQOMKWTDLA----- 1892
Db 1829 LBSHATMBACKNEFVIRPAGBELKALYEERPMGSHLSRQTESVPRQOMKWTDLA----- 1888
Qy 1893 ESITISNLYSPYFPLEVAREFVMOALAEAVETNOVNRDPVGSNENMLFLPLIKLVRL 1952
Db 1889 EVVDNIRSLYSQFPDLDVDRDFMALDEAVQINQJLHNRDPVGSNENMLFLPLIKLVRL 1948
Qy 1953 LTVGMRRDEDVKLLINTPMTDPSFDEKGEDEHKKGLIHHMAGAKLQMCYLLQHLN 2012
Db 1949 LTVGMRRDEDVKLLINTPMTDPSFDEKGEDEHKKGLIHHMAGAKLQMCYLLQHLN 2008
Qy 2013 DIQLRHVRBAIIAFAHDFVGDLOTDQRLRYTEIKOSDLSAVALAKTRFRCPPREQMA 2072
Db 2009 DIQLRHVRBAIIAFAHDFVGDLOTDQRLRYTEIKOSDLSAVALAKTRFRCPPREQMA 2068
Qy 2073 IISFKHLEBEDYENCPGEBELIARNNEFHTTMAHVSJHALQBPDAAB-NQEBEATPGAF 2131
Db 2069 IISFKHLEBEDYENCPGEBELIARNNEFHTTMAHVSJHALQBPDAAB-NQEBEATPGAF 2128
Qy 2132 GKLNNINTVKELEBAKALIEEPKKTPEEKRYLQIOTVYMAESQIETPLVNEMS 2191
Db 2129 GKLNNINTVKELEBAKALIEEPKKTPEEKRYLQIOTVYMAESQIETPLVNEMS 2188
Qy 2192 LTVROQYDAVGEILIRALEKTYVINAKTKLDVAEMWGLSQIRALLPQMSQSEELMRKEL 2251
Db 2189 LTVROQYDAVGEILIRALEKTYVINAKTKLDVAEMWGLSQIRALLPQMSQSEELMRKEL 2248
Qy 2252 WGLVNNHTFQHPDLIRVLRVHENYAVVMNTLGRRAQOSDAQPSQPVABDSKEKOTR 2311
Db 2249 WGLVNNHTFQHPDLIRVLRVHENYAVVMNTLGRRAQOSDAQPSQPVABDSKEKOTR 2308
Qy 2312 HEMVYVACCRFLCYFCRTGRQONKAMPDHDPLLENSNIIILSPRSLRGSTPLDVAYSSLWE 2371
Db 2309 HEMVYVACCRFLCYFCRTGRQONKAMPDHDPLLENSNIIILSPRSLRGSTPLDVAYSSLWE 2368
Qy 2372 NTELLALREHYLEKIAVLSRQGSQNSSEIVEKGPPLDGMPVSEGERYLDFARFCVWYN 2431
Db 2369 NTELLALREHYLEKIAVLSRQGSQNSSEIVEKGPPLDGMPVSEGERYLDFARFCVWYN 2428
Qy 2433 GSEVEENANLVIRLLIRREPCGPAALRGEGSLKALIVDANKMSERIADRRKLRENEQEG 2491
Db 2429 GSEVEENANLVIRLLIRREPCGPAALRGEGSLKALIVDANKMSERIADRRKLRENEQEG 2487
Qy 2492 D---VNFHPLPESDEDDYIDTGAAILNFYCTLYDLGRCAPDAGVILAGKNESTRARA 2548
Db 2488 TTMVNHFBPPLPESDDDDYIDTGAAILNFYCTLYDLGRCAPDAGVILAGKNESTRARA 2547
Qy 2549 IIRSLVPLEDQGVSLRFTLANNPAGGERPAGSDMPSGLIPGHKQSVGLFLERVYGIETQ 2608
Db 2548 IIRSLVPLEDQGVSLRFTLANNPAGGERPAGSDMPSGLIPGHKQSVGLFLERVYGIETQ 2607

Qy	2609	ELPFXLLEBEALPDLRATMTLMDRNDGCSDMALSNRRYISGSIPLIKAHYFNEAEY	2668
Db	2608	ELFRLLEBEALPDLRATMTLMDRNDGSSDVALANRRYISGSIPLITTSKRYNEADNY	2667
Qy	2669	ASLIDATHTYVRLYSKNNMRLTKGOREAVSDPLVALTSAOESMLKLRKLTVDVSKLSE	2728
Db	2668	ASLIDATHTYVRLYSKNNMRLTKGOREAVSDPLVALTSSMOGSMLKLRKLTVDVSKLTE	2727
Qy	2729	YTTVALRLTLTHYERCANYGSGTGAGQCAFASDDEKRLTMMLFSNIFDSLXKNDYEP	2788
Db	2728	YTTVALRLTLTHYDRCAKYGSGTG- GQGLYGSSSDDEKRLTMMLFSNIFDSLXKNDYEP	2786
Qy	2789	LFGKRLPCLTIAGCALPPDYSLSKNYDDEFPYG-KEQAGDLDNPDYDQPIINTSVLNN	2847
Db	2787	LFGKRLPCLTIAGCALPPDYSLSKNYDDELFGARSOQAGPBDGP-YNQPIINTSVLNN	2845
Qy	2848	DLNTIVQKFSSEHYHDMAWSRKLENGWVYGEGWSDSQKTHPRLKPYNNLNDY-----EKER	2902
Db	2846	DLNTIVQKFSSEHYHDMAWSRKLENGWYTGDDWSDSQKTHPRLKPYNNLNDYVESIBER	2905
Qy	2903	YKEPVRESLKALLAIIGVSEHSEVDIPESSNNFSNMRQSGSGGAPPELVTDSATPPDYNH	2962
Db	2906	YKEPVRESIKALLAIIGVSEHSEADVPILTSGSIRQSG-----PNAWDSSTPEFNHYN	2960
Qy	2963	PVDMTNLTLSRENNQMAERLADNADNADIAPKKKKKEELVT 3000	
Db	2961	PIDMTNLTLSRENNQMAERLADNADNADIAPKKKKKEELIT 2398	

XX	ADME68878 standard; protein; 5127 AA.
XX	ADME68878;
XX	17-JUN-2004 (first entry)
DE	Drosophila melanogaster ryanodine receptor protein SEQ ID NO:122.
KM	ryanodine receptor; insect ion channel; insecticide; pesticide;
KW	calcium balance disruption; receptor calcium release mechanism.
XX	Drosophila melanogaster.
OS	
PN	WO2004027042-A2.
XX	
PD	01-APR-2004.
XX	
PP	23-SEP-2003; 2003WO-US029834.
XX	
PR	23-SEP-2002; 2002US-0412795P.
PR	18-NOV-2002; 2002US-0427324P.
XX	
PA	(DUPO) DU PONT DE MEMOURS & CO E I.
XX	
P1	Caspar T, Cordova D, Gutierrez S, Raun JI, Smith RM, Wu L,
P1	Tao Y;
XX	
DR	WPI; 2004-295411/27.
PT	New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT	for isolating other pest ryanodine receptors and in developing screens to
PT	identify insecticidally active compounds.
XX	
PS	Disclosure; SEQ ID NO 122; 687bp; English.
XX	
CC	The present invention describes an isolated nucleotide fragment (1)
CC	comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC	having an amino acid sequence identity of at least 80% when compared to a
CC	polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC	128, 130, 144, or 145; or (b) the complement of (a). (1) comprises a
CC	nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC	1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant

sequence, comprising (1) operably linked to at least one regulatory sequence; (2) a transformed host cell comprising the recombinant construct; (3) a method to isolate (1) encoding ryanodine receptors and related polypeptides; (4) an isolated polypeptide having ryanodine receptor activity; (5) a method for evaluating at least one compound for its ability to modulate calcium homeostasis; (6) a method for evaluating at least one compound which modulates ryanodine receptor activity; (7) an isolated nucleic acid fragment encoding an insect ion channel comprising at least two fully defined polypeptide sequences selected from SEQ ID Nos. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56, 120-126; (8) a method for identifying a nucleic acid sequence encoding an insect ion channel; (9) a method for expressing an isolated nucleic acid fragment encoding a toxic insect ion channel; and (10) recombinant construct comprising in the 5' to 3' direction a promoter operably linked to an isolated nucleic acid fragment encoding a toxic insect ion channel. The isolated nucleotide fragment (1) encoding a ryanodine receptor is useful for the isolation of other pest ryanodine receptors and developing of screens to identify insecticidally active compounds. The nucleic acid fragments are useful as pesticides, fragments of protein for antibody production, fragments of protein for determination of the structure of insecticide binding sites and in the identification of insecticides that disrupt the calcium balance in cells through other messengers that interact with the receptor calcium release mechanism. The present sequence is used in the exemplification of the present invention.

Query Match	Similarity	79.5% ; Score 12516.5 ; DB 8 ; length 5127 ;
Match Local Similarity	78.8% ; Pred. No. 0 ;	
Batches 2387 ;	Conservative 263 ; Mismatch 312 ; Indels 67 ; Gaps 21 ;	
QY	1	MAABGASBODVYFLRTEDMVLCTSTATGERVCLAAEGFNHCFLENIADKNIPDL 60
Db	1	MAABEGG-SEGDDVYFLRTEDMVLCTATGERVCLAAEGFNHCFLENIADKNIPDL 59
QY	61	SQCFVFEQALSVRALDELVTAAAGSEFGKGTGSHRTLILGNALLHNLAMDVLACT 120
Db	60	SQCFVFEQALSVRALDELVTAAAGSEFGKGTGSHRTLILGNALLHNSMDVLACT 119
QY	121	SSSDOKLAFVGLQOHSQGECAWTLTHPASKSBEKRVGDDLIVSAATERYLTHTK 180
Db	120	SSSDOKLSFDVGLQOHSQGECAWTLTHPASKSBEKRVGDDLIVSAATERYLTHTK 179
QY	181	ENEVSYINASHFVTHMSVOPVGTGISMKYVGVYFGDVLRFPGDECLTIPSTWKDG 240
Db	180	ENESYINASHFVTHMSVOPVGTGISMKYGVYFGDVLRFPGDECLTIPSTWREA 239
QY	241	GQNTIVYEGGSVMSQANSLRLELARTKMGAGFLNWTHPMRIRHTTGRYLGVNDONEL 300
Db	240	GQNTIVYEGGVMAQASRLRLELARTKMGAGFLNWTHPMRIRHTTGRYLGVNDNEL 299
QY	301	LYSSEKTTTASCACLFQEKQDKQVLEDLDLYTGAPIIKYGGSTIYVOHSEGTLM 360
Db	300	LYKKEBSIAITTYTCLQEKQDKQVLEDLDLYTGPILIKYGTIYIVQHCETSLM 359
QY	361	KSYETKKKGKGVKYEKQALIHESGKMDGLDFSKSQEBSRTARVIRKCSLPTKPLNGL 420
Db	360	KSYETKKKGKGVKYEKQALIHESGKMDCLDFSKSQEBSKTAARVIRKCSLPTKPL 419
QY	421	ETLOENRRHSMFPASVNLGEMVCLDLINYPADPDEMEHEKQKFRALRNQDLFOE 480
Db	420	ETLOSNRRHSIFPOKVMINEMVCLDLINYPSPEDMEHEKQKFRALRNQDLFOE 479
QY	481	EGTLNLLLEAIDKINVTISQGLAGFLAAGBSGGSWEMISGYLQLAALIKGNHTCAQ 540
Db	480	EGVNTLLLEAIDKINVTISQGLAFLAAGBTGQSWLITLYLQLAALIKGNHTCAQ 539
QY	541	FANSNRLNMTLFSRLGSOASGEGTGLDVLHCVLIDSEBALNMKDEHIKYLISLEKGR 600
Db	540	FANSNRLNMTLFSRLGSOASGEGTGLDVLHCVLIDSEBALNMKDEHIKYLISLEKGR 599
QY	601	DPKVLIVLCISLVNGVAVNASSQNNICDYLIPGNLLLTALVDHVSVAEPNIFVGVGEG 660

Db	600	DPKVDLVCISLVCNGVAVRSSQNNICDFLEPKRULLQTLVLVDHVASIRPNITFYGVYDG	655
Qy	661	SAVYKRWFEVYTMHIEKTHMMPHLRIGMANTTYVYVPGGGEKMGANGVDDLYSYGF	720
Db	660	SSMYQKWFEVYTMHIEQTHMMPHLRIGMANTSYVYVPGGKKMGANGVDDLYSYGF	719
Qy	721	DGAYMSGGRKTPVNRTHAEEPYIRKGDYIGCALDLYPIINFMNGRYVYGSFYNFLE	780
Db	720	DGAFYMTGGRKTLVVDALPEEBPIKKGVDYGAIDLSPVITTFPNQKGVKVSFPDFMID	779
Qy	781	GMFFPVISSSLGCRPLIGGHRGLRYAPRGYSPLVESLLPQOILSLEPGFYGNLSK	840
Db	780	GMFFPVMGSSSLGCRFLFGGDHGLKFRAPRGFSALVQCLMPQOILSDPCTFYGNLAK	839
Qy	841	PALAPPLVODDTAEVPTPVDTLQTLPTVYQOIKDLAENIHENAMANKIEAGMYGDO	900
Db	840	NVLAPGFWLIEDDTAVVPKRVDTGTVLTSVDQIKELAENIHENAMANKIEAGMSWEH	899
Qy	901	REDLKHHPCLVPERLPPAEKRYOIQALAVOTLKITLALGYISLDPKPARIRNRLNE	960
Db	900	RDDYHRIHPCLTHPEFKLPAAEKRYNOQLAVOTLKITLISLGYITTDKPKPARIRPRELNE	959
Qy	961	PFMOSNGKPAPLDISATLTPROMELVDOLAENHNMAREPQOQMGTYGAINESDHR	1020
Db	960	IFMQNGKPAPLDISAVTLTPKLELDVQALENHNIMAREIQOQMGTYGAINESSEHR	1019
Qy	1021	SPHLVPYKVDALIKKANDTASEVFRTLVYGYMLDEPTGBOHEALLLEASKOKODFR	1080
Db	1020	SPHLVPYAKVDEAIKKANRDTASEVFRTLVYGYLDPFTGBOETALLALEKORLKFAFR	1079
Qy	1081	TYRAEKYAVSSGKMYFEPEITITAGPMRYGMADHAPGMILGODENSMAFDGYNEEKY	1140
Db	1080	TYRVERNYAVTSKMYFEFEVILTSGRMKVGMARADCYGAMIGSEDTISMAFDGHNEEKY	1139
Qy	1141	SGNTESEKONAVGVGVPLDIDKITSFSLNGELMDALGGETTPADV--QGNPFPA	1198
Db	1140	GGVSESPGQCGPGGIVGVPLDLADHTISFSLNGELMDALGGETTPADVABGFPA	1199
Qy	1199	CTLGAGQKARLYYGQDVNTLKFTTCGLQEGYEPFCVMKKEIDVTMYTKDOPIFENTDEM	1258
Db	1200	CTLGAGQKARLYYGQDVDSLKFTTCGLQEGYEPFCVMRRPYTHMYTKDOPIFENTDEM	1255
Qy	1259	IDTRIDVTRIPAGSDTPPCLKISHTFETMEKANMEFLRLSLPVICHNEFTIDEAKARW	1318
Db	1260	PDCRIDVTRIPGADTPPHLKISHNTFETMEKANMEFLRLSPVCMGEFTISEGKARW	1319
Qy	1319	VEIKDROQILMKEA-VEAOW-----PAHIDQIMSGFMNIDIKGLHYE-DNOBELPSKM	1371
Db	1320	DEIKKQRLMKEAETIAOMOVQTOAAMHDHLKGGFMWNNDIKGLTRNFDHDALEAHM	1379
Qy	1372	KRLSPRPKRSKSMTEGVTIQVNNLQPCQVNGMHSTSEAEAMAKDLAGLTPDDKDX	1431
Db	1380	MRGPRPRPKRSKSLTRNIT---PEIDMSAADDEMQRSTSE-----VLDMNGGLBEMDDKC-K	1430
Qy	1432	RGRSPFKFRSKRGESSDPAKRSKSTDPSPSDTSEBERGARARNPOIKVSQANORYNG	1491
Db	1431	RGRSPFKFEF-SKKSRDQGREK-MGARLTDTSLERENTYAHGRNVVNOQMTTAPTLRLNN	1488
Qy	1492	MNAPRSRNNLYGSGVGLMAMPYTORKQMTTSLAQSTFVYNGEIPRAECGLKLINEFY	1551
Db	1489	AEIPSPV-----POGPKOLSGNIGQOQEVETSGDEMFAECGLKLINEFY	1534
Qy	1552	GVRIYPGQDPFHYVIGWTTQYTHLSKQFNOSKTVKYSVITTDVDRVVENVNQOSCMV	1611
Db	1555	GVRIYPGQDPHYVYGVWTTQYTHLSRBNKKNKRRKRSVYIEDDYEMAIKIDMQSCVY	1594
Qy	1612	RADELINWMAEATAKGASQGMFLGCSVDTSISVSFTCEGKDTISFKKMEPETGLPFAI	1671
Db	1595	RADELINWYTOADASKGASQGMFVGCAPDTATGIRFTCEGKDTISHRMWMEPDYGLFAI	1654
Qy	1672	FVEATSKILLQIELGRSATSLPLAAVYPTSDKAVIPOPFRPLKYOCLKPHQMARVPOK	1731
Db	1655	FVEATSKILLQIELGRPTTLPPLSAVYPTSPKHNINPQSPRLKYOCLKRPQMARVPTA	1714

QY	1732	LQVHALKJSDIRGSMUCEADVSMALAHIPBEDRCIDILBPIENDKJLSFSHSHTLTYYA	1791
Db	1715	LQVHALKJSDVRGSMUCEADVSMALAHIPBEDRCIDILBPIENDKJLSFSHSHTLTYYA	1774
QY	1792	LCYOSNRAAALCTHVDOKJLVAIOSOWMSGJROGFIDLALHJESHAITMBAJCN	1851
Db	1775	LCYOSNRAAALCOHVDOKJLVAIOSOWMSGJROGFIDLALHJESHAITMBAJCN	1834
QY	1852	BEVJPLGBELKALYBEPDMGHSLSLQTESVPMQKMTDI-----ABSITE	1897
Db	1835	EYIIPDLGELKELEYSDDEMOHSLSLQTESVPMQKMTDI-----ABSITE	1894
QY	1898	ISNLSYPPFLVAFARFPMQALAEVETNOYHNRPVGSSENNLFLPLIKLVDRLILVGM	1957
Db	1895	IDOLYSPPFLVAFARFPMQALAEVETNOYHNRPVGSSENNLFLPLIKLVDRLILVGM	1954
QY	1958	MRDDVDKTLIMNPEMTWDSFDKEGDGHRKGLJLHMMABGALQMCYLLQHLNDIOLR	2017
Db	1955	LTDVDOKLWIMDPEMTWDSFDKEGDGHRKGLJLHMMABGALQMCYLLHNYDLOLR	2014
QY	2018	HREVALIAFAHDFVGDLOTQDLRRYTEIKOSDLPASAALKTEBFCRPREONNALISFK	2077
Db	2015	HREVALIAFHSDFVGDLOTQDLRRYTEIKOSDLPASAALKTEBFCRPREONNQILCFK	2074
QY	2078	HLEBEDKENCPCGSEELIARNEPFDTLMAVSHALQEPDAENOB-PEAKPGAFKJYN	2136
Db	2075	NLEPDDQNCQGLHGLRGLDFHDSLMQKVSINALQEPGVEGTALAEVYGTGPIYKYN	2134
QY	2137	IIMNVKLEBBAKALIEBPKKTPEBKKRYLLOITVMMABESQIEPTKJLVREMSLLVRQ	2196
Db	2135	FIINVKLEBEBKVEBPKKTPEBVRKVALIKTIVABESQIENKJLVREMSLLLRQ	2194
QY	2197	YDAGSELIRALEKYYVINAKTKJLVAEMWYGLSQIRALLPVQMSQEEBEMRKJMLJYN	2256
Db	2195	YDYGELVRLAEKTYVINTPARDVAEMWYGLSQIRALLPVQMSQEEBELMRKJMLJYN	2254
QY	2257	NHTEFOHPDLIRVLVHENWVAVMWNTLIGRRAQOASDAQPSQOPVAE--DSKEKDTSHM	2314
Db	2255	NATFFQHPDLIRIRLVHENWVAVMWNTLIGRRAQOASDA-PTQSEVAAGAPSKEKDTSHM	2313
QY	2315	VVACCRFLCYCRGRONOKAMPHPFLFLENSITLRSRSLRGSTPDLVAYSSLMENTE	2374
Db	2314	VVACCRFLCYCFCRGRONOKAMPHPFLPDLNANITLARPSLRSTPLDVAYSLSMENTE	2373
QY	2375	LALALREHYLEKJLVYLSRCSLQSNSELYEKGYDLCMDPVEGERYUDPLRFCVWVAGES	2434
Db	2374	LALALREHYLEKJLVYLSRCSLQSNSELYEKGYDLCMDPVEGERYUDPLRFCVWVAGES	2433
QY	2435	VEENANVIRILIRRPCLGPALRGESEGLIKALIVDANKMSERJADBRKJLREMOEGDV-	2493
Db	2434	VEENANVIRILIRRPCLGPALRGESEGLFPAIVEANRMSERISDRCKMDD-BAGETIA	2492
QY	2494	--NFSHPRESDEDEDYITDGAALINYYCTVLVDLGRCAPDAGYIALGNKESLRAARILR	2551
Db	2493	GLNFTHPRLPEGEDEDEDYITDGAALINYYCTVLVDLGRCAPDASYIEGKJESLRAARILR	2552
QY	2552	SLVPLEDLQGLVLSRFLTNPPAAGEBPKSDMBSGLRGKHQSGVFLERYVYGETOELF	2611
Db	2553	SLVPLEDEDOGLVLSKFTLSOTPAPEEBPKSDMBSGGLPNNKQSVLPLERYVYGBAODLF	2612
QY	2612	YKLEBBAFLPLDRAATMLDBNDGCESDMALSMNRYYGNSITPLILIKHAYVEENAEVASTL	2671
Db	2613	YRLLEBAFLPLDRLRATITLDSKDSGSEDMALAMNRYIGNSLTILPLIKHSKYYNEAEVASTL	2672
QY	2672	LDATLHTVYRISKRMJTKGQREAVSDPVALTSQMPAMJLKJLRJTVDSKJSEYTT	2731
Db	2673	LDATLHTVYRISKRMJTKGQREAVSDPVALTSQMPAMJLKJLRJTVDSKJSEYTT	2732
QY	2732	VALMLLTLHYERCAKYYGSGTGAAGAGASDEDEKJLTMLLFSNITPSSLKQMYBEPPLFG	2791
Db	2733	VALMLLTLHYERCAKYYGSGT--QGGGASGASDEDEKJLTMLLFSNITPSSLKQMYBEPPLFG	2791

Qy	2792	KALCLCIAIGCALPPDYSLSKNYDPEFGKGAQAGDLDPQYDPDPITSSVALANDNT	2854
Db	2792	KALCLCIAIGCALPPDYSLSKNTBEDYGRQMGAP--DQPPMPPIIDITNVHLNDLNTS	2849
Qy	2852	IVQRFSEHYHMAASRKILENGVYGEGSDSOXKTPRLKPNMLNDYKEKRYKEPVRESL	2911
Db	2850	LVQRFSEHYHMAASRLLEGATYICDINSDDRGKPRKLPNMLSEYREKRYDPVRECL	2909
Qy	2912	KALLAIGMSVHSEVDIPDSNNRSSMKRQSKSGGRPEI--VTDSATPPDYNPHPYDMNTL	2965
Db	2910	KGLLAIGMTVHSEVSEVALNHRGSTRQSK-----PQINERQNEGSPFNYPNHPYDMNTL	2964
Qy	2970	TLSRQMOMAEERLADNADIDIAKKKKEEL	2998
Db	2965	TLSRQMOMAEERLAEENSHDIWAKKKNEEL	2993
RESULT 8			
ID	ADM68877	standard; protein; 5113 AA.	
AC	ADM68877;		
XX	17-JUN-2004	(first entry)	
DT			
XX	Drosophila melanogaster ryanodine receptor protein SEQ ID NO:121.		
DE			
XX	ryanodine receptor; insect ion channel; insecticide; pesticide;		
KM	calcium balance disruption; receptor calcium release mechanism.		
XX			
OS	Drosophila melanogaster.		
XX			
PN	MO2004027042-A2.		
PD			
XX	01-APR-2004.		
PF	23-SEP-2003; 2003WO-US029834.		
XX			
PR	23-SEP-2002; 2002US-0412795P.		
PR	18-NOV-2002; 2002US-0427324P.		
XX			
PA	(DUPO) DU POINT DE NEMOURS & CO E I.		
XX			
P1	Caepar T, Cordova D, Gutierrez B, Rauch JJ, Smith RM, Wu L;		
P1	Tao Y,		
PT			
XX			
DR	WPI, 2004-295411/27.		
PS			
XX	Disclosure; SEQ ID NO 121; 687bp; English.		
CC			
XX	The present invention describes an isolated nucleotide fragment (1)		
CC	comprising: (a) a nucleic acid sequence encoding a ryanodine receptor		
CC	having an amino acid sequence identity of at least 80% when compared to a		
CC	polypeptide selected from the group consisting of (a). (1) comprises a		
CC	128, 130, 144, or 146; or (b) the complement of (a). (1) comprises a		
CC	nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.		
CC	1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant		
CC	construct comprising (1) operably linked to at least one regulatory		
CC	sequence; (2) a transformed host cell comprising the recombinant		
CC	construct; (3) a method to isolate (1) encoding ryanodine receptors and		
CC	related polypeptides; (4) an isolated polypeptide having ryanodine		
CC	receptor activity; (5) a method for evaluating at least one compound for		
CC	its ability to modulate calcium homeostasis; (6) a method for evaluating		
CC	at least one compound which modulates ryanodine receptor activity; (7) an		
CC	isolated nucleic acid fragment encoding an insect ion channel comprising		
CC	at least two fully defined polypeptide sequences selected from SEQ ID		
CC	NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,		
CC	120-126; (8) a method for identifying a nucleic acid sequence encoding an		
CC	insect ion channel; (9) a method for expressing an isolated nucleic acid		

	fragment encoding a toxic insect ion channel, and (10) recombinant
CC	construct comprising in the 5' to 3' direction a promoter operably linked
CC	to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC	The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC	useful for the isolation of other pest ryanodine receptors and developing
CC	of screens to identify insecticidally active compounds. The nucleic acid
CC	fragments are useful as pesticides, fragments of protein for antibody
CC	production, fragments of protein for determination of the structure of
CC	insecticide binding sites and in the identification of insecticides that
CC	disrupt the calcium balance in cells through other messengers that
CC	interact with the receptor calcium release mechanism. The present
CC	sequence is used in the exemplification of the present invention.
XX	
XX	Sequence 5113 AA:
	Query Match 79.3%; Score 12489.5; DB 8; Length 5113;
	Best Local Similarity 78.8%; Pred. No. 0;
	Matches 2376; Conservative 271; Mismatches 315; Indels 53; Gaps 20;
Oy	1 MAABEGASBODDVSFLRTBEDVCLCTATGSEYVCLAAGEGNRHCFLENTADKXIPDL 60
Db	1 MAABEGG-SEDDDSVFLRTEBDVTLSCTATERVCLAAEGGNHCFFLENTADKNVPDL 59
Oy	61 SGCPLVEQLALSVBALDELVTAPASENGKGSQSHRTLTYGNALILRHNSDMVLACST 120
Db	60 SQCPFVIEQLATSVBALDELVTAPASENGKGSQHRTLTYGNALILRHNSDMVLACST 119
Oy	121 SSSDOKLAFVDGLQOHSOGSEACMWTLTPASQRSEGEKVARGDDLIVSVATERYLHTTK 180
Db	120 SSSNDKLSFDVGLDEHSGERACMTVHPASQRSEGERVARGDDLIVSVATERYLHTTK 179
Oy	181 ENEVSIYNASFHTWMSVOPYGTSISRMKYGVYFGGDVLPFHGGDECLTIPSTWKDG 240
Db	180 ENESIVNASFHTWMSVOPYGTGISRMKYGYVGGDVLPFHGGDECLTIPSTWKG 239
Oy	241 GQNVLYREGSVMQAASIRPLEELARTKMGGFINWHPMIRITTRGRYLVGUNDQNLX 300
Db	240 GQNVLYREGVMAQASRLMPLIELARKTMGGFINWHPMIRIHITGRYLVGUNDNELI 299
Oy	301 LVSRREATTASCAFLROEKDOKOVLEDKOLBYTAGPIIKYGSTVIQHSSETGLMISTY 360
Db	300 LVKKEBASIAITTCCLAQEKODEKVELDEDOLAVIGSPIIKKGPITYIVQGCEFSIMASTY 359
Oy	361 KSYETKKGKGVAVEEKOAILHEEGKMDDGLDFSQBEESTNAVIRKCSLLFTKFINGL 420
Db	360 KSYETKKGKGVAVEEKOAILHEEGKMDDCLDFRSQEESTAYAIRKCSLLFTOFITAL 419
Oy	421 ETLDENRRHSFPASVNLGEMVNCLELIINFAPDDEMHEEEKONFRALARNOOLFQE 480
Db	420 ETLDSNRRHSIFPKVNLNEMVNCLELIINFSQPEDMEHEEEKONFRALARNOOLFQE 479
Oy	481 EGILNLLILEAIDKINVTTSGOFLAGLAGDESQGWEMISGYLTOLLAIIKGNHTNCAQ 540
Db	480 EGVNLNLLIEAIDKINIITSOGFLASFLAGDETGSQWDLISYTLQLALAIKGNHTNCAQ 539
Oy	541 FANSNRNLNMLFSLRGSOASGEGTGMDLVLCVLIDSPALNMEDDEHIKVIIISLEKHGR 600
Db	540 FANSNRNLNMLFSLRGSOASGEGTGMDLVLCVLLIDSPALNMEDDEHIKVIIISLEKHGR 599
Oy	601 DPKYLDVLCSTCVANGVAVRSSQNNICDYLLPGKULLIQTLAVDHVSSVRNIIVGARYBG 660
Db	600 DPKYLDVLCSTCVANGVAVRSSQNNICDPFLIPGKULLIQTLAVDVHASIRPNIFEVRVDG 659
Oy	661 SAAYRKMYFEVYTMHRIKTTMMHLIRGMANTTGVYPYPGGSGKMGNGVGDLLYSYGF 720
Db	660 SSMYQMYFEVYTMHIRQTTHMPHLIRGMANTTGVYPYPGGSGKMGNGVGDLLYSYGF 719
Oy	721 DGATLWSGGRKTPTNRTAEAPYIRKGDVIGCALDLTVPIINFENGVRYVGSFTNFMLE 780
Db	720 DGATLWTGKRCTLVVDALPEEPFIIRKGDVIGVALDSLVPITTFPFGVKVAGSRDFLD 779
Oy	781 GMPPPVVISCGSKSCRFLLGSEHGRLRYAADBGYSPLVESLIPQOILISLEPCFFGNISK 840

QY 2984 DNAADIMAKKKEEL 2998
:|||||
DB 2965 ENSHDIWAKKKEEL 2979

RESULT 9
ADM68876
ADM68876 standard; protein; 5127 AA.
ADM68876,
17-JUN-2004 (first entry)
Drosophila melanogaster ryanodine receptor protein SEQ ID NO:120.
ryanodine receptor; insect ion channel; insecticide; pesticide;
calcium balance disruption; receptor calcium release mechanism.
Drosophila melanogaster.
MO2004027042-A2.
01-APR-2004.
23-SEP-2003; 2003WO-US029834.
23-SEP-2002; 2002US-0412795P.
18-NOV-2002; 2002US-0427324P.
(DUPO) DU PONT DE NEMOURS & CO E I.
Caesar T, Cordova D, Gutierrez S, Rauh JT, Smith RM, Wu L;
Tao Y,
WPI, 2004-295411/27.
New isolated nucleotide fragment encoding a ryanodine receptor, useful
for isolating other pest ryanodine receptors and in developing screens to
identify insecticidally active compounds.
Disclosure; SEQ ID NO 120; 687bp; English.

CC The present invention describes an isolated nucleotide fragment (1)
CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (1) comprises a
CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC construct comprising (1) operably linked to at least one regulatory
CC sequence; (2) a transformed host cell comprising the recombinant
CC construct; (3) a method to isolate (1) encoding ryanodine receptors and
CC related polypeptides; (4) an isolated polypeptide having ryanodine
CC receptor activity; (5) a method for evaluating at least one compound for
CC its ability to modulate calcium homeostasis; (6) a method for evaluating
CC at least one compound which modulates ryanodine receptor activity; (7) an
CC isolated nucleic acid fragment encoding an insect ion channel comprising
CC at least two fully defined polypeptide sequences selected from SEQ ID
CC NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC insect ion channel; (9) a method for expressing an isolated nucleic acid
CC fragment encoding a toxic insect ion channel; and (10) recombinant
CC construct comprising in the 5' to 3' direction a promoter operably linked
CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC The isolated nucleotide fragment (1) encoding a ryanodine receptor is
CC useful for the isolation of other pest ryanodine receptors and developing
CC of screens to identify insecticidally active compounds. The nucleic acid
CC fragments are useful as pesticides; fragments of protein for antibody
CC production; fragments of protein for determination of the structure of
CC insecticide binding sites and in the identification of insecticides that
CC disrupt the calcium balance and in the identification of insecticides that
CC interact with the receptor calcium release mechanism. The present
CC sequence is used in the exemplification of the present invention.

XX
SQ Sequence 5127 AA;
Query Match 79.2%; Score 12465.5; DB 8; Length 5127;
Best Local Similarity 78.4%; Pred. No. 0;
Matches 2375; Conservative 272; Mismatches 315; Indels 67; Gaps 21;

QY 1 MAEARGASGEQDDVFLRTEDMVCLSCTATGRCVCLAAEGFQNRHCFLENIADKNI PPDL 60
DB 1 MAEARGG-SEQDDVFLRTEDMVTLSCTATGRCVCLAAEGFQNRHCFLENIADKNI PPDL 59
QY 61 SOCVFVTEQALSVPRLQELVTAAAGSETGKGTSGRHTLLYGNAILLRHLSNMYLACTST 120
DB 60 SOCVFVTEQALSVPRLQELVTAAAGSETGKGTSGRHTLLYGNAILLRHLSNMYLACTST 119
QY 121 SSSODKLAFDVLQOHSQGEACMHTLHPASKORSSEGEKRVQDDLIIVSVATERYLHTK 180
DB 120 SSSNDKLSPDVLQOHSQGEACMHTVHPASKORSSEGEKRVQDDLIIVSVATERYLHTK 179
QY 181 ENEVSIYNASFFVTHMSVQPYGTGISRMKYGVYFGGDVLRFFHGDECLTTPSTWKG 240
DB 180 ENEGSIYNASFFVTHMSVQPYGTGISRMKYGVYFGGDVLRFFHGDECLTTPSTWGRA 239
QY 241 GQNIIVYEGGSVMSQARSIMRLRLARTKAGGFIMWTHPMIRHTTGRYLLGVNDONEL 300
DB 240 GQNIIVYEGGVMAQARSIMRLRLARTKWTGGFIMWTHPMIRHTTGRYLLGVNDONEL 299
QY 301 IYSREATTASCAFCILROEKDDQKQVLEBDKQLEVI GAPIIKYGDSTVIYQHSBTGLMSY 360
DB 300 IYKREBASTATTFPCILROEKDEKQVLEBDKQLEVI GSPILIKYGDVTVIYQHSBTGLMSY 359
QY 361 KSEYTKKKGVGKVEEKOAILHEGKMDGDLDSRSQSEBSRTARVIRKCSLFTKFINGL 420
DB 360 KSEYTKKKGVGKVEEKOAILHEGKMDGDLDSRSQSEBSRTARVIRKCSLFTKFINGL 419
QY 421 ETLQENRRHSWFPASVNI GEMVYCIEDLINYAQPDEDEHEHEKONKFPALNNRQDLFOE 480
DB 420 ETLQSNRRHSIFQKYNINEMWCMEDLILNYSQPEDDEHEHEKONRFPALNNRQDLFOE 479
QY 481 EGIILVILIEADIKINIVTSGFLAGFLGDESGGSEWMSGYLYOLLAIRKGNHTNCQ 540
DB 480 EGIILVILIEADIKINIVTSGFLAGFLGDESGGSEWMSGYLYOLLAIRKGNHTNCQ 539
QY 541 FANSRLRLMLFRLLSQASGSEGTGMLDVJHCVLISPEALNNRDEHIKVIISLEKGR 600
DB 540 FANSRLRLMLFRLLSQASGSEGTGMLDVJHCVLISPEALNNRDEHIKVIISLEKGR 599
QY 601 DKPVLDTVCSLCVNGVAVRASSQNNICDYLPGKNLLQTLAVDHVSVRPNI FVGARYG 660
DB 600 DKPVLDTVCSLCVNGVAVRASSQNNICDYLPGKNLLQTLAVDHVSVRPNI FVGARYG 659
QY 661 SAVYRKMYREVTMDHIEKTHMPPHRLRGMANVTGVPVPGGEGKGGNGVDDLYSYGF 720
DB 660 SSYMKQWFEVYTMHDIEQTHMPPHRLRGMANVTGVPVPGGEGKGGNGVDDLYSYGF 719
QY 721 DSAVYMSGGRKTPVNRTHAEBPYIRKGDVIGCALDVIVIIIMFNGVAVTSGFTYFNL 780
DB 720 DSAVYMSGGRKTLVVDALPEBPFIKGDVIGALDVIVIIIMFNGVAVTSGFTYFNL 779
QY 781 GMPFPVYSCSSSLSCRFLLGSEHGLRYAABGVSPLYESLLPQOITSLPECFYFNLK 840
DB 780 GMPFPVMSSSSLSCRFLLGSEHGLRYAABGVSPLYESLLPQOITSLPECFYFNLK 839
QY 841 RALAGPVLVQDDTAVPVPVDTLQTLPTVYEQIDKLAENIHEWAMNKIAGMMYGGQ 900
DB 840 NVTLAPVMLIEDTAVPKPKVDVTGVLPSVQIKKLAENIHEWAMNKIAGMMYGGH 899
QY 901 REDLKHIRHCYLPFRPLPABRGYDIQLAVOTLKTIALGYTISLDPKPARIRNVL PNE 960
DB 900 RQDYHRIHCLTHFEKLPABRGYDIQLAVOTLKTIISIGYITTYMDKPPARIRPRL PNE 959
QY 961 PEMQNGYKPAFLDLSAVTLTPRKMDLVQDLAENTHTNWARERIQQGWTYGLNEDSMR 1020
DB 961 PEMQNGYKPAFLDLSAVTLTPRKMDLVQDLAENTHTNWARERIQQGWTYGLNEDSMR 1020

Db 960 IMQNGNYKPAULDISAVTLTPKLEBLVDQLAENTHNLWABERIOQGWTYGLNDESENH 1019
Qy 1021 SPHLVPPYKVDALIKKANBDTASETVRTLVTGYMLDPPTGEQHEALLLEASKOKADDER 1080
Db 1020 SPHLVPYAKVDAIKKANBDTASETVRTLVTGYMLDPPTGEQHEALLLEASKOKADDER 1079
Qy 1081 TYRAEKNTAVSSGKTYFEFEILLTAGPMRYGMAHADMAPGMMIQQODENSAFPGYNEEKY 1140
Db 1080 TYRAEKNTAVSSGKTYFEFEILLTAGPMRYGMAHADMAPGMMIQQODENSAFPGYNEEKY 1139
Qy 1141 SNTESFGQMAVGVNVGVFLDLIDTISFSLNGELMLDAGETTPAV--QGNFVFA 1198
Db 1140 ASISHFVRYEADGVTCFIDVKEQTISFSLNGELMLDAGETTPAV--QGNFVFA 1199
Qy 1199 CTLGVOQKARLTYYGQDVNTLKYFTTQGLQEGYEPFCVNNKRDVTHWYTKOPIFENTDEM 1258
Db 1200 CTLGVOQKARLTYYGQDVNTLKYFTTQGLQEGYEPFCVNNKRDVTHWYTKOPIFENTDEM 1259
Qy 1259 IDTRIDVTRI PAGSDTPCLKISHNTFETMEKANNFELSLPVI CHNEFIDEAKARRW 1318
Db 1260 PCRIDVTRI PEGADTPPHLKISHNTFETMEKANNFELSLPVI CHNEFIDEAKARRW 1319
Qy 1319 VEIKRQOOLMKEA--VEAQM-----PAHIDQIMRSGFTMNDIKGLHYE--DNOBELSSCK 1371
Db 1330 DEIKRQYRLMREAEIAQMVOYQOAAHNDHMLKGGFNNNDIKGLTRNFDEHADAEDEM 1379
Qy 1372 KKLPERPKSGMTRGVTIQNYNNLQPGQVNGMHRSTSEBAWAKYDLGAQGLTPDDKQK 1431
Db 1380 MGPMPRPKSGSLTRNIT---FETDMSALDEMOSTS-----VLDMNGLGSEMDKK-K 1430
Qy 1432 RGRSPKPFKRGESSDRKSKSTPDPFSDTEVSPERGARRNPQIKVSQANQRYNG 1491
Db 1431 RGRSPKPFKRGESSDRKSKSTPDPFSDTEVSPERGARRNPQIKVSQANQRYNG 1488
Qy 1492 MWARSRTMLYSGVGLMAMATPTQDRKQNTTSTLAQSAFETYGNEIPLFAECLKLINEY 1551
Db 1489 AEIPSPV-----PQGRKJSSNLQGOQPVETSGDEFDFAECLKLINEY 1534
Qy 1552 GVRIYFGQDPTHVYIGMVTTOYHLHSKD FNQSKVTGSVYITDDYRVVENVROSQWY 1611
Db 1555 GVRIYFGQDPTHVYIGMVTTOYHLHSKD FNQSKVTGSVYITDDYRVVENVROSQWY 1594
Qy 1612 RADELINYMABATAKASQGMFICGSVDSTGSVSFTCEGKOTSPKFMABETKLPFAI 1671
Db 1595 RADELINYMABATAKASQGMFICGSVDSTGSVSFTCEGKOTSPKFMABETKLPFAI 1654
Qy 1672 FVEATSKETLOIEIGRSATSLPLSAAVLPFSDKHYIROPFRLTKOCLKPHOMAVPNOS 1731
Db 1655 FVEATSKETLOIEIGRSATSLPLSAAVLPFSDKHYIROPFRLTKOCLKPHOMAVPNOS 1714
Qy 1732 LOVHALKLSDIGMSMLCEDAVSMLAHIPEDRCIDILEPIEMDKLSFHSHTLTLYA 1791
Db 1715 LOVHALKLSDIGMSMLCEDAVSMLAHIPEDRCIDILEPIEMDKLSFHSHTLTLYA 1774
Qy 1792 LCYQSNYRAAHLCTHVQKOLLVYAIQSOYNSGPIRQGFYDLLIALHESHAATTWEACK 1851
Db 1775 LCYQSNYRAAHLCTHVQKOLLVYAIQSOYNSGPIRQGFYDLLIALHESHAATTWEACK 1834
Qy 1852 BEVITLGPRLKALYEPRMGHLSIQTSVAPRQMKMTDI-----AESITR 1897
Db 1835 BEVITLGPRLKALYEPRMGHLSIQTSVAPRQMKMTDI-----AESITR 1894
Qy 1898 ISNLSYPYPLFEVAFVMOALAEAVETQVHNRDVPVGSNENLFLPLKLDVRLLYVOM 1957
Db 1895 IDQVSPKPLEVAFVMOALAEAVETQVHNRDVPVGSNENLFLPLKLDVRLLYVOM 1954
Qy 1958 MKEDEVKLLIMTNEPMTDPSFDEKGDHRKGLLHMKNABGAKLQMCYLLQHLNDIQLR 2017
Db 1955 LTDEVOQRLLVMIIDETWQAFERBEGKDBHRKGLLTMKNABGAKLQMCYLLQHLNDIQLR 2014
Qy 2018 HRVEALIAFAHDFVGLDQTDRLRYTEIKQSDLPASVAAKKTREBRCPREBQMAILSFX 2077
Db 2015 HRVESIIAFSHDFVGLDQTDRLRYTEIKQSDLPASVAAKKTREBRCPREBQMAILSFX 2074

Qy 2078 HLEEDKENCPCGEBELIARMMEFHDTLMAHVSIALHJOEBDAENQ--PEAKGAFGLKVN 2136
Db 2075 NLEPDQONCTCGELRGLRGLDFHDSLMQKVSILNLOEPDVGEGRAIEBVKGTPTIKYV 2134
Qy 2137 IINTYKELBEEKALIEBPPKTPPEKFRKYLQITVMAABEQOITPKLVREMPSLVNO 2196
Db 2135 FINTYKELBEEKAVEBEPKTPPEBFRKYLQITVMAABEQOINPKLVREMPSLVNO 2194
Qy 2197 YDAGELIRALEKTYVNAKTLQDVAEMVVGSLQIRALLPVQMSQOEBELMKRLKVN 2256
Db 2195 YDAGELIRALEKTYVNAKTLQDVAEMVVGSLQIRALLPVQMSQOEBELMKRLKVN 2254
Qy 2257 NHTFQHPDLIRVLEVHENVNAVMNNTIGRAQAQSDAOPSQPAE--DSKEDTSHM 2314
Db 2255 NATFQHPDLIRVLEVHENVNAVMNNTIGRAQAQSDA--PTQSEVAEAGAPSEKDTSHM 2313
Qy 2315 VVACCRFLCYFRTGRQOKAMFDFPDLLENSNILLRSPILRGSTPLDVAYSILMENTE 2374
Db 2314 VVACCRFLCYFRTGRQOKAMFDFPDLLENSNILLRSPILRGSTPLDVAYSILMENTE 2373
Qy 2375 LALALREHYLEKIAVYLSRGLQSNSELVEKGYPDLGMDPVYEGRYLDFLRQVWNGES 2434
Db 2374 LALALREHYLEKIAVYLSRGLQSNSELVEKGYPDLGMDPVYEGRYLDFLRQVWNGES 2433
Qy 2435 VEENANLYIRLLIRREPCIGPALRGEGBGLKAIYDANKMSERLADRRKREMEQGDV- 2493
Db 2434 VEENANLYIRLLIRREPCIGPALRGEGBGLKAIYDANKMSERLADRRKREMEQGDV- 2492
Qy 2494 --NBSHPLPESDEDEYIDTGAAILNPFCTYLDLGRCAPDAGVYALGNBSLBARAILR 2551
Db 2493 GLNFTHPLEBGEDEYIDTGAAILNPFCTYLDLGRCAPDAGVYALGNBSLBARAILR 2552
Qy 2552 SLVPLEDIOGVLSLFTLNPAGERBPKSDMPSGLIGHQOSVGLFLERYVIGITOEFL 2611
Db 2553 SLVPLEDIOGVLSLFTLNPAGERBPKSDMPSGLIGHQOSVGLFLERYVIGITOEFL 2612
Qy 2612 YKLEAEFLPDLRAATMLDRNDGCSDMALSNRYIGNSILPLIKHAYFYNAENYASL 2671
Db 2613 YKLEAEFLPDLRAATMLDRNDGCSDMALSNRYIGNSILPLIKHAYFYNAENYASL 2672
Qy 2672 LDATHTYVYRSLKNNMLTKGOREAVSDPLVALTSQMOBAMLIKLRKULVDVSKSEYTT 2731
Db 2673 LDATHTYVYRSLKNNMLTKGOREAVSDPLVALTSQMOBAMLIKLRKULVDVSKSEYTT 2732
Qy 2732 VALRLTLHYERCAKYGSTAGOGAPGASDSBEKRLTMPLFSNIFDSLSKXDYBEPFLG 2791
Db 2733 VALRLTLHYERCAKYGSTAGOGAPGASDSBEKRLTMPLFSNIFDSLSKXDYBEPFLG 2791
Qy 2792 KALPCLIAIGCALPPDYSLSKNYDEPYGKEQAAGDLDPQYDQPOPINTSSVALNNDLMT 2851
Db 2792 KALPCLIAIGCALPPDYSLSKNYDEPYGKEQAAGDLDPQYDQPOPINTSSVALNNDLMT 2849
Qy 2852 IYQKSEHYHMAASRKIENGVTGEGWSDQKTHPRILKPYNMLNDYKERYKEPYREEL 2911
Db 2850 IYQKSEHYHMAASRKIENGVTGEGWSDQKTHPRILKPYNMLNDYKERYKEPYREEL 2909
Qy 2912 KALLAIGSVHSEVDIPSNRRSSMRROSKSGGRPEI--VYDSATPPDYNHVDMNTL 2969
Db 2910 KALLAIGSVHSEVDIPSNRRSSMRROSKSGGRPEI--VYDSATPPDYNHVDMNTL 2964
Qy 2970 TISREMOMARLADNAHDIWAKKKEEL 2998
Db 2965 TISREMOMARLADNAHDIWAKKKEEL 2993

RESULT 10
ADM68766
ID ADM68766 standard; protein, 5109 AA.
XX
AC ADM68766;
XX
DT 17-JUN-2004 (first entry)

XX Drosophila melanogaster ryanodine receptor protein SEQ ID NO:10.
 DE ryanodine receptor; insect ion channel; insecticide; pesticide;
 KM calcium balance disruption; receptor calcium release mechanism.
 XX Drosophila melanogaster.
 OS
 PN MO2004027042-A2.
 XX
 PD 01-APR-2004.
 XX
 XX 23-SEP-2003; 2003WO-US029834.
 PF
 PR 23-SEP-2002; 2002US-0412795P.
 PR 18-NOV-2002; 2002US-0427324P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 P1 Caspar T, Cordova D, Gutierrez S, Rauch JJ, Smith RM, Wu L;
 P1 Tao Y;
 XX
 XX WPI, 2004-295411/27.
 DR N-PSDB; ADM68765.
 DR
 PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
 PT for isolating other pest ryanodine receptors and in developing screens to
 PT identify insecticidally active compounds.
 XX
 PS Claim 15; SEQ ID NO 10; 687P; English.
 XX
 CC The present invention describes an isolated nucleotide fragment (1)
 CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
 CC having an amino acid sequence identity of at least 80% when compared to a
 CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
 CC 120, 130, 144, or 146; or (b) the complement of (a). (1) comprises a
 CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
 CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
 CC construct comprising (1) operably linked to at least one regulatory
 CC sequence; (2) a transformed host cell comprising the recombinant
 CC construct; (3) a method to isolate (1) encoding ryanodine receptors and
 CC related polypeptides; (4) an isolated polypeptide having ryanodine
 CC receptor activity; (5) a method for evaluating at least one compound for
 CC its ability to modulate calcium homeostasis; (6) a method for evaluating
 CC at least one compound which modulates ryanodine receptor activity; (7) an
 CC isolated nucleic acid fragment encoding an insect ion channel comprising
 CC at least two fully defined polypeptide sequences selected from SEQ ID
 CC NO. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
 CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
 CC insect ion channel; (9) a method for expressing an isolated nucleic acid
 CC fragment encoding a toxic insect ion channel; and (10) recombinant
 CC construct comprising in the 5' to 3' direction a promoter operably linked
 CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
 CC The isolated nucleic acid fragment (1) encoding a ryanodine receptor is
 CC useful for the isolation of other pest ryanodine receptors and developing
 CC of screens to identify insecticidally active compounds. The nucleic acid
 CC fragments are useful as pesticides, fragments of protein for antibody
 CC production, fragments of protein for determination of the structure of
 CC insecticide binding sites and in the identification of insecticides that
 CC disrupt the calcium balance in cells through other messengers that
 CC interact with the receptor calcium release mechanism. The present
 CC sequence is used in the exemplification of the present invention.
 XX
 SQ Sequence 5109 AA;
 Query Match 79.1%; Score 12460.5; DB 8; Length 5109;
 Best Local 81milarity 78.7%; Pred. No. 0;
 Matches 2371; Conservative 273; Mismatches 316; Indels 53; Gaps 20;

QY 61 SQCFVFIHQALSVRALQELVTAAAGSETKGSGHRTLLYGNALLRHLSNDMYLACTST 120
 DB 60 SQCFVFIHQALSVRALQELVTAAAGSETKGSGHRTLLYGNALLRHLSNDMYLACTST 119
 QY 121 SSSODKLAFDVGLQOHSGGEACWMTLHPASIKORSBGEKVRVGDDLLVSVAVERLYHTTK 180
 DB 120 SSSNDKLSFDVGLQSHSGGEACWMTLHPASIKORSBGEKVRVGDDLLVSVAVERLYHTTK 179
 QY 181 ENEVSIYNASPHVTHMSVQPYGTGISRMKYYGVYFGGDLVRFPHGDECLTTPSTWTKG 240
 DB 180 ENEGSIYNASPHVTHMSVQPYGTGISRMKYYGVYFGGDLVRFPHGDECLTTPSTWTKG 239
 QY 241 GQNIYVEGSSVMSQARSMLRLBLARTWAGGFIMWHPKIRIHTTGRYGVNDQNELY 300
 DB 240 GQNIYVEGSSVMSQARSMLRLBLARTWAGGFIMWHPKIRIHTTGRYGVNDQNELY 299
 QY 301 LVSREATTAACAPLROEKDOQVLEDKLEVGAIIYKSGSTVVOHSEGTMLTSTY 360
 DB 300 LVKKEBASIAVTTTCLRQEKDEKVLKDLVYGSPIIKYGDVTIVQHCETSLMTSTY 359
 QY 361 KSYETKKGKGVKVEBKQALHEEGKMDGDLFSSRQSESRRTARYRKCSLFTFKINGL 420
 DB 360 KSYETKKGKGVKVEBKQALHEEGKMDGDLFSSRQSESRRTARYRKCSLFTFKINGL 419
 QY 421 ETLQENRRHSMFPASVNIQENMCLDILINYPADPEDMEHEKONKPRALRNQDLFOE 480
 DB 420 ETLQENRRHSMFPASVNIQENMCLDILINYPADPEDMEHEKONKPRALRNQDLFOE 479
 QY 481 EGIANTLIEAIDKINVTISQGLAFLAGDSGGSEMEISGYLYQLALLIKGNTNCAQ 540
 DB 480 EGIANTLIEAIDKINVTISQGLAFLAGDSGGSEMEISGYLYQLALLIKGNTNCAQ 539
 QY 541 FANSRLNMLPSRLGSOASGEGTGLDYLHCVLDSPEALMMMDHEIKVILSLEKGR 600
 DB 540 FANSRLNMLPSRLGSOASGEGTGLDYLHCVLDSPEALMMMDHEIKVILSLEKGR 599
 QY 601 DPKVLVDVLSLQVNGAVAVRSSONNICDYLLPGKRLAQTLAVDVHSSVSRPNI FVGRVYG 660
 DB 600 DPKVLVDVLSLQVNGAVAVRSSONNICDYLLPGKRLAQTLAVDVHSSVSRPNI FVGRVYG 659
 QY 661 SAIVRKMYFEVYTMHIEKTTMMPLRIGMANTTGYVYPGGGKKGNGVGGDLVSYGCF 720
 DB 660 SSMQKMYFEVYTMHIEKTTMMPLRIGMANTTGYVYPGGGKKGNGVGGDLVSYGCF 719
 QY 721 DGAYVMSGGRTPVNRHTAABPYIRKGDVIGCALDLATYPIINFMNGVAVVGSFTNPLLE 780
 DB 720 DGAYVMSGGRTPVNRHTAABPYIRKGDVIGCALDLATYPIINFMNGVAVVGSFTNPLLE 779
 QY 781 GMFPFVISCSSKLSLCPFLAGSEHGLRYAADEGSPVLESLLPOQILSLBPCFYGNLSK 840
 DB 780 GMFPFVISCSSKLSLCPFLAGSEHGLRYAADEGSPVLESLLPOQILSLBPCFYGNLSK 839
 QY 841 RALAGPPLVODDTAFVPTPVDTLOITLPTVEQIRDKLAENIHEMWANKI BAWMYTDQ 900
 DB 840 RALAGPPLVODDTAFVPTPVDTLOITLPTVEQIRDKLAENIHEMWANKI BAWMYTDQ 899
 QY 901 REDLAKHIPCIVPRRRLPRAKRYDIOAVOTKTITLALGYTISLDKRPALIRVRLNE 960
 DB 900 REDLAKHIPCIVPRRRLPRAKRYDIOAVOTKTITLALGYTISLDKRPALIRVRLNE 959
 QY 961 PFMOSNGYKPAPLDLSAVTLTPPKDELVDQALAEWTHNLMARERIQGGTYGLENDSQMR 1020
 DB 960 PFMOSNGYKPAPLDLSAVTLTPPKDELVDQALAEWTHNLMARERIQGGTYGLENDSQMR 1019
 QY 1021 SPHLVPEKVDALIKKANRDASSETVRLTVYGYMLDPTGSEOHALLLEASKOKQADFR 1080
 DB 1020 SPHLVPEKVDALIKKANRDASSETVRLTVYGYMLDPTGSEOHALLLEASKOKQADFR 1079
 QY 1081 TYRAEKYAVSSGKMYFEFELITLGPVNRVGAHADMAFGMMLGDDENSMAVDGYNLEKYY 1140
 DB 1080 TYRAEKYAVSSGKMYFEFELITLGPVNRVGAHADMAFGMMLGDDENSMAVDGYNLEKYY 1139
 QY 1141 SGNTESEFCQNAVGVDVGVFDLLIDKTIISFSLNGBELMDALGSETTADV--QGDNFVPA 1198

Db 1140 AGSIFHFGRVLEAGVIGCFIDVKAQTISFSLNGELMDALGGETTFADVTAAGGVAPA 1199
Qy 1199 CTLGVGQKARLTVGGDVNTLKYFTTCGLQEGEYPCVANNKRDVTHMYTKQPIFENTEM 1258
Db 1200 CTLGVGQKARLTVGGDVNTLKYFTTCGLQEGEYPCVANNKRDVTHMYTKQPIFENTEM 1259
Qy 1259 IDTRIDVTRIPAGSTPPCLKTSNTFETMEKAMEFLRLSLPVICNNEPIDEAKARW 1318
Db 1260 PDCRIDVTRIPAGSTPPCLKTSNTFETMEKAMEFLRLSLPVICNNEPIDEAKARW 1319
Qy 1319 VEIKRQGLIMKEA-VEAQM-----PAHIDQIMSGFTMNDIKGLHYE-DNQBELPSSKM 1371
Db 1320 DEIKRQGLIMKEAIIAQMVOYQALAHNDHMLKGFNNNDIKGLTRNPDHDAEADHM 1379
Qy 1372 KRLPSRPKSGSMRTGVTIONYNLQPGCVNHHSTSEAEWAKYDLAQGLTPDDKDX 1431
Db 1380 MRGPRPRPKSGSLTNIT---PETMSAALDMQSTG-----VLDNMGLEBMDCK-K 1430
Qy 1432 RGRSPFKFRSKGESSDPAKSRKSTDPESDTEVSPERGARRPNFQIKVSQANQYNG 1491
Db 1431 RGRSPFKFRSKGESSDPAKSRKSTDPESDTEVSPERGARRPNFQIKVSQANQYNG 1488
Qy 1492 MNARSRTNLVGSQGLMMATPTDQRKQMTSTLAQSAETVYGNIEPDAECIKLINEFY 1551
Db 1489 AEIPSPV-----PGPKOLSGSNLQGOQEVETSGDMFAECIKLINEFY 1534
Qy 1552 GVRILPGQDPTHVYIGWTTQYHLHSDPNOSKVTKSIVITDDYRVAENVNROSQYV 1611
Db 1555 GVRILPGQDPTHVYIGWTTQYHLHSDPNOSKVTKSIVITDDYRVAENVNROSQYV 1594
Qy 1612 RADELINVEWMAEATKAGASQGMFICGSVDTSQVSPFCBGKDTSPKFMETKLPAL 1671
Db 1595 RADELINVEWMAEATKAGASQGMFICGSVDTSQVSPFCBGKDTSPKFMETKLPAL 1654
Qy 1672 FVEATSKILLQIEIGRATSLPLSAAYLPTSPKHVTPQRPRLKYQCKXPOMAVPNQS 1731
Db 1655 FVEATSKILLQIEIGRATSLPLSAAYLPTSPKHVTPQRPRLKYQCKXPOMAVPNQS 1714
Qy 1732 LQVHALKLSDIRGMSMLCEDAVSMALAHIPEDRCIDILPEIEMDKLSFHSHTTLVAA 1791
Db 1715 LQVHALKLSDIRGMSMLCEDAVSMALAHIPEDRCIDILPEIEMDKLSFHSHTTLVAA 1774
Qy 1792 LQVOSNYAAHALCTHVDQKOLLVYIQOSYMSGRLRGFPYDLLALHLESHATTWEACKN 1851
Db 1775 LQVOSNYAAHALCTHVDQKOLLVYIQOSYMSGRLRGFPYDLLALHLESHATTWEACKN 1834
Qy 1852 EFVILPGLBELKALYEBPDMGHSRLQTESVAPQOMKTDIASTEISNLYSPYPLEVA 1911
Db 1835 EFVILPGLBELKALYEBPDMGHSRLQTESVAPQOMKTDIASTEISNLYSPYPLEVA 1894
Qy 1912 RBFVQALAEAVETQVHNRPVGVGSNNLPLPLKLDVRLLLVGMDEDEVKLLIMTN 1971
Db 1895 RBFVQALAEAVETQVHNRPVGVGSNNLPLPLKLDVRLLLVGMDEDEVKLLIMTN 1954
Qy 1972 PETWDPSTFKGCKDHRKGLLHMKAAGAKLQMCYLLQHLNDIQLRHRVAAIIAFANDPV 2031
Db 1955 PETWDPSTFKGCKDHRKGLLHMKAAGAKLQMCYLLQHLNDIQLRHRVAAIIAFANDPV 2014
Qy 2032 GDLQTDQARRYTEIKQSLPBAVAAKTRERPCPREQMANILSKHLEEDKXCPGGE 2091
Db 2015 GDLQTDQARRYTEIKQSLPBAVAAKTRERPCPREQMANILSKHLEEDKXCPGGE 2074
Qy 2092 ELIARMEFHDTLMAHVLALQBPDAENOE-PAKKGAGKLYKININTYKALEEBEKA 2150
Db 2075 ELIARMEFHDTLMAHVLALQBPDAENOE-PAKKGAGKLYKININTYKALEEBEKA 2134
Qy 2151 IEPPPKKTPBEKFRKVLIIQITVMAAESQIETPKLVREMFSLVAYQDAVELIRALEKT 2210
Db 2135 IEPPPKKTPBEKFRKVLIIQITVMAAESQIETPKLVREMFSLVAYQDAVELIRALEKT 2194
Qy 2211 YVIAKTKLDVAEMVGLSQTALLPVQMSQEBEELAKRLMKLVNNTFFQHPDLIRVL 2270
Db 2270 YVIAKTKLDVAEMVGLSQTALLPVQMSQEBEELAKRLMKLVNNTFFQHPDLIRVL 2270

Db 2195 YVITRRARDVAEMVGLSQTALLPVQMSQEBEELAKRLMKLVNNTFFQHPDLIRVL 2254
Qy 2271 RVHENVMAVMNNTLIGRAQAQSDAPSQVAA--DSKXKDTSHMNVVACCRFLCYGRT 2328
Db 2255 RVHENVMAVMNNTLIGRAQAQSDA-PTQSEVAAEGAPSKKOTSHMNVVACCRFLCYGRT 2313
Qy 2329 GRONQKAMFDPFDLLENSNILLRSPRLSGSTPLDVAYSILMENTELALAREHYLEKIA 2388
Db 2314 GRONQKAMFDPFDLLENSNILLRSPRLSGSTPLDVAYSILMENTELALAREHYLEKIA 2373
Qy 2389 VYLSRQGLQSNSELVEKGPDLGMDPVGESEYTLFLRCVAVNQSVEENANLVYRLIR 2448
Db 2374 VYLSRQGLQSNSELVEKGPDLGMDPVGESEYTLFLRCVAVNQSVEENANLVYRLIR 2433
Qy 2449 RPECIGPALRGEGBGLKALIVDANKMSERLADRRKLREMEQGDV--NFSPPLPESDED 2505
Db 2434 RPECIGPALRGEGBGLKALIVDANKMSERLADRRKLREMEQGDV--NFSPPLPESDED 2492
Qy 2506 EDYIDTGAALINFPCTIVDLIGRCAPDAGVYALGNESLRAARAILRSLVPLEDLQGVSL 2565
Db 2493 EDYIDTGAALINFPCTIVDLIGRCAPDAGVYALGNESLRAARAILRSLVPLEDLQGVSL 2552
Qy 2566 RFTLNPPAAGERPKSDMPGSLIPGHKQSVGLFLERYVGIETOLEFYKLEBEAFLPDRA 2625
Db 2553 RFTLNPPAAGERPKSDMPGSLIPGHKQSVGLFLERYVGIETOLEFYKLEBEAFLPDRA 2612
Qy 2626 ATMLDRNDGCSDMALSNRRYIGNSILPLILKHAFFYNEAENVASLLDATLHTVYRLSKN 2685
Db 2613 ATMLDRNDGCSDMALSNRRYIGNSILPLILKHAFFYNEAENVASLLDATLHTVYRLSKN 2672
Qy 2686 RMLTKGQREAVSDPLVALTSAMQPSMLKILRKTIVDSKLSSETTVVALRLTLHYERCA 2745
Db 2673 RMLTKGQREAVSDPLVALTSAMQPSMLKILRKTIVDSKLSSETTVVALRLTLHYERCA 2732
Qy 2746 KYTSGTAGOGAFGASSDEEKRLTMMLFSNIFDSLXMDVPEPLFGKALPCLIAIGCALP 2805
Db 2733 KYTSGTAGOGAFGASSDEEKRLTMMLFSNIFDSLXMDVPEPLFGKALPCLIAIGCALP 2791
Qy 2806 PDVSLSNKYVDDEFYKGEQAAGDLNDNPQYDPPQINTSSVALNNDNTIYOKSEBHYHDAWA 2865
Db 2792 PDVSLSNKYVDDEFYKGEQAAGDLNDNPQYDPPQINTSSVALNNDNTIYOKSEBHYHDAWA 2849
Qy 2866 SRKLENGVYIGEGMSDSQKTHPLKPYNMLNDYKERYKEKYPVESLQALLAIGSVESHE 2925
Db 2850 SRKLENGVYIGEGMSDSQKTHPLKPYNMLNDYKERYKEKYPVESLQALLAIGSVESHE 2909
Qy 2926 VDISNRRSSMRQSKSGRPREIIVTDSATPFQVNPVPMYTNLTLSREOMMAERLADN 2985
Db 2910 VDISNRRSSMRQSKSGRPREIIVTDSATPFQVNPVPMYTNLTLSREOMMAERLADN 2962
Qy 2986 AHDIWAKKKEEL 2998
Db 2963 SHDIWAKKKEEL 2975

RESULT 11
ADM68762
ID ADM68762 standard; protein; 5104 AA.
XX
XX ADM68762;
XX
XX 17-JUN-2004 (first entry)
XX
XX Periplaneta americana ryanodine receptor protein SEQ ID NO:6.
XX
XX ryanodine receptor; insect ion channel; insecticide; pepticide;
XX
XX calcium balance disruption; receptor calcium release mechanism.
XX
XX Periplaneta americana.
XX
XX W02004027042-A2.
XX
XX 01-APR-2004.
PD

PX		23-SEP-2003; 2003WO-US029834.
PR		
XX		
XX		23-SEP-2002; 2002US-0412795P.
PR		
PR		18-NOV-2002; 2002US-0427324P.
PA		
XX		(DUPO) DU PONT DE NEMOURS & CO E. I.
XX		
F1	Casper T, Cordova D, Gutteridge S, Raub JU, Smith RM, Wu L,	
P1	Tao Y,	
DR	WPI, 2004-295411/27.	
N-P	N-PSDb), ADM68761.	
PT	New isolated nucleotide fragment encoding a ryandoline receptor, useful	
PT	for isolating other pest ryandoline receptors and in developing screens to	
XX	identify insecticidally active compounds.	
PS		
XX	Claim 15, SEQ ID NO 6, 687pp, English.	
CC		
CC	The present invention describes an isolated nucleotide fragment (I)	
CC	comprising: (a) a nucleic acid sequence encoding a ryandoline receptor	
CC	having an amino acid sequence identity of at least 80% when compared to a	
CC	polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,	
CC	128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a	
CC	nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.	
CC	1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant	
CC	construct comprising (II) operably linked to at least one regulatory	
CC	sequence; (2) a transformed host cell comprising the recombinant	
CC	construct; (3) a method to isolate (I) encoding ryandoline receptors and	
CC	related polypeptides; (4) an isolated polypeptide having ryandoline	
CC	receptor activity; (5) a method for evaluating at least one compound for	
CC	its ability to modulate calcium homeostasis; (6) a method for evaluating	
CC	at least one compound which modulates ryandoline receptor activity; (7) an	
CC	isolated nucleic acid fragment encoding an insect ion channel comprising	
CC	at least two fully defined polypeptide sequences selected from SEQ ID	
CC	NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,	
CC	120-126; (8) a method for identifying a nucleic acid sequence encoding an	
CC	insect ion channel; (9) a method for expressing an isolated nucleic acid	
CC	fragment encoding a toxic insect ion channel; and (10) recombinant	
CC	construct comprising in the 5' to 3' direction a promoter operably linked	
CC	to an isolated nucleic acid fragment encoding a toxic insect ion channel.	
CC	The isolated nucleotide fragment (I) encoding a ryandoline receptor is	
CC	useful for the isolation of other pest ryandoline receptors and developing	
CC	of screens to identify insecticidally active compounds. The nucleic acid	
CC	fragments are useful as pesticides, fragments of protein for antibody	
CC	production, fragments of protein for determination of the structure of	
CC	insecticide binding sites and in the identification of insecticides that	
CC	disrupt the calcium balance in cells through other messengers that	
CC	interact with the receptor calcium release mechanism. The present	
CC	sequence is used in the exemplification of the present invention.	
XX		
SQ	Sequence 5104 AA;	
Query Match	79.0%; Score 12445; DB 8; Length 5104;	
Best Local Similarity	78.3%; Pred. No. 0;	
Matches 2283;	Conservative 266; Mismatches 294; Indels 100; Gaps 32;	
OY	1 MAEAGGASBODDVSFLRTEDMVCISCTATGSRVCLAAEGFNRCIFLENTADKNIIPDL 60	
DB	1 MADSE-GSSEDDVAFRLTEDMVCISCTATGSRVCLAAEGFNRCIFYENLTADKNIIPDL 59	
OY	61 SOCVFVIQDALSVRALLOELVTAAAGSBTKG-GTSGGHRTLLTYGNALILRLHNSDMYLACIS 119	
DB	60 SOCVFVIEQALSVRALLOELVTATTSSOBGKGGTGGSGHRTLTYGNALLRLHNSDMYLACIS 119	
OY	120 TSSSQDKLAFDVGLQQHSGGBACMWTLTPASHKORSEGEKRVGVDDLIIIVSVATERYHTT 179	
DB	120 TSSSNDKLSPFDVGLQBHSGBACMWTVHPDASKORSEGEKRVGVDDLIIIVSVATERYHTA 179	
OY	180 KENEYSIYNVASRYVTHMSVOPRGITGISRNKYGYGVPGGVLPFRFGSGDECLTIPESTWKD 239	
OY	180 KENEYSIYNVASRYVTHMSVOPRGITGISRNKYGYGVPGGVLPFRFGSGDECLTIPESTWKD 239	
DB	180 KENEYSIYNVASRYVTHMSVOPRGITGISRNKYGYGVPGGVLPFRFGSGDECLTIPESTWKD 239	

QY	240	GGONIVVYEGGSWNSQARSILMRLELATPKAGGFINMYHPRIHITITGRVIGYNDONEL	299
Db	240	SGONIVIVEGGSVMSQASILMRLELATPKAGGFINMYHPRIHITITGRVIGYNNENNEL	299
QY	300	YLVSRREATYASCAFLRQEKDDQKQVLEDDLELVICAPITIKYDSTVIVQHSSETGLMS	359
Db	300	HLVCRERBTYASSFFPLRQEKDDKXILEDKLELVICAPITIKYDSTVIVQHSSTGLMLT	359
QY	360	YKSJETKKKGVKYEKQALIHBEKMDGDLDPSSRQSEBSRTARVTRKSSLTFTKING	419
Db	360	YKSJETKKKGVKYEKQAVLHBEKMDGDLDPSSRQSEBSRTARVTRKSSLTFTQEI9G	419
QY	420	LETLQENRRHMFASVYVLTGEMWMLCEDLNYFQAPQBPDMHEHEKONKFRALNRROLFO	479
Db	420	LENLQSNRRSLFCSFVNLNEMVNCLEBLNYFQAPQBSDEHEHEKONKFRALNRROLFO	479
QY	480	EEGLINLILAEIDKXINVTSGFLAGFLAGDSGQSWBMTSGYLYOLLAALIKGNHTNCA	539
Db	480	EEGLINLILAEIDKXNITTSQGFVWS-LAGDSGQSDMYISGYLYOLLAALIKGNHTNCA	538
QY	540	QPANSNRINMT.FSRIGQASGEGTGM.DV.LHC.VLIDSPBALNMKRDHIXIKIISLBEDHG	599
Db	539	QFANTNRINMT.FSRIGQASGSEGTGM.DV.LHC.VLIDSEBALNMKRDHIXIKIISLBEGHG	598
QY	600	RDPKVL.DV.LGSLCYGNGVAVASSONNICD.VL.PGKNLLLOTLADHYSSV.PN.FVGRVE	659
Db	599	RDPKVL.DV.LGSLCYGNGVAVASSONNICD.FL.PGKNLLLOTLADHYASV.PN.FVGRVHS	658
QY	660	GSAYVRKMYFEVYMDHIEKTHMMPHLRIGMANTTGVYVPGGSEKMGNGVGDLSYSG	719
Db	659	GSAYVRKMYFEVALIDHYEGTTHLMPHLRIGMANTAGVYVPGGSEKMGNGVGDLSYSFG	718
QY	720	PDGATV.MSGGKRT.PVNRTHABEPYTRKCDVIG.CHALD.VLP.IINMENGVRVTRGSFTNPL	779
Db	719	PDGSLT.MVGKRSSEV-MPGEISINIKKGDVIG.CHALD.VLP.IITFTLNGQVLQVQAFRDNPL	777
QY	780	EGMPFVYVSCSSKSCRFPLGEGHGRLEYYAPBEGSPVLESIL.FQOQILSEPCYFNGLS	839
Db	778	DOMFPVYVSCSSKSGCRFLGDDHGRLEKFTPPDESP.FLESIL.FQOQILTDPCYFNGLS	837
QY	840	KRALAGPPLVQDDTA.FVVP.PVDVLTQ.LT.PTYVEQIRDKLAENIHEMMANNTKEAGMYTGD	899
Db	838	KCVL.LGPMYVEDDTAFVNPVDVTSKVLT.PSYIENIKDCLANIHMMANNTKEAGWOYGD	897
QY	900	QREDLAKH.PCLVPERKLP.PRAEKYDIO.LAVQTLKTI.LAGYVLSLXKPPARINVR.LPN	959
Db	898	KRNDTRKTH.PCLIOFKLP.PRAEKYDSQ.LAVQTLKTYV.LALGYHLSINDPERSIKTVR.LPN	957
QY	960	BPFMOSNGYKAP.LDLSIAVLT.JTPKMDLE.VPDDLAENTHNL.MARERIQQSWTGLNEDSDMH	1019
Db	958	BPFMOSNGYKAP.LDLSAINLS.SGMKEBILIDQLAENTHNL.MAKENIQQSWTGLNBELOML	1017
QY	1020	RS.PHL.VPYKYDDAIKKANRDYASVYVTL.LVYGM.LDPTGEOHEA-LIL.EASKQKQAD	1078
Db	1018	RS.PHL.VPYKVDDAIKKANRDYASVYVTL.LVYGYNDLP.PGTENAEATL.LIDENYTR.YLT	1077
QY	1079	FRTYRAEKQVAVSSGKWYFEFEI.LTAGEMRYRGMAHADMA.PQMMLGODNSNAPFGYNEEK	1138
Db	1078	FRTYRAEKTYVAVASGKWYFEFEILTNGRMGAR.PTCS.PGQYQISDENSNAFPGYNEEK	1137
QY	1139	VYS.GNTSES.FFGQ.MAGDVAVGF.LD.LIDKTIISFSLNGBELMLMALGGETTFADVQDGNFVPA	1198
Db	1138	LYMGTAABEFGRQ.MQGVQVAVGF.LDMDHTISFSLNGBELMLMDTIGGETTFSSVQGBGFVPA	1197
QY	1199	CTLGVGQAR.LLT.YGQDVNTLT.KYFTTCGLQ.EGEBYEPCCVNMKQDVYHMYTKQPIREBNDM	1258
Db	1198	PLT.LGQAR.KLTLFGQDVNSLKYFTTCGQ.EGEBYEPCCVNMKKPYVYMYTKQPIREBND--	1256
QY	1259	IDTR.IDVYRIPAGS.TP.PCLKAI.SNHT.FEPMKAMNEF.LRLSLPYI.CHNHF.IDEABEKARYM	1318
Db	1257	FSSV.IDVYRIPAGS.TP.PCLKAI.SNHT.FEPMERANNEF.LRLSLPYI.CLP.NF.IDEGBEKQRYM	1316

QY	1319	VEIKROQILMEAEQWAPAHIDIMSGFPMNIDKGLH--YEO----	NOBELPSS----	1368
Db	1317	Q6IRIRQ6HLLQOS--EHATPAIEIQMSGFSMSIDIKGLHRCYSDDPVENDEMMENTAPL		
QY	1370	----IKAKRLPSHPPRKGSMTNR--GVYIQNYNNLQCGOVNMGMRSTSEAEKAYDL----	GA 1420C	
Db	1376	PEPRGNQOPPPPPRPRKGSLSRBDLTIEN-----DOKL-----RSSSELNFINYNQONNG	1427	
QY	1421	Q6LTDPDKDKXGGRSPFKFKRGESSDPAKSRKSKTDPDPDSTVEVPERGARPNN--	1477	
Db	1428	QDINDDDKK-KXGRSPFRPFSSKKGSPSDNPK--RAKTPDPAPARN--VRSRNAARHPNTLN	1483	
QY	1478	----POIKYSQANORNGNMAPSRSTNLVGSQVGNMAMPPT-QDR--KQMTTSTLQSA	1529	
Db	1484	EXITPOIRY-----SQMDKLITLPPALPDRGGPKMWSFTPSSAG	1522	
QY	1530	TEVGNELFDAQELKLINEFYGVAYIPGQDPDTHYIGMVTTOYHAGSDFNQSVTKSS	1589	
Db	1523	IEFVGNELFDEBCLKLINEYYGVAYIPGQDPDTHYVGMVTTQPHLSKDSQNHVTKST	1582	
QY	1590	VITDDYDRVVENVRQSCVMYRADELINVEMAEYATGASQMGFTGSVDTSGSVFT	1649	
Db	1583	VTVVDEHNRIETESIDROSCVMYRSDELINVEVNDSSGKAGASQMAIGFIDIANGVMSFT	1642	
QY	1650	CEGKQTSPEFKPEBETPKLPPALFVGNATSKETIQITELGSAISPLSAVLEPDSKHYTPQ	1709	
Db	1643	CEGKTSPEFKPEBETPKLPPALFVGNATSKETIQITELGSAISPLSAVLEPDSKHYTPQ	1702	
QY	1740	PPRLKVOCLKPHQARVPNOSLOVHALKLSIDIRGSMVLCDAVSMALATHPEEDRCIDI	1769	
Db	1703	PPRLKVOCLKPHQARVPNDSLHHTLKSLDJKMSLILCEDPVSMATHPEEDRCIDI	1762	
QY	1770	LEPIEMDKLSFHSHTLTLYAALCYQSNYRAHAALCTHVQKOLLLYAIQSYMSGPIRQ	1829	
Db	1763	LEPIEMDKLSFHSHTLTLYAALCYQSNYRAHAALCTHVQKOLLLYAIQSYMSGPIRQ	1822	
QY	1830	FYDILLIAHLSHAHTMAKCKNEVITPIGPELKALYEEDPMGHSIRISQTSVAPQOKMT	1889	
Db	1823	FYDILLIAHLSHAHTMAKCKNEVITPIGHEITLYALYDPOGHSIRISQTSVAPQOKMT	1882	
QY	1890	DIAESITEISNLSYFPLEVARPEFVMOALA.EAVETNOVHNHRDVGGSNEULFPLIKLV	1949	
Db	1883	EISVDIDNVRKILSYFPLOVREYMAALBEAYLVANOYHRDPIGGSNEULFPLIKLV	1942	
QY	1950	DRLLLVGMARDEVEKLLIMTNPETWDSFJKEGKDEBERKGLLHMKAEGAKLQMCYLIO	2009	
Db	1943	DRLLLVGMARDEVEKLLIMNPEWDSFJQOGDDEHRKGLLHMKAEGAKLQMCYLILH	2002	
QY	2010	HLNDIQLHREVALIAPAHADVGLQDTQLRRTYEIKOSDLPASVAAKTREFPCPREQ	2069	
Db	2003	HLNDIQLHREVALISFYSQVNIQIDQLRHYVEIKOSDLPASVAAKTREFPCPREQ	2062	
QY	2070	MNALISFPHLEEDKENCPCGEELIARBNRPHDTLMAHVSJLHAIQEDDAE-----NOE	2123	
Db	2063	MNALISFPHLSDSDKENCILGDELRERNRBNRNEKLMQIILVALQSEDDGLDINNIRE	2122	
QY	2124	PEAKRGAFGLYNIINTYKLEEBEAKAIEBPCKTPEKFRKVLQITVMAEBSQIETP	2183	
Db	2123	-----GKIKQYNNFINAVKO--BANENGLNEHEKKIPREIAPKVLITTVMAEBSQIETP	2176	
QY	2184	KLVBEMSSLVROYDANGELIRALEKTYVINAKTKLDVAMWGLSOIRALLPVQMSQEB	2243	
Db	2177	KLVBEMSSLVROYDSVGEILIRALEKTYVINAKTKEDOVAQWVGLSGIRISLLPVQMSQEB	2236	
QY	2244	BEIMRKULMKNVNHTEFQHPDILRLRYVHEHNNAVNMNTLGRRAQOSQAPSSQVY-A	2302	
Db	2237	BEIMRERIMKLVNHNTEFQHPDILRLRYVHEHNNAVNMNTLGRRAQOS--QPGSTVYTG	2294	
QY	2303	EDS-----KEKQTSHEMVVACSRFLICYFCRTSRQOKAMPHPDILNNSVITLISRPILRG	2358	
Db	2295	QDGEITVPEKQTSHEMVVACSRFLICYFCRTSRQOKAMPHPDILNNSVITLISRPILRG	2354	
QY	2359	STPLDVAVSSIMENTELALAREHYLEKIAVLVSRGLOSNSELVEKGYDGLQMDPVEGE	2418	

Db	2355	STPLDVAASISLMENETLALAREHLEKTAIAYLSRCGQSSSELI EKGYPLDGMDFAGE	2414
Qy	2419	RYLDFLRFCVWVNGSEVSENNANLVRLIRAREPCIGPALRQEGEGLLKAIYDANKMSERI	2478
Db	2415	RYLDFLRFCVWVNGSEVSENNANLVRLIRAREPCIGPALRQEGEGLLKAIYDANKMSERI	2474
Qy	2479	ADRRK-LREMEQGDVNFSPHLPSSDEDEDYIDTGAALINFCYTLVDLGRCAPDAGVIA	2537
Db	2475	AERRKFLRESGQNOETQLDHPFLPESSEDEDEDYIDTGAALINFCYTLVDLGRCAPDGSVIA	2534
Qy	2538	LGKNSLBARALINSIVLEPDLOCVLSIRFLTNPPAAGEEPKXDMBSGLIRGHKQSVGL	2597
Db	2535	LGKNSLBARALINSIVLEPDLOCVLSIRFLTNPPAAGQDRPKSDMBGGLIRGHKQSVYL	2594
Qy	2598	FLERYVGIETDELFPYKLEBAFLPDLPRAATYLDNRDGCESPMALSMNRYIGNSILPLLIK	2657
Db	2595	FLERYVGIEMQELFPYLLEBAFLPDLPRAATYLDNRDGCESPMALSMNRYIGNSIVPLIIG	2654
Qy	2658	HAFYNEAENYASILIDATLHTVYLSKQRMLTGQREAVSDFLVALTSQMOPSWLLKLLR	2717
Db	2655	HSKFYESDNYANILIDATLHTVYLSKQRMLTGQREAVSDFLVALTSQMOPSWLLKLLR	2714
Qy	2718	KLTYDVSLGSLTYTVAARLLTLHERCAKTYGSGAQQGAFGASDDEKULTMMLPSNIF	2777
Db	2715	KLTYDVSNLSYTTVAARLLTLHAHRCAKYGGSG-0QGIYGASSDEKULTMMLPSNIF	2773
Qy	2778	DSLKMDPEPLFGKALPCLIAIGCALPPDYSLSKNYDDEFPYG-KEQAGDLNDPOYPDQ	2836
Db	2774	DSLKMDYDPLFGKALPCLISATIGCALPPDYSLSKNYDDEFGSKNYIQGSPDG-YNPQ	2832
Qy	2837	PINTSVSVALNNDLTIYQKSEHYHDAMASRKLENGWVYBGMSDSQKTHPRLKPYMMLN	2896
Db	2833	PINTNSIYLDNDANSIVHKSEHYHDAMARKLENGWVYBGQFNDVKNSHPLKPYMMLS	2892
Qy	2897	DYERKRYKEPVRSELSKALLAIGMSVSESYVDIPENNFSNRQSGSGRPPPEIYTSATP	2956
Db	2893	EYERKRYKEPVRSELSKALLAIGMSIEHSENDAPLANNRGSVRRQSKS-----NENVTP	2944
Qy	2957	FDYNPHPVDMTNLTLSREMONMARLADNADHDIWAKKKKEIYV	2999
Db	2945	FDYNPFPIDMTNLTLTIREMONMARLADNSHDIAWAKKKKEIYV	2987
RESULT 12			
ABB65257			
ID	ABB65257	standard; protein; 5107 AA.	
AC	ABB65257;		
XX			
DT	26-MAR-2002	(first entry)	
XX			
DE	Drosophila melanogaster	polypeptide SEQ ID NO 22563.	
XX			
KW	Drosophila; developmental biology; cell signalling; insecticide;		
KW	pharmaceutical.		
XX			
OS	Drosophila melanogaster.		
XX			
MO	MO200171042-A2.		
EN			
XX			
PD	27-SEP-2001.		
XX			
PE	23-MAR-2001; 2001WO-US009231.		
XX			
PR	23-MAR-2000; 2000US-0191637P.		
PR	11-JUL-2000; 2000US-00614150.		
XX			
PA	(PEKE) PE CORP NY.		
XX			
TI	Venter UC, Adams M, Li PWD, Myers EW;		
XX			
WI	PI; 2001-6556860/75.		
XX			

DR N-PSDB, AB09360.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from *Drosophila* and for elucidating cell signaling and cell-cell
PT interactions.
PS Disclosure, SEQ ID NO 22563, 21np + Sequence Listing, English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from *Drosophila*. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB01840-AB01845), expressed DNA
CC sequences (AB01840-AB01845) and the encoded proteins (AB01840-AB01845).
CC AB01840-AB01845). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WFO at http://wfo.int/pub/published_pcr_sequences
XX
XX Sequence 5107 AA/
SQ
Query Match 78.6%; Score 12384; DB 4; Length 5107;
Beet Local Similarity 78.3%; Pred. No. 0;
Matches 2356; Conservative 272; Mismatches 314; Indels 66; Gaps 20;
QY 22 MYCLSTATGGERVCLAEFGNHCLENIADNIPEDLSQCVFVEQALSYALQELVT 81
DB 1 MTLTGTATGGERVCLAEFGNHCLENIADNIPEDLSQCVFVEQALSYALQELVT 60
QY 82 AAGSETGKTGSGHRTLLYGNAILLRHNSDMYLACLSTSSODKLAFLVGLQDSGEA 141
DB 61 AAGSETGKTGSGHRTLLYGNAILLRHNSDMYLACLSTSSNDKLSFVGLQDSGEA 120
QY 142 CMTTLPBARKSSEKKNVGDLLIVSATERYATTTKENYISYNASPTHYMSVOY 201
DB 121 CMTTLPBARKSSEKKNVGDLLIVSATERYATTTKENYISYNASPTHYMSVOY 180
QY 202 GTGISMKYVYFGSDVLRFPFGDECLTIPSTWKGQGNIVVEGGSVNSQASLNR 261
DB 181 GTGISMKYVYFGSDVLRFPFGDECLTIPSTWKGQGNIVVEGGSVNSQASLNR 240
QY 262 LELATKMGAGFINTWPMIRIHTTGRYGVNDONELYVSHBAATTSACFLQEKD 321
DB 241 LELATKMGAGFINTWPMIRIHTTGRYGVNDONELYVSHBAATTSACFLQEKD 300
QY 322 DQKQVLEDDLVYGNPIIKYGSYTYVQSHSEGLSYKSYTTKKGVGKVEKQALIH 381
DB 301 DQKQVLEDDLVYGNPIIKYGSYTYVQSHSEGLSYKSYTTKKGVGKVEKQALIH 360
QY 382 BEGKMDGDLFBSRQSEBSRTAVIRKCSLFTKFTNGLETTLOENRHSMPFASVNLGEM 441
DB 361 BEGKMDGDLFBSRQSEBSRTAVIRKCSLFTKFTNGLETTLOENRHSMPFASVNLGEM 420
QY 442 VNCLEDLINFAQPDDEMEHEKONKFRALRNKQDLFOEBGILNLLBAIDKINVTISGQ 501
DB 421 VNCLEDLINFAQPDDEMEHEKONKFRALRNKQDLFOEBGILNLLBAIDKINVTISGQ 480
QY 502 FLAAGFLAGBSGSGSWMISGYQLAAITKGNHTCAQFANSNRLNMLPSRLGQASGE 561
DB 481 FLAAGFLAGBSGSGSWMISGYQLAAITKGNHTCAQFANSNRLNMLPSRLGQASGE 540
QY 562 GTGMDLVHLCVLLIDSEBALNMMDBHKYISLLEHGRDPKLDVLSLGVNGVAVNS 621
DB 541 GTGMDLVHLCVLLIDSEBALNMMDBHKYISLLEHGRDPKLDVLSLGVNGVAVNS 600
QY 622 GGNICDYLPGKLLQTLVDHVASVNPILFVGVEGSAVRYKFFEVYMDHIKETH 681
DB 601 GGNICDYLPGKLLQTLVDHVASVNPILFVGVEGSAVRYKFFEVYMDHIKETH 660
QY 682 MNPHLRIGNANTTGYYPYGGGSKGNGVGDLLYSYGPDAVYLSGGKRTPVNRTABE 741
DB 661 MNPHLRIGNANTTGYYPYGGGSKGNGVGDLLYSYGPDAVYLSGGKRTPVNRTABE 720

QY 742 PYTRKGDVIGCALDVLTPPIINFMNGVYRTSGFTNPLEGMFPVYSCSSKSLCRLVLGG 801
DB 721 PYTRKGDVIGCALDVLTPPIINFMNGVYRTSGFTNPLEGMFPVYSCSSKSLCRLVLGG 780
QY 802 BHGRLEYAPBEGSPVLESILPQOILSLBPCFPGLSKRALAGPVLVODDTPAVTPVD 861
DB 781 BHGRLEYAPBEGSPVLESILPQOILSLBPCFPGLSKRALAGPVLVODDTPAVTPVD 840
QY 862 TLQITLPTVEQIRDKLAENIHMMAMNKILEAGMYGDORBDLAKTHPLVPEERLPPAE 921
DB 841 TLQITLPTVEQIRDKLAENIHMMAMNKILEAGMYGDORBDLAKTHPLVPEERLPPAE 900
QY 922 KRYDIOAVQTLKTIILALSYISLDEKPRIRNVRPLNEPFGNSGKAPADLSAVTIT 981
DB 901 KRYDIOAVQTLKTIILALSYISLDEKPRIRNVRPLNEPFGNSGKAPADLSAVTIT 960
QY 982 PKMDELVDLANNTNLMARERIQQGWTYGLNEDSNHNSPHLVPRKVDADLKKANRPT 1041
DB 961 PKMDELVDLANNTNLMARERIQQGWTYGLNEDSNHNSPHLVPRKVDADLKKANRPT 1020
QY 1042 ASETVRTLIVYGYMDPPYBOHEALLLSASKOKQADFRTPYAEKNYAVSSGKMYEPEFI 1101
DB 1021 ASETVRTLIVYGYMDPPYBOHEALLLSASKOKQADFRTPYAEKNYAVSSGKMYEPEFI 1080
QY 1102 LTAGPVRVGMADHAPGMMLGODENSWAPDGYNEEKVYSGMTSEFGQMAVGVDVGL 1161
DB 1081 LTAGPVRVGMADHAPGMMLGODENSWAPDGYNEEKVYSGMTSEFGQMAVGVDVGL 1140
QY 1162 DLIDKTSFSLNGELMDLAGEITTPADV--GGDNVPRCTIGYQKALITIGQDVNTLK 1219
DB 1141 DLYKQTFISFSLNGELMDLAGEITTPADVAGVGVPACTIGVQKALITIGQDVNTLK 1200
QY 1220 YFTTGLQGYEPCVNMKRDVTHWYTKQPIFENTDEMTDIRIDVTRIPAGSDTPCKL 1279
DB 1201 YFTTGLQGYEPCVNMKRDVTHWYTKQPIFENTDEMTDIRIDVTRIPAGSDTPCKL 1260
QY 1280 ISHNTPEYMEKANMEBLRLSLPVIKNEPIDEAKARVWEIKDRQOILMKEA--VEAQN- 1337
DB 1261 ISHNTPEYMEKANMEBLRLSLPVIKNEPIDEAKARVWEIKDRQOILMKEA--VEAQN- 1320
QY 1338 ---PAHIDQIRSGTMDIDIGLHYE--DNQELPSSKKKPLPSRPPRGSMTRGYTIGN 1392
DB 1321 VOTQAAHMDHMLKGGNNMDIKGLTENPDEHDAEDHMMKRPNRPGRGSLTRNT--- 1377
QY 1393 YNNLQGVNGMHRSTSEBAEMAKYDLAGOGLPDDKQKRGSPPFKPSKGESSDRAK 1452
DB 1378 FETDMSAALDENQSTSTST---VLDNNGLGSEMDK-KRGSPPKFP-SKSGRDSREK 1430
QY 1453 SRKSKTPDPSPDTEVSPERGAARRPNQIKVSOANORVNGMARNPSRTNLYGSOVGIMNAT 1512
DB 1431 MGARTLDSLBRNTVAHGRVAVVNOQMTTRAPTLRINNAETPPSPV----- 1476
QY 1513 PTQDRKQMTSTLQASATTVGNEIFDAECLKLINEFYGVRIYGPQDPTHYITIGVTTQ 1572
DB 1477 PTQDRKQMTSTLQASATTVGNEIFDAECLKLINEFYGVRIYGPQDPTHYITIGVTTQ 1535
QY 1573 YHLHSGDNQSKVYTSVITTDYDVRVENNRQSCYMRABEIVNBAATKAGASG 1632
DB 1556 YHLHSGDNQSKVYTSVITTDYDVRVENNRQSCYMRABEIVNBAATKAGASG 1595
QY 1633 MFTGCVDTSTGVSFTGKXDTSEFKKMEPETKLPALFVBAITSKEILQIEIGSATSLS 1692
DB 1596 MFTGCVDTSTGVSFTGKXDTSEFKKMEPETKLPALFVBAITSKEILQIEIGSATSLS 1655
QY 1693 PLGSAVLTPTSDKGVIPDPFRLKVOCLKPHQARVNPQSLQVHALKSLDIRGSMUCEDA 1752
DB 1656 PLGSAVLTPTSDKGVIPDPFRLKVOCLKPHQARVNPQSLQVHALKSLDIRGSMUCEDA 1715
QY 1753 VSMALAHTEPDRCDILEPIEMDKLSFHSHTLTLYALCYQSNYRAHNAICTHYDQO 1812
DB 1716 VSMALAHTEPDRCDILEPIEMDKLSFHSHTLTLYALCYQSNYRAHNAICTHYDQO 1775
QY 1813 LLYAIGQVMSGPLRQGFYDLILALHLSHAATTMEACKNEFVYPLGPELKALEYEPPDMGH 1872

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Db 1776 LLYAISEWISGSLRGQFDLLIALHESHAITMECKEYITPLAEKEKELSDSEMOH 1835
Qy 1873 SLRSLOTESVRPQMKMTDI-----AESITSEISNLYSPYFPLEVAREFMQA 1918
Db 1836 SLRSILTESVRPQLARTEITRPVIATSSMPSVSEPIPDIDQXSKFPLEVARGVME 1895
Qy 1919 LMEAVETNOYVNRDPVGSNENI.PLLIKLVDRLLVGMKRDDEKELMTNPEWTDP 1978
Db 1896 LKDAVINOVHNRDPVIGWTENI.FPLIKLTDRLLVGLTDEDEVORLWIMIDPEWDA 1955
Qy 1979 FDEKGEDEHRKGLLHKMGAGALQMCYLLQHLNDIQLHRVRAIIAPADPFQDQOTD 2038
Db 1956 FEEBGEDEHRKGLLHKMGAGALQMCYLLHLYDTQLRRVRSIIAFSHDFVGDQOTQ 2015
Qy 2039 LRRYTEIKOSDLPESAVALAKTRFRCPRPEQNNAAISFKHLEEDKENCPCGEBELARMA 2098
Db 2016 LRRYTEIKOSDLPESAVALAKTRFRCPRPEQNNAAISFKHLEEDKENCPCGEBELARMA 2075
Qy 2099 EPHDTLMAVSHALQEPDAENQD-PEAKPAFGKLYNIIINTVKELSEBAKAIIEPPK 2157
Db 2076 DEFDSIMOKVSLNALQEPDVEBGTALIEVKTGPIYTKLYNFINTVKELSEBKEVEPEKK 2135
Qy 2158 TPEEKRYKLIQTIYVMAEESQIETPKVREMSLLVROYDANGELIRALEKTYVNACT 2217
Db 2136 TPEEVFRKYLITVMAEESQIENPKLVREMSLLRQYDVGELVRALEKTYVINTA 2195
Qy 2218 KLDVAMWVGLSQIRALLPYQMSQEEBELMRKLMKLVNHTFQHPDILRVLRVHENM 2277
Db 2196 RDVAMWVGLSGIRALLPYQMSQEEBELMRKLMKLVNHTFQHPDILRVLRVHENM 2255
Qy 2278 AVMMNTLGRRAQSDAPSSQPVAF-DSKEKDTSHENVACCRFLYFCRTGRONQKA 2335
Db 2256 AVMMNTLGRRAQSDA-PTQSEVAGAPSKEDKDTSHENVACCRFLYFCRTGRONQKA 2314
Qy 2336 MEDHPELLENINIIISRSISLGTBLDVAYSISLMENTLALAREHYLEKIAVYLSRG 2395
Db 2315 MEDHPELLENINIIISRSISLGTBLDVAYSISLMENTLALAREHYLEKIAVYLSRG 2374
Qy 2396 LOSNSELVEKGYPDLCMDPEVEGERYDPLRFQVWNGESVEENANVIRLIRREPCLP 2455
Db 2375 LOSNSELVEKGYPDLCMDPEVEGERYDPLRFQVWNGESVEENANVIRLIRREPCLP 2434
Qy 2456 ALRGESEGLKALVDANKKSERIADRRLREMEQEDV--NFSHPLPSDEDEVDYDTG 2512
Db 2435 ALRGESEGLFRAIVEANRMSERISDRCKMD-EAEGTLAGLNTFHPLEPGEDEVDYDTG 2493
Qy 2513 AAILNFTCTVLDLGCAPDAGYIALGKNESLARAIIASVPLEBLOGLVLSIRFTLNP 2572
Db 2494 AAILNFTCTVLDLGCAPDAGYIALGKNESLARAIIASVPLEBLOGLVLSIRFTLNP 2553
Qy 2572 AAGEBPKSDMPSGLIPGHKQSVGLERVYGIETQELFYKLEBAFLPDLRAATLNDN 2632
Db 2554 AGEERPKSDMPSGLIPGHKQSVGLERVYGIETQELFYKLEBAFLPDLRAATLNDN 2613
Qy 2633 DGCESDMALSNRRIYIGNSILPLLIKHAYFYNEANENYASLLDALTHTVYLSKRMULTKQ 2692
Db 2614 DGCESDMALSNRRIYIGNSILPLLIKHAYFYNEANENYASLLDALTHTVYLSKRMULTKQ 2673
Qy 2692 RAVSDFLVALTSANQPSMLKILKRLTYDVSKLSTYTTVALRLTLHERCAKTYGSG 2752
Db 2674 RAVSDFLVALTSANQPSMLKILKRLTYDVSKLSTYTTVALRLTLHERCAKTYGSG 2732
Qy 2753 AQOGAFGASDEBEKRLTMMFLFSNIPDSLSKMDYEPFLFGKALPCIIAICALPPDYSLSK 2812
Db 2733 AQOGAFGASDEBEKRLTMMFLFSNIPDSLSKMDYEPFLFGKALPCIIAICALPPDYSLSK 2792
Qy 2813 NYDDEFYGRQAAGLDNPDQYDPOPIINTSSVALNDLNTIYOKFSEHYHDANASRKIENG 2872
Db 2793 NYDDEFYGRQAAGLDNPDQYDPOPIINTSSVALNDLNTIYOKFSEHYHDANASRKIENG 2850
Qy 2873 WYGGCMSQSOKTHRLKRYNMLNDYKERRYKPEPVRESIKALLAIGMSYHSEVDIPSN 2932

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Db 2851 WTYGDIRSDNRKHPRLKPYNMLSEYERERYDPAVRECKLGLALIGVHSEVEVALNH 2910
Qy 2933 RSMRROSQSGRPPRI--VTDSATFPDYNPVPVMTNLTLREMONMARLADNADIM 2990
Db 2911 RSTRROSQ-----PQINFGQSGSPFNPNPVPKSNLTLREMONMARLADNADIM 2965
Qy 2991 AKKKKEEL 2998
Db 2966 AKKKKEEL 2973

RESULT 13
AD68881
ID AD68881 standard; protein; 5112 AA.
XX
XX ADM68881;
AC
XX
XX 17-JUN-2004 (first entry)
DT
XX
XX Drosophila melanogaster ryanodine receptor protein SEQ ID NO:125.
DE
XX
XX ryanodine receptor; insect ion channel; insecticide; pesticide;
KW calcium balance disruption; receptor calcium release mechanism.
OS Drosophila melanogaster.
PN
XX WO2004027042-A2.
PD
XX 01-APR-2004.
PF
XX 23-SEP-2003; 2003WO-US029834.
XX
XX 23-SEP-2002; 2002US-0412795P.
PR
XX 18-NOV-2002; 2002US-0427324P.
XX
XX (DURO) DU PONT DE MEMOURS & CO E. I.
PA
XX Caspar T, Cordova D, Gutteridge S, Rauh JJ, Smith RM, Wu L;
PI Tao Y;
PI MPI; 2004-295411/27.
XX
XX New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT for isolating other pest ryanodine receptors and in developing screens to
PT identify insecticidally active compounds.
XX
XX Disclosure; SEQ ID NO 125; 687bp; English.
PS
XX
XX The present invention describes an isolated nucleotide fragment (I)
CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC construct comprising (I) operably linked to at least one regulatory
CC sequence; (2) a transformed host cell comprising the recombinant
CC construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC related polypeptides; (4) an isolated polypeptide having ryanodine
CC receptor activity; (5) a method for evaluating at least one compound for
CC its ability to modulate calcium homeostasis; (6) a method for evaluating
CC at least one compound which modulates ryanodine receptor activity; (7) an
CC isolated nucleic acid fragment encoding an insect ion channel comprising
CC at least two fully defined polypeptide sequences selected from SEQ ID
CC NO. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC insect ion channel; (9) a method for expressing an isolated nucleic acid
CC fragment encoding a toxic insect ion channel; and (10) recombinant
CC construct comprising in the 5' to 3' direction a promoter operably linked
CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC useful for the isolation of other pest ryanodine receptors and developing
CC of screens to identify insecticidally active compounds. The nucleic acid

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CC fragments are useful as pesticides, fragments of protein for antibody
 CC production, fragments of protein for determination of the structure of
 CC insecticide binding sites and in the identification of insecticides that
 CC disrupt the calcium balance in cells through other messengers that
 CC interact with the receptor calcium release mechanism. The present
 CC sequence is used in the exemplification of the present invention.

XX Sequence 5112 AA;

Query Match 78.4%; Score 12354; DB 8; Length 5112;

Best Local Similarity 78.2%; Pred. No. 0;

Matches 2359; Conservative 265; Mismatches 337; Indels 54; Gaps 21;

QY 1 MAEAGSAGSODDVSFLRTEDVCLSTATGERVCLAEFGNRFLENIAADKNIPDL 60
 DB 1 MAEAGS-SEGDVSVFLRTEDVCLSTATGERVCLAEFGNRFLENIAADKNIPDL 59
 QY 61 SGCVFPIEQLALSVRALOEVLTAAGSTGCTGSGHRTLLYGNAILLRHNSDMYLA 120
 DB 60 SGCVFPIEQLALSVRALOEVLTAAGSTGCTGSGHRTLLYGNAILLRHNSDMYLA 119
 QY 121 SSSODLAFDVLGLOHSGRACWTLHPASKORSEBKRVGDDLLVSAATERYHTTK 180
 DB 120 SSSNDLAFDVLGLOHSGRACWTLHPASKORSEBKRVGDDLLVSAATERYHTTK 179
 QY 181 ENEVSIVNASFVYTHNSVOPVGTGSRMKVGVYFGDVLRFPHGDECLITPSTWKD 240
 DB 180 ENEGSIVNASFVYTHNSVOPVGTGSRMKVGVYFGDVLRFPHGDECLITPSTWKD 239
 QY 241 GONIVYIEGGSVMSQARSRLRLATKAAGFINNYHPRIRHITTTGRLVANDONELY 300
 DB 240 GONIVYIEGGSVMSQARSRLRLATKAAGFINNYHPRIRHITTTGRLVANDONELY 299
 QY 301 LVSRBATATASCAFCRLROEKDOKYLEDKLEVTAPITIKYGDSTVIYOHSTGIML 360
 DB 300 LVKGEASATATTSFV-DEKDEKYLEDKLEVTAPITIKYGDSTVIYOHSTGIML 358
 QY 361 KSEYTKKKGVKVEKQALILHEGKMDGLDFRSQSEBSRTAVLRKCSLTFKEING 420
 DB 359 KSEYTKKKGVKVEKQALILHEGKMDGLDFRSQSEBSRTAVLRKCSLTFKEING 418
 QY 421 ETLQENRRHSMEFASVNLGEMVCLDILNYPAOPDEMEHEKONKPRALRRDOLF 480
 DB 419 ETLQENRRHSMEFASVNLGEMVCLDILNYPAOPDEMEHEKONKPRALRRDOLF 478
 QY 481 EGIILNLTALIKINIVTSGPLAGLAGDESGQSEMTSGYXOLLAIIKENHNCQ 540
 DB 479 EGIILNLTALIKINIVTSGPLAGLAGDESGQSEMTSGYXOLLAIIKENHNCQ 538
 QY 541 PANSNRLNMLFSLRGSQASGEOTGMDLVLCVLIIDSPALNMNRDEHIVYISLEK 600
 DB 539 PANSNRLNMLFSLRGSQASGEOTGMDLVLCVLIIDSPALNMNRDEHIVYISLEK 598
 QY 601 DPKVLDVLCSLCVGVNGVAARSSONNICDYLPGKNLLLOTALVDVHVSVPNIFV 660
 DB 599 DPKVLDVLCSLCVGVNGVAARSSONNICDYLPGKNLLLOTALVDVHVSVPNIFV 658
 QY 661 SAVYRKVFYETMDHIEKTHMPLRIGHANTTGYVPPFGGSEKKGNGVGDLYSGP 720
 DB 659 SAVYRKVFYETMDHIEKTHMPLRIGHANTTGYVPPFGGSEKKGNGVGDLYSGP 718
 QY 721 DGAYLMSGRKTPVNTTHABEPIYIRKGDVYGCALDITVPIINFMFGVNTGFTF 780
 DB 719 DGAFLMTGSKTIVYDALPBEPIYIRKGDVYGCALDITVPIINFMFGVNTGFTF 778
 QY 781 GMPFVYISGSKLSCLFLLGEGHGLRYAPGYSPLVBSLLPQOILSLBPCFYGNLS 840
 DB 779 GMPFVYISGSKLSCLFLLGEGHGLRYAPGYSPLVBSLLPQOILSLBPCFYGNLS 838
 QY 841 RALAGPVLVODDPAFVPTVDTLQITLPTVEQIRKLAENITHMANMKIEAGMYG 900
 DB 839 RALAGPVLVODDPAFVPTVDTLQITLPTVEQIRKLAENITHMANMKIEAGMYG 898

QY 901 REDLKHIPCLVEFERLPAEKRYDIOAVOTKITLALGYISLKPAPRIANVLPNE 960
 DB 899 RDYHRIHPLCTFEFLPAEKRYDIOAVOTKITLALGYISLKPAPRIANVLPNE 958
 QY 961 PFMQSGYRPAIDLSAVLTLPKMDLVNOLMENTNIMARREIOGWTYGLNEDDMR 1020
 DB 959 IFMQNGYRPAIDLSAVLTLPKMDLVNOLMENTNIMARREIOGWTYGLNEDDMR 1018
 QY 1021 SPHLVYPRKVDIAIKKANRDTASEYVRLTLVGYMDLPTPGEOLLEASKODAFR 1080
 DB 1019 SPHLVYPRKVDIAIKKANRDTASEYVRLTLVGYMDLPTPGEOLLEASKODAFR 1078
 QY 1081 TYRAENYAVSSQKMYFEFEILLTAGEMRYGMAHADNAPGMIGQDENSAPDGYNEKY 1140
 DB 1079 TYRAENYAVSSQKMYFEFEILLTAGEMRYGMAHADNAPGMIGQDENSAPDGYNEKY 1138
 QY 1141 SGTESFGOMAVGVVGFPLDIDITISPLANGELLMALGGETPAVY--QGDNPVA 1198
 DB 1139 SGTESFGOMAVGVVGFPLDIDITISPLANGELLMALGGETPAVY--QGDNPVA 1196
 QY 1199 CTGVGQKARLTGQDVTILKYFTTGLQEGYEPFCVNNKRDVTHYTKOPIFENTDM 1258
 DB 1199 CTGVGQKARLTGQDVTILKYFTTGLQEGYEPFCVNNKRDVTHYTKOPIFENTDM 1256
 QY 1259 IDTRIDVTIRI PAGESDTPCLKISHNTFETMERKANMFLSLPVCNPEIDEAKRW 1318
 DB 1259 IDTRIDVTIRI PAGESDTPCLKISHNTFETMERKANMFLSLPVCNPEIDEAKRW 1316
 QY 1319 VEIKRQOLIMKRA-VEAQM-----PAHIDQIRSGFTMMDIKGLHYE-DNGEELSSSK 1371
 DB 1319 VEIKRQOLIMKRA-VEAQM-----PAHIDQIRSGFTMMDIKGLHYE-DNGEELSSSK 1369
 QY 1372 KRLPSRPRKSGSTRGVITONVNNLPGOVNGHRSISEMAKXYLAGOGLTPDDKOK 1431
 DB 1372 KRLPSRPRKSGSTRGVITONVNNLPGOVNGHRSISEMAKXYLAGOGLTPDDKOK 1429
 QY 1432 RGRSPKPRKSGSTRGVITONVNNLPGOVNGHRSISEMAKXYLAGOGLTPDDKOK 1491
 DB 1432 RGRSPKPRKSGSTRGVITONVNNLPGOVNGHRSISEMAKXYLAGOGLTPDDKOK 1489
 QY 1492 RGRSPKPRKSGSTRGVITONVNNLPGOVNGHRSISEMAKXYLAGOGLTPDDKOK 1551
 DB 1492 RGRSPKPRKSGSTRGVITONVNNLPGOVNGHRSISEMAKXYLAGOGLTPDDKOK 1549
 QY 1552 GRIYVPGDPTHYVIGMTTTOYHLSKDFNOSKVTSSVITDDYRVVENVROSQWY 1611
 DB 1552 GRIYVPGDPTHYVIGMTTTOYHLSKDFNOSKVTSSVITDDYRVVENVROSQWY 1609
 QY 1612 RADELTYNEVMAEATAGASQGMFICGSVDSTGSVFTCEGKDTSEFKPMEBETKLP 1671
 DB 1612 RADELTYNEVMAEATAGASQGMFICGSVDSTGSVFTCEGKDTSEFKPMEBETKLP 1669
 QY 1672 FVEATSKELIOLBLGSAATSLPSAVALPDSKGVLPQFPPLKYQCLKPHOMARV 1731
 DB 1672 FVEATSKELIOLBLGSAATSLPSAVALPDSKGVLPQFPPLKYQCLKPHOMARV 1729
 QY 1732 LOVHALKSDIGKMSLCEDAVSMALHATPEEDRCIDILEPEMKGLSFPHSHTLL 1791
 DB 1732 LOVHALKSDIGKMSLCEDAVSMALHATPEEDRCIDILEPEMKGLSFPHSHTLL 1789
 QY 1792 LCYOSNYRAAHLCTHVDOKULLYALOSQYMSGPLRQGFYDILLALHLSHATTEAC 1851
 DB 1792 LCYOSNYRAAHLCTHVDOKULLYALOSQYMSGPLRQGFYDILLALHLSHATTEAC 1849
 QY 1852 EYVITPLGPELKLAYEEDPKGSLRSIQTESVPPQKMTDIASITIEISLWYBPFL 1911
 DB 1852 EYVITPLGPELKLAYEEDPKGSLRSIQTESVPPQKMTDIASITIEISLWYBPFL 1909
 QY 1912 RFRWQALAEAVETQVNRDVPVGSNENLPLPLKLYORLLVGMARDEDEYKLIIM 1971
 DB 1912 RFRWQALAEAVETQVNRDVPVGSNENLPLPLKLYORLLVGMARDEDEYKLIIM 1969
 QY 1972 PETWPSFDKSGDEHHRKGLHMKVAGAKLQMCYLLQHLANDIQLHHRVBAIIAFA 2031
 DB 1972 PETWPSFDKSGDEHHRKGLHMKVAGAKLQMCYLLQHLANDIQLHHRVBAIIAFA 2029


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Db      1954  PETWQAFERBSGDEHRRKGLTMTKABGKLDQCILNHLVTDTQLRHRVESTIIASHDV  2013
Qy      2032  GDLQTDOLRRYTEIKOSDLP5AVAAKTRFCPPREONNAIISFKHLEEDKENCPCGE  2091
Db      2014  GDLQTDOLRRYTEIKOSDLP5AVAAKTRFCPPREONNAIISFKHLEEDKENCPCGE  2073
Qy      2092  ELIAPNEFHDTLMAHVSILHALQEPDAENQ-PEAKPGAFGKLNININTVTELEBEAKA  2150
Db      2074  ELRGLGPHDLMQVSNALQEPGVGTALIEEYKTPIRKYNFINTVTELEBEPKE  2133
Qy      2151  IEPPKTPPEEKFRKVLQITVNMAREEQIETPKVREMFSLVNGYAVGELIRALEKT  2210
Db      2134  VEEPEKTPPEEVRKVLKTIIVSMAREEQIENPKVREMFSLVNGYAVGELIRALEKT  2193
Qy      2211  VYINAKTKLDVAMVWGLSQIRALLPVQMSQEEBELMRRLVNNHTFQHPDLIRVL  2270
Db      2194  VYINRARDVAMVWGLSQIRALLPVQMSQEEBELMRRLVNNHTFQHPDLIRVL  2253
Qy      2271  RVHENVMAMNTLGRRAQASDAQSSQPAE--DSKEKOTSHENVAVACRFLCYPCRT  2328
Db      2254  RVHENVMAMNTLGRRAQASDAQSSQPAE--DSKEKOTSHENVAVACRFLCYPCRT  2312
Qy      2329  GRQNGKAMPDHPDLLENSTIISPSISLSTPLDVAYSIMENNELALAEHYLEKIA  2388
Db      2313  GRQNGKAMPDHPDLLENSTIISPSISLSTPLDVAYSIMENNELALAEHYLEKIA  2372
Qy      2369  VYLSRCGLQSNSEIVEKGYPDLGMPDVEGERYLDPLFCVWVNGESVEENANLVIRLIR  2448
Db      2373  VYLSRCGLQSNSEIVEKGYPDLGMPDVEGERYLDPLFCVWVNGESVEENANLVIRLIR  2432
Qy      2449  REECLGPAIRGEGGLKAIYDANKMSERLADRRLKREMOQGDV---NFSHPLPESDED  2505
Db      2433  REECLGPAIRGEGGLKAIYDANKMSERLADRRLKREMOQGDV---NFSHPLPESDED  2491
Qy      2506  EBYITGAAIINFCTYVDLLRCAPDAGVIALGKNESIRAAIIRSLVPLEDLQGVSL  2565
Db      2492  EBYITGAAIINFCTYVDLLRCAPDAGVIALGKNESIRAAIIRSLVPLEDLQGVSL  2551
Qy      2566  RFTLNPPAAGEERPKSDMPGSLIPGKQGVGFLEEVYGIETFOELFYKLLBEAPLPDLA  2625
Db      2552  KTLTGQTAAGEERPKSDMPGSLIPGKQGVGFLEEVYGIETFOELFYKLLBEAPLPDLA  2611
Qy      2626  ATMLDRDQCESDMLSMNRVYIGNSILPLLIRKHAFFYNEAENYASILDATHTVYRLSK  2685
Db      2612  ATMLDRDQCESDMLSMNRVYIGNSILPLLIRKHAFFYNEAENYASILDATHTVYRLSK  2671
Qy      2666  RMLTGGQREAVSDPLVALTSQMPAMLKTLRKLTVDSKLSBYTTVALRLTLHFDRCA  2745
Db      2672  RMLTGGQREAVSDPLVALTSQMPAMLKTLRKLTVDSKLSBYTTVALRLTLHFDRCA  2731
Qy      2746  KYGSGTGAQGAFASSDEKRLTMMPLFSNIPDSISKMDYBEPLFGKALPCLIAIGCALP  2805
Db      2732  KYGSGTGAQGAFASSDEKRLTMMPLFSNIPDSISKMDYBEPLFGKALPCLIAIGCALP  2790
Qy      2806  PDYSISKYVDDEFYGEQAAGLDLNPQYDQPIINTSSVALNNDLNTIYQKSEHYHDAWA  2865
Db      2791  PDYSISKYVDDEFYGEQAAGLDLNPQYDQPIINTSSVALNNDLNTIYQKSEHYHDAWA  2848
Qy      2866  SRKINGVYGEQSDOKTHPRLLKRYNMLNDYEKERYEPEVRESIKALLAIGSVESHE  2925
Db      2849  SRRLTGGWYVGDIRSDNDKSHRLKRYNMLSEYERERYDPAVECKIGLLAIGVTEHSE  2908
Qy      2926  VDIPENNSSMRQSKSGRPPET--VDSATPDPDNPVPMVMTLTSREOMNAERLA  2983
Db      2909  VEPPLNHRGSTRQSK-----PQINEFQNEGSPFNPNPVMMSNLTSREOMNAERLA  2963
Qy      2984  DVAADIWAKKKKEEL  2998
Db      2964  ENSHDIWAKKKKEEL  2978

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RESULT 14

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ADM68880
ID      ADM68880  standard; protein; 5126 AA.
XX
AC      ADM68880;
XX
DT      17-JUN-2004  (first entry)
XX
DE      Drosophila melanogaster ryanodine receptor protein SEQ ID NO:124.
XX
KW      ryanodine receptor; insect ion channel; insecticide; pesticide;
KW      calcium balance disruption; receptor calcium release mechanism.
XX
OS      Drosophila melanogaster.
XX
PN      WO2004027042-A2.
XX
PD      01-APR-2004.
XX
PF      23-SEP-2003; 2003WO-US029834.
XX
PR      23-SEP-2002; 2002US-0412795P.
PR      18-NOV-2002; 2002US-0427324P.
XX
PA      (DUPO ) DU PONT DE NEMOURS & CO E I.
PI      Caspar T, Cordova D, Gutteridge S, Rauch JJ, Smith RM, Wu L,
PI      Tao Y;
XX
DR      WPI; 2004-295411/27.
XX
PT      New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT      for isolating other pest ryanodine receptors and in developing screens to
PT      identify insecticidally active compounds.
XX
PS      Disclosure; SEQ ID NO 124; 687bp; English.
XX
CC      The present invention describes an isolated nucleotide fragment (1)
CC      comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC      having an amino acid sequence identity of at least 80% when compared to a
CC      polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC      128, 130, 144, or 146; or (b) the complement of (a). (1) comprises a
CC      nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC      1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC      construct comprising (1) operably linked to at least one regulatory
CC      sequence; (2) a transformed host cell comprising the recombinant
CC      construct; (3) a method to isolate (1) encoding ryanodine receptors and
CC      related polypeptides; (4) an isolated polypeptide having ryanodine
CC      receptor activity; (5) a method for evaluating at least one compound for
CC      its ability to modulate calcium homeostasis; (6) a method for evaluating
CC      at least one compound which modulates ryanodine receptor activity; (7) an
CC      isolated nucleic acid fragment encoding an insect ion channel comprising
CC      at least two fully defined polypeptide sequences selected from SEQ ID
CC      NOS. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC      120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC      insect ion channel; (9) a method for expressing an isolated nucleic acid
CC      fragment encoding a toxic insect ion channel; and (10) recombinant
CC      construct comprising in the 5' to 3' direction a promoter operably linked
CC      to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC      The isolated nucleotide fragment (1) encoding a ryanodine receptor is
CC      useful for the isolation of other pest ryanodine receptors and developing
CC      of screens to identify insecticidally active compounds. The nucleic acid
CC      fragments are useful as pesticides, fragments of protein for antibody
CC      production, fragments of protein for determination of the structure of
CC      insecticide binding sites and in the identification of insecticides that
CC      disrupt the calcium balance in cells through other messengers that
CC      interact with the receptor calcium release mechanism. The present
CC      sequence is used in the exemplification of the present invention.
XX
SQ      Sequence 5126 AA:

```

Query Match 78.3%; Score 12338; DB 8; Length 5126;
 Best Local Similarity 77.9%; Pred. No. 0;
 Matches 2359; Conservative 266; Mismatches 336; Indels 68; Gaps 22;

QY 1 MAEAGGASQDDVSLRTEDNVCLSTCTATGEBVCLAAEGFGRNHCLENNIADKNIPDL 60
DB 1 MAEAGG-SEQDDVSLRTEDNVCLSTCTATGEBVCLAAEGFGRNHCLENNIADKNIPDL 59
QY 61 SQCVVIBALSVRLAQELVTAAGSTGCGTSGHRTLYGNAILLRHNSDMYLA 120
DB 60 SQCVVIBALSVRLAQELVTAAGSTGCGTSGHRTLYGNAILLRHNSDMYLA 119
QY 121 SSSODKAPDVGLOQHSQGEACMWTLPAPSKORSEGEKRVGDDLLVAVATERVYATTK 180
DB 120 SSSNDKLSFDVGLQHSQGEACMWTLPAPSKORSEGEKRVGDDLLVAVATERVYATTK 179
QY 181 ENEVASIVNASFVYTHNSVOPYGTGSRMKYGVVFGDYLRFPHGDECLITPSTYKDG 240
DB 180 ENEQOSIVNASFVYTHNSVOPYGTGSRMKYGVVFGDYLRFPHGDECLITPSTYKGBA 239
QY 241 GGNIVYVYEGGSVMSQARSILMRLELATKAGGFIMYHMRIRHITTGRIYGVNDQNEIX 300
DB 240 GGNIVYVYEGGSVMSQARSILMRLELATKAGGFIMYHMRIRHITTGRIYGVNDQNEIX 299
QY 301 LVSRBEATVASCACFLAROEKDDKOYLLEDKLEVIGAPIIKYGDSTVIVOHSEGTALSY 360
DB 300 LVKKEBASIAITTFSM-QEKDDEKAVLEDKDLVIGSPIIKGDTIVIVQHCSTSLMISY 358
QY 361 KSEYTKKKGVKVEEKQALIHBEKGMDGLDFSRQSEBSRTARVIRKCSLPTFKINGL 420
DB 359 KSEYTKKKGVKVEEKQALIHBEKGMDGLDFSRQSEBSRTARVIRKCSLPTFKITML 418
QY 421 ETLQENRRHSMPFASVNLGBMWCLDELINYPADPEDEMEHEKONKPRALNRRQDLFOE 480
DB 419 ETLQSRRRHSIFQKVNLEMWCLDELINYPADPEDEMEHEKONKPRALNRRQDLFOE 478
QY 481 BEILMLILPAIKINITYSGPLAGLADDESGQSEMTSGYLYOULALITGNHNCQO 540
DB 479 BEVLMILPAIKINITYSGPLASLADDETGQSDVLSLYLYOULALIKGNHNCQO 538
QY 541 FANSRLNMLFSLRGSQASGEGTGMMDVLCVILDEPALNMNRDEHIKIVISLEKHGR 600
DB 539 FANSRLNMLFSLRGSQASGEGTGMMDVLCVILDEPALNMNRDEHIKIVISLEKHGR 598
QY 601 DPKVLDVLCSLCVGNGVAVRBSQNNICDYLPGKNLLQTLVDHVSVRPNIFVGRVAG 660
DB 599 DPKVLDVLCSLCVGNGVAVRBSQNNICDYLPGKNLLQTLVDHVSVRPNIFVGRVAG 658
QY 720 SAVYRMYFEVYTMDEHKTTHMPLRIGMANTGVVYPPGGGKKGNGVGDLYSGYF 720
DB 659 SMTYQKMYFEVYTMDEHKTTHMPLRIGMANTGVVYPPGGGKKGNGVGDLYSGYF 718
QY 721 DCAVYLSGGRKTPVNRTHABEPPYIRKGDVIGCALDLPILINFMFGVYVTSFTFNE 780
DB 719 DCAVYLSGGRKTPVNRTHABEPPYIRKGDVIGCALDLPILINFMFGVYVTSFTFNE 778
QY 781 GMEFPVYSCSKLSCFPLLGEHGRLYAABEGVSPVLESLLPQOITLDEPCFYGNLSK 840
DB 779 GMEFPVYSCSKLSCFPLLGEHGRLYAABEGVSPVLESLLPQOITLDEPCFYGNLSK 838
QY 841 RALLAGEPVLVODTAFVPTPYDTLOTLPTVBOIRKLABNHEKMANKIEAGMYGQ 900
DB 839 NYLAGFWLIEDDTAFVPEKVDITGVLPSSVDQIKKELABNHEKMANKIEAGMYGWH 898
QY 901 REDLKHIFHCIVPEEPLPAEKRYDOLAVOLTUKTILAGUYISLDPKPARIRNVLPME 960
DB 899 RQDYNHIFCLTHFEKLPAAEKRYDOLAVOLTUKTILAGUYISLDPKPARIRNVLPME 958
QY 961 PFMQNGYKAPADLSAVTLTPQMDLVOLALENTNLWABERIOQSWTYGLNEDSDMR 1020
DB 959 IFMQNGYKAPADLSAVTLTPQMDLVOLALENTNLWABERIOQSWTYGLNEDSDMR 1018
QY 1021 SPHLVYPRYDAIKKANNDTASVYRTLLVGVYMLDPTGEGHEALLIASHQKQADR 1080
DB 1019 SPHLVYPRYDAIKKANNDTASVYRTLLVGVYMLDPTGEGHEALLIASHQKQADR 1078

QY 1081 TYRAENYAVSSGKTYFEFEITTAGPMRYGAHADMARPMHICODENSAFPGYNEKY 1140
DB 1079 TYRVENYAVSSGKTYFEFEITTAGPMRYGAHADMARPMHICODENSAFPGYNEKY 1138
QY 1141 SGNTPSGKQMAVGVVGVFLDLIDKTSFSLNGELMDALGERTPAV--QGDNFVA 1198
DB 1139 GGVSSFGKQCGPDDVGVFLDLADHTTISFSLNGELMDALGERTPAV--QGDNFVA 1198
QY 1199 CTLAGVQKARLTYGQDVTILKYFTTCGLQEGYAPPCVNNKRDVTHYTKQDPIFENTDEM 1258
DB 1199 CTLAGVQKARLTYGQDVTILKYFTTCGLQEGYAPPCVNNKRDVTHYTKQDPIFENTDEM 1258
QY 1259 IOTRIDVTRI PAGSDTPCLKTSHTFETMEKANEFLRLSPV CANEFIDBAEKARW 1318
DB 1259 PCORIDVTRI PAGADTPPHLKISHNTFETMEKANEFLRLSPV CMGEFISEOBKARW 1318
QY 1319 VERIKROQILMEKA-VEAQM-----PAHQDQMSGEFTMNDIKGLHYE-DNOEBLPSMKA 1371
DB 1319 DEIKROQILMEKA-VEAQM-----PAHQDQMSGEFTMNDIKGLHYE-DNOEBLPSMKA 1371
QY 1372 KRLSPRPKSGMTGVTIIONYNNLOPGQNGMHRSTSEAKYDLGAQGLTPDDKDK 1431
DB 1379 MEGPNRPKSGMTGVTIIONYNNLOPGQNGMHRSTSEAKYDLGAQGLTPDDKDK 1429
QY 1432 RGRSPFPKSGMTGVTIIONYNNLOPGQNGMHRSTSEAKYDLGAQGLTPDDKDK 1491
DB 1430 RGRSPFPKSGMTGVTIIONYNNLOPGQNGMHRSTSEAKYDLGAQGLTPDDKDK 1487
QY 1492 MNAKPSRTLYSGQGLMNAFTPODRKQNTTTLAQSARETYGNELFDEBCLKLINEY 1551
DB 1488 MNAKPSRTLYSGQGLMNAFTPODRKQNTTTLAQSARETYGNELFDEBCLKLINEY 1533
QY 1552 GVRIVGQDPTHYVIGWTTQYHLSKDFNSKQTSYIITDDYRVVENYRQSCYV 1611
DB 1534 GVRIVGQDPTHYVIGWTTQYHLSKDFNSKQTSYIITDDYRVVENYRQSCYV 1593
QY 1612 RADELVNEVBAATKAGSQMGFICGSVDTSGVSFTCEGKQTSKFMDEBETKLPAL 1671
DB 1594 RADELVNEVBAATKAGSQMGFICGSVDTSGVSFTCEGKQTSKFMDEBETKLPAL 1653
QY 1672 FVBAATSKELIOTELGRSATSPLSAVLPSTOKVYIPOPFPALQOCLKPHQMARVPNS 1731
DB 1654 FVBAATSKELIOTELGRSATSPLSAVLPSTOKVYIPOPFPALQOCLKPHQMARVPNS 1713
QY 1732 LQVHALKSIDRIGMSLCEDAVSMLAHNPEEDRCIDILEPIEMDKLSFHSHTLLTYA 1791
DB 1714 LQVHALKSIDRIGMSLCEDAVSMLAHNPEEDRCIDILEPIEMDKLSFHSHTLLTYA 1773
QY 1792 LQVHALKSIDRIGMSLCEDAVSMLAHNPEEDRCIDILEPIEMDKLSFHSHTLLTYA 1851
DB 1774 LQVHALKSIDRIGMSLCEDAVSMLAHNPEEDRCIDILEPIEMDKLSFHSHTLLTYA 1833
QY 1852 BFVYLPGLKALYBEPDMGHSLSLQTESVROPKMTDI-----ABSTYE 1897
DB 1834 BFVYLPGLKALYBEPDMGHSLSLQTESVROPKMTDI-----ABSTYE 1893
QY 1898 ISNIVSPFLEVARFVWQALAEAVETNOVNNRPOVGSNNELPLKIDYRLILVGM 1957
DB 1894 ISNIVSPFLEVARFVWQALAEAVETNOVNNRPOVGSNNELPLKIDYRLILVGM 1953
QY 1958 MDEDEVEKLLIMTNPETMPSFDEKGEDEHKGILHMKAAEAKLOMCTILOHLNDIOQR 2017
DB 1954 MDEDEVEKLLIMTNPETMPSFDEKGEDEHKGILHMKAAEAKLOMCTILOHLNDIOQR 2013
QY 2014 HREVASIASHDFVGLQTDQRLRYEIKQSDLPASAFAKTKFERCPREOMNOQLCPK 2073
DB 2078 HREVASIASHDFVGLQTDQRLRYEIKQSDLPASAFAKTKFERCPREOMNOQLCPK 2073
QY 2078 HREVASIASHDFVGLQTDQRLRYEIKQSDLPASAFAKTKFERCPREOMNOQLCPK 2136
DB 2074 HREVASIASHDFVGLQTDQRLRYEIKQSDLPASAFAKTKFERCPREOMNOQLCPK 2133
QY 2137 INTVYALBEBAKAIEBPKKTPBEKFRKVLQITIVNMAESQIETPKLVREMFSLVQ 2196

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Db      2134 FNTVLEBEGPKEVEPEKTPPEEVRKVLITIVSMBESQIENPKVREMFSLLEQ 2193
      2197 YDVGELIPALKEKTVYINAKTKLDVAMWVGLSQIRALLPVQMSQEEELMRKMLKN 2256
      2194 YDTVGLVALBETKTYINTRARDVAEMWVGLSQIRALLPVQMSQEEELMRKMLKN 2253
      2257 NHTFQHPDLIRLVYHENVMAVMNTLGRRAQSQDAOSPQVAE--DSKEDTSHM 2314
      2254 NATFFQHPDLIRLVYHENVMAVMNTLGRRAQSQDA--PTQSEVVEGAPEKEDTSHM 2312
      2315 VVACCFELCYFQRTGQONKAMPDHFDFLENNIILSRPSLRGSPPLVAASLMEHNE 2374
      2313 VVACCFELCYFQRTGQONKAMPDHFDFLENNIILSRPSLRGSPPLVAASLMEHNE 2372
      2375 LALALREHYLEKIAVLSRQGLQSNSELYEKGYPDLGMPVPEGERTLDFELFCVWNGES 2434
      2373 LALALREHYLEKIAVLSRQGLQSNSELYEKGYPDLGMPVPEGERTLDFELFCVWNGES 2432
      2435 VEENANLVIRLIRREPECLGPALRGEGGLKALVDANKMSERIADRRKLREMEQGDV- 2493
      2433 VEENANLVIRLIRREPECLGPALRGEGGLFRAIVANMSERISDRCKMD- EAGTIA 2491
      2494 --NESHPLRESDDEYIDTGAAILNFCYIVDLGRCAPDAGVIALGNESIRARAILR 2551
      2492 GLNFTHPLPEGEDEYIDTGAAILNFCYIVDLGRCAPDAGVIALGNESIRARAILR 2551
      2552 SLVPLEDLQGVLSLRFETLNNPAAGEERPKSDMPSGILPQHKOSVGLFELRVYGIETQELF 2611
      2552 SLVPLEDLQGVLSLRFETLNNPAAGEERPKSDMPSGILPQHKOSVGLFELRVYGIETQELF 2611
      2612 YKLEBAFLPDLRAATMDRNDGCSBDMALSMNRYGNSILPLLIGHAYFNEAENVASL 2671
      2612 YKLEBAFLPDLRAATMDRNDGCSBDMALSMNRYGNSILPLLIGHAYFNEAENVASL 2671
      2672 LDATHTVRLSKRWLTGOREAVSDFLVALTSAMOPMLKLRKLVDSKLSSEYTT 2731
      2672 LDATHTVRLSKRWLTGOREAVSDFLVALTSAMOPMLKLRKLVDSKLSSEYTT 2731
      2732 VALRLTLTHYERCAKAYYSTGAGQAFGASDBEKKLTMMLFNSIPDSLSKMDYEPFLFG 2791
      2732 VALRLTLTHYERCAKAYYSTGAGQAFGASDBEKKLTMMLFNSIPDSLSKMDYEPFLFG 2791
      2732 VALRLTLTHYERCAKAYYSTGAGQAFGASDBEKKLTMMLFNSIPDSLSKMDYEPFLFG 2791
      2791 KALPCLIAIGCALPPYSLYSKNTDEYDYGQWAP--DQPYQWPNPIDTNNVHLDDNLS 2848
      2852 IYQKSEHHADMAWASKIENGWYVYGGWDSQKTHRLKPYMMNDYERKEKPEYRESL 2911
      2849 IYQKSEHHADMAWASKIENGWYVYGGWDSQKTHRLKPYMMNDYERKEKPEYRESL 2908
      2912 KALLAIGWSEHSEVDIPENRRSSMRQSGSGRPPPI--VTDSATPFYNNPYPVDMTTL 2969
      2909 KELLAIIGWSEHSEVDIPENRRSSMRQSGSGRPPPI--VTDSATPFYNNPYPVDMTTL 2963
      2970 TLSREWQNNABRIADNDIWAKKKKEEL 2998
      2964 TLSREWQNNABRIADNDIWAKKKKEEL 2992

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RESULT 15
ID      ADM68812 standard; protein; 5126 AA.
XX      ADM68812;
XX      17-JUN-2004 (first entry)
XX      Drosophila melanogaster ryanodine receptor related protein seq ID NO:56.
XX      ryanodine receptor; insect ion channel; insecticide; pesticide;
XX      calcium balance disruption; receptor calcium release mechanism.
XX

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OS      Drosophila melanogaster.
PN      WO2004027042-A2.
XX
XX      01-APR-2004.
XX
XX      23-SEP-2003; 2003WO-US029834.
XX
XX      23-SEP-2002; 2002US-0412795P.
XX
XX      18-NOV-2002; 2002US-0427324P.
XX
XX      (DUPO ) DU PONT DE MEMOIRS & CO E I.
XX
XX      Caspar T, Cordova D, Gutteridge S, Rauh JJ, Smith RM, Wu L;
XX      Tao Y;
XX      WPI; 2004-295411/27.
XX
XX      New isolated nucleotide fragment encoding a ryanodine receptor, useful
XX      for isolating other pest ryanodine receptors and in developing screens to
XX      identify insecticidally active compounds.
XX
XX      Example 4; SEQ ID NO 56; 687bp; English.
XX
XX      The present invention describes an isolated nucleotide fragment (I)
XX      comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
XX      having an amino acid sequence identity of at least 80% when compared to a
XX      polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
XX      128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
XX      nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
XX      1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
XX      construct comprising (I) operably linked to at least one regulatory
XX      sequence; (2) a transformed host cell comprising the recombinant
XX      construct; (3) a method to isolate (I) encoding ryanodine receptors and
XX      related polypeptides; (4) an isolated polypeptide having ryanodine
XX      receptor activity; (5) a method for evaluating at least one compound for
XX      its ability to modulate calcium homeostasis; (6) a method for evaluating
XX      at least one compound which modulates ryanodine receptor activity; (7) an
XX      isolated nucleic acid fragment encoding an insect ion channel comprising
XX      at least two fully defined polypeptide sequences selected from SEQ ID
XX      NOS. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
XX      120-126; (8) a method for identifying a nucleic acid sequence encoding an
XX      insect ion channel; (9) a method for expressing an isolated nucleic acid
XX      fragment encoding a toxic insect ion channel; and (10) recombinant
XX      construct comprising in the 5' to 3' direction a promoter operably linked
XX      to an isolated nucleic acid fragment encoding a toxic insect ion channel.
XX      The isolated nucleotide fragment (I) encoding a ryanodine receptor is
XX      useful for the isolation of other pest ryanodine receptors and developing
XX      of screens to identify insecticidally active compounds. The nucleic acid
XX      fragments are useful as pesticides, fragments of protein for antibody
XX      production, fragments of protein for determination of the structure of
XX      insecticide binding sites and in the identification of insecticides that
XX      disrupt the calcium balance in cells through other messengers that
XX      interact with the receptor calcium release mechanism. The present
XX      sequence is used in the exemplification of the present invention.
XX
XX      Sequence 5126 AA:
XX
XX      Query Match      78.3%; Score 12338; DB 8; Length 5126;
XX      Best Local Similarity 77.9%; Pred. No. 0;
XX      Matches 2359; Conservative 266; Mismatches 336; Indels 60; Gaps 22;
XX
XX      1 MAEAGGASQDDVFLRTEDMVCSCTATGRCVLAEGFGNRHCFLEINADKNIPPL 60
XX      1 MAEAGG-SEQDDVSLFRTEDMVTLSCRTGRCVLAEGFGNRHCFLEINADKNIPPL 59
XX
XX      61 SQCVFVIGQALSVRALQELVTPAAGSETGKGTSGHRTLLYGNAILLRHNSDMYLAQST 120
XX      60 SQCVFVIGQALSVRALQELVTPAAGSETGKGTSGHRTLLYGNAILLRHNSDMYLAQST 119
XX
XX      121 SSSQDKLAFVQGLQGHSGEACWMTLHPASQSGEGRVAVDDLLIVSVATERVLTHTK 180
XX      120 SSSNDKLSFDVGLQSHSGEACWMTVHPASQSGEGRVAVDDLLIVSVATERVLTHTK 179

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QY 181 ENEVSI VNASFHVTHMSVOPVYGTGSI RMKYGVVFGDVLAREFHGDECLTIPSTWTKDG 240
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 DB 240 GONI VYIEBGS VMAQARSIMRLSLARTKAGGFIMKTHPMRI RHITGGYLVGNDONELV 299
 QY 301 IYSREATA SCAPCLROEKDO KOVLEDKDLEVGAP IIKYGDSTVYIOHSEGTGMLSY 360
 DB 300 IYKKEBAS IATTFPSW - QEKDEK KVLBEKDELEVISPIIKGDTVYIOHSEGTSLMSLY 358
 QY 361 KSYETKKGKGVYEEKQALIHESGKMDGLDPSRQSEBSRTARVIRKCSLFTXFINGL 420
 DB 359 KSYETKKGKGVYEEKQALIHESGKMDGLDPSRQSEBSRTARVIRKCSLFTXFINGL 418
 QY 421 ETLQENRRHSMPFASVNLGEMVNCLEDLINYPAQPEDEMEHEBKONKPRALNRODLFOE 480
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 DB 599 DBKVLIDVLCISLCVGNVAVRSSONNICDYLPGKINLLQTLVDHVASVRPIPVGRVAG 658
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 QY 781 GMPFVVISGSKSLSCRFLLGGBHGRLYVAPBGVSPVLESLLPQOILSLBPCFYFNGLSK 840
 DB 779 GMPFVVISGSKSLSCRFLLGGBHGRLYVAPBGVSPVLESLLPQOILSLBPCFYFNGLSK 838
 QY 841 RALLAGPVLVODDTPAPVTPVDLTQITLPTVYVQIRKKAENIHEMAMKIEAGMAYGQ 900
 DB 839 RALLAGPVLVODDTPAPVTPVDLTQITLPTVYVQIRKKAENIHEMAMKIEAGMAYGQ 898
 QY 901 REDLKHIFCLVFERLPPAEKRYDQLAVQTLKTIILGYIISLDKPPAIRNVLPRNE 960
 DB 899 REDLKHIFCLVFERLPPAEKRYDQLAVQTLKTIILGYIISLDKPPAIRNVLPRNE 958
 QY 961 PFMQNGYKAPLDLSAVTLTPKMDLVQDLAENTINLWABERIIOGWTYGLNEGSDMR 1020
 DB 959 IFMONGYKAPLDLSAVTLTPKMDLVQDLAENTINLWABERIIOGWTYGLNEGSDMR 1018
 QY 1021 BSHLVYPRVYDALKKANODTASSETVRLTLYGYMLDPTPGHSEKALLBASKOKADAR 1080
 DB 1019 BSHLVYPRVYDALKKANODTASSETVRLTLYGYMLDPTPGHSEKALLBASKOKADAR 1078
 QY 1081 TYRAEKNYAVSAGKAFYFEBIITAGPMRYGMAMADMAPGMMLGODNSNAPDGYNEKKY 1140
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 QY 1141 SGNTSEFGKQWAVGVFLDIDKTIISFLNGELMLDALGGETTFADV--OGDNFVDA 1198
 DB 1139 GGVNSBFGKQCGGDIIVGFLOLADHTISFLSNGELMLDALGGETTFADVTAAGVGFVDA 1198
 QY 1199 CTLGCGQKARLTYGQDVNTLKTFTTGCLOBGEPFCYNNKRDVTHYTKOPIFENTDEM 1258
 DB 1199 CTLGCGQKARLTYGQDVNTLKTFTTGCLOBGEPFCYNNKRDVTHYTKOPIFENTDEM 1258

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 DB 1319 VRIKROQILMEKA -VEAOW-----PAHTDOIMBEGFTMNDIKGLHYE -DNOBELPSSOW 1378
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 DB 1379 MGRPNRPKSGSLTNNIT---FETMSALDEMOGSTS-----VDMNGLGEMDDKX -K 1429
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 DB 1954 MEDEVEKLLIMTNPBTMDPSFDKSGDEBHRKGLLMKNAEAGAKLOMCTYLLQHLNDIQRL 2013
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 DB 2074 HLEBEDKXCPGGBELIARNEFHTIMAHVSLHLAQBEPDAENGE -PEAKGAGKGLN 2133
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 DB 2134 IINTVKELEBBAKALIEBPPKTPPEKFRKVLQITIVNMAESQIETPKLVREMFSLVRO 2193
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Db 2313 VVACRFFLCYFCRTGRQNOQAMPDHPDPLDDNANILLARPSLKSGSTPLDVAYSISLMENTE 2372
QY 2375 LALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDILGMDPVEGERYLDPLRFCVWNGES 2434
Db 2373 LALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDILGMDPVEGERYLDPLRFCVWNGES 2432
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Db 2433 VEBNNANLVIRLLIRREPCGLPALRGEGLKAIYDANKSERIADRRKIRENEOEGDY- 2491
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Db 2492 GINFTHPLESGSDEBYIDTGAAILNFYCTIVDLGRCAPDAGVIALGKNESLRARAIIIR 2551
QY 2552 SLVPLEDLOGVLSLRFTLNPPAAGEBRPKSDMPSGLIPGHKOSVGLFLERYVGIETQELF 2611
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Job time : 329 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using BW model

Run on: April 14, 2006, 14:38:23 / Search time 2288 Seconds
(without alignments)
10846.330 Million cell updates/sec

Title: US-10-668-767-127_COPY_1000_4000

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Sequence: 1 gcatagggcgcgccatcat.....cctaagaaagagcgactg 3001

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications NA Main:

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2: /cgn2_6/pdata/1/pubna/US08_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	3001	100.0	15387	7	US-10-668-767-127
2	2857	95.2	15303	7	US-10-668-767-145
3	2847.4	94.9	15679	7	US-10-668-767-1
4	2841	94.7	15405	7	US-10-668-767-129
5	2839.4	94.6	15429	7	US-10-668-767-143
6	1620.4	54.0	15606	10	US-11-097-143-22562
7	1617.2	53.9	16363	7	US-10-668-767-9
8	1542.2	51.4	15413	7	US-10-668-767-7
9	1335.4	44.5	15315	7	US-10-668-767-5
10	1319	44.0	15845	7	US-10-668-767-3
11	1150	38.3	24336	10	US-11-097-143-22561
12	668	22.3	4078	6	US-10-305-720-1154
13	668	22.3	14302	7	US-10-276-774-552
14	668	22.3	15731	9	US-10-887-553A-490
15	646.6	21.5	15359	7	US-10-276-774-500
16	646.6	21.5	15359	9	US-10-887-553A-489
17	646.6	21.5	15359	9	US-10-450-763-4960
18	622.8	20.8	15453	8	US-10-723-860-5796
19	618.4	20.6	15563	7	US-10-764-425-48
20	618.4	20.6	15563	9	US-10-887-553A-491
21	597	19.9	15583	9	US-10-450-763-12305
22	597	19.9	15820	9	US-10-450-763-23337
23	104.8	3.5	321	6	US-10-029-386-16105

24	104.8	3.5	597	6	US-10-029-386-2405	Sequence 2405, Ap
25	81.6	2.7	535	5	US-10-027-632-59310	Sequence 59310, A
26	81.6	2.7	535	6	US-10-027-632-59310	Sequence 59310, A
27	81.6	2.7	643	5	US-10-027-632-51124	Sequence 51124, A
28	81.6	2.7	643	6	US-10-027-632-51124	Sequence 51124, A
29	71	2.4	1800	9	US-10-450-763-23334	Sequence 23334, A
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31	70	2.3	608	4	US-09-925-065A-169265	Sequence 169265, A
32	61.2	2.0	587	3	US-09-864-761-8415	Sequence 8415, Ap
33	60.8	2.0	196	3	US-09-864-761-25143	Sequence 25143, A
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36	54.8	1.8	486	9	US-10-450-763-23333	Sequence 23333, A
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38	53.6	1.8	600	9	US-10-972-079-73805	Sequence 73805, A
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41	50.2	1.7	639	9	US-10-450-763-12306	Sequence 12306, A
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44	42.4	1.4	496	5	US-10-027-632-77061	Sequence 77061, A
45	42.4	1.4	496	5	US-10-027-632-77062	Sequence 77062, A

ALIGNMENTS

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RESULT 1
US-10-668-767-127
; Sequence 127, Application US/10668767
; Publication No. US2004017111A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Raulh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, LiHong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
; LENGTH: 15387
; TYPE: DNA
; ORGANISM: Heliothis virescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(15384)
; OTHER INFORMATION:
; FEATURE:
; OTHER INFORMATION: pXL-Hv7
; US-10-668-767-127
Query Match 100.0%; Score 3001; DB 7; Length 15387;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1000 GTCATAGGCGGCCCATCATCAAAATATGTAAGTCTCCACCGTCATTTGCACATTCGAG 1059
QY 61 ACTGCTTGTGCGCTGTCTTATTAAGCTTACGAAACGAAGAAGGAGTGGGTTAAAGTA 120
DB 1060 ACTGCTTGTGCGCTGTCTTATTAAGCTTACGAAACGAAGAAGGAGTGGGTTAAAGTA 1119
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Db 3280 AAGTGAAGTCTGAGTCTGAGTCTTAAAGGCTGAGCACTATGAGGGCTGGCTGGCTGAC 3339
Qy 2341 GCTGATATGCAACAGATATGCTCGGACAAAGAGAACTTTGGGCAATTTGATGAT 2400
Db 3340 GCTGATATGCAACAGATATGCTCGGACAAAGAGAACTTTGGGCAATTTGATGAT 3399
Qy 2401 TACAAATGAGAAAAGTGTACAGCGGTAACTAGATCTTTTGGGCAATGAGCTGTT 2460
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Db 3460 GGTACGATGAGGGGGGTCTTCTAGATCTCAATTTGATGAGTAAAGTCTTCACTCAT 3519
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Db 4000 G 4000

RESULT 2

US-10-668-767-145
; Sequence 145, Application US/10668767
; Publication No. US2004017111A1
; GENERAL INFORMATION:
; APPLICANT: Casper, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutierrez, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, LiHong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: B1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 145
; LENGTH: 15303
; TYPE: DNA
; ORGANISM: Heliothis virescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(15300)
; OTHER INFORMATION:
; FEATURE:
; OTHER INFORMATION: pXL-HV6
US-10-668-767-145
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Best Local Similarity 97.0%; Pred. No. 0;
Matches 2911; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
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Db 1255 ACTAAGTTTATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1314
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Db 1855 GGTAAAGGCGGTGCGGTGCGCTGTCACAGAAACAATCGACATCTTGTCTGCGCGGC 1914
Qy 901 AAGAAGCTGTGCTGCAAACTGCGCTCGTGAATCAAGTATCTAGTCCGTCCGAACATC 960
Db 1915 AAGAAGCTGTGCTGCAAACTGCGCTCGTGAATCAAGTATCTAGTCCGTCCGAACATC 1974
Qy 961 TTCTGGGTGCGATGAAAGGGTCGGCACTGTACCGCAAAATGGTATCTTGAAGTGAATG 1020
Db 1975 TTCTGGGTGCGATGAAAGGGTCAGCCGTGTACCGCAAAATGGTATCTTGAAGTGAATG 2034
Qy 1021 GACCAATAGAGAAAGAACACATATGATGCCACATCTACCGATAGAGATGGGCCAACAT 1080
Db 2035 GACCAATAGAGAAAGAACACATATGATGCCACATCTACCGATAGAGATGGGCCAACAT 2094
Qy 1081 ACTGGTATATGTCCCATACCCGCGCGGTGGCGAATAATGGAGGTAAACGCGTGGAGAT 1140
Db 2095 ACTGGTATATGTCCCATACCCGCGCGGTGGCGAATAATGGAGGTAAACGCGTGGAGAT 2154
Qy 1141 GACCTGTATCTGTACGGGTTCGACGGCGCTTACCTTGTGTCCGGGGGAGAGAACTCC 1200
Db 2155 GACCTGTATCTGTACGGGTTCGACGGCGCTTACCTTGTGTCCGGGGGAGAGAACTCC 2214
Qy 1201 GTCAATAGAGATCTATGCTGAAGAGCCTTATATTAAGAAAGGTGACGTGATAGTTGGCA 1260
Db 2215 GTTATATAGACTCATGTGTGAAGAGCCTTATATTAAGAAAGGTGACGTGATAGTTGGCA 2274
Qy 1261 TTGGAAGCTGACGGTACCCATATCACTTCACTGTTCAACGGAGCGGGGTGACGGGATCC 1320
Db 2275 TTGGAAGCTGACGGTACCCATATCACTTCACTGTTCAACGGAGCGGGGTGACGGGATCC 2334
Qy 1321 TTCAACCACTTCAATCTGGAAGGCAATGTTCTTCCGGGTCACTAGCTGTCTAGTAACTG 1380
Db 2335 TTCAACCACTTCAACCTGGAAGGCAATGTTCTTCCGGGTCACTAGCTGTCTAGTAAATG 2394
Qy 1381 AGTGTGCGGTCTCTGCTGGGGGAGAGAACAGGTGCTCTCCGTACCGGGCTCCGAAGGC 1440
Db 2395 AGTGTGCGGTCTCTGCTGGGGGAGAGAACAGGTGACCTCCGTACCGGGCTCCGAAGGC 2454
Qy 1441 TACTCTCCCTGTGAGAGTCTCTCTGCGGAGAGATCTCAGCGTGGAGCCGTGCTTC 1500
Db 2455 TACTCTCCCACTGTGAGAGTCTCTCTGCGGAGAGATCTCAGCGTGGAGCCGTGCTTC 2514
Qy 1501 TACTTCGGCAACTGTGCCAAGCGGGCCCTGCTGGAACCCCGCTAGTACAGAGAGATACG 1560
Db 2515 TACTTCGGCAACTGTGCCAAGCGGGCCCTGCTGGAACCCCGCTAGTACAGAGAGATACG 2574
Qy 1561 GCCTTCTGCTCTACACTGTGATTAATTTACAGATTAATCTGCTCTACATATGTGAACAA 1620
Db 2575 GCTTTTGTGCTCTACACTGTGATTAATTTACAGATTAATCTGCTCTACATATGTGAACAA 2634
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Db 2635 ATTAGAGTAAAGCTAGCTGAATAATATACAGAAATGTGGCTATGAATTAAGTGAAGCA 2694
Qy 1681 GGGTGAATGTAACGGGAGAACAGAGAAAGATTTGCAAGATCCACCCCTGCTGTGCC 1740
Db 2695 GGGTGAATGTAACGGGAGAACAGAGAAAGATTTGCAAGATCCACCCCTGCTGTGCC 2754
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Db 2755 TTTCAGGCACTCCCACTGCTGAGAAAGATTAAGATCAATCACTGCTGTGAGACACTC 2814
Qy 1801 AAGAATATCCGGGCTGGGCTGATACATCAGCTTAAGCTTAAGCTCCAGCAGGATCCGC 1860
Db 2815 AAGAATATCCGGGCTGGGCTGATACATCAGCTTAAGCTTAAGCTCCAGCAGGATCCGC 2874
Qy 1861 AACGTTGCTGTGCGCAAGAACTTTCAATGCAAGTCCAAAGGCTTCAAGCCAGCACTC 1920
Db 2875 AACGTTGCTGTGCGCAAGAACTTTCAATGCAAGTCCAAAGGCTTCAAGCCAGCACTC 2934
Qy 1921 GACCTGAGTGTGTCAACCTTGAACCCAAATGGAATGAGCTAGTGAACAGCTGGCTGAG 1980

Db 2935 GATCTGAGTGTGTCAACCTTGAACCCAAATGGAATGAGCTAGTGAACAGCTGGCTGAG 2994
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Db 2995 AACACACAAACCTTTGGGCGAGGAGAGGATACAGAGGGAATGAACTTATGAGCTTAAT 3054
Qy 2041 GAGGACTCGGACATGCAATCGTTCCCGGCACTGTGGTGCATACCCGAAGGTTGACGATGCC 2100
Db 3055 GAGGACTCGGACATGCAATCGTTCCCGGCACTGTGGTGCATACCCGAAGGTTGACGATGCC 3114
Qy 2101 ATCAAGAAAGGCAACAGGAGACAGGCTCGGAGACTGTGAGAACCCCTGCTGTCTACGG 2160
Db 3115 ATCAAGAAAGGCAACAGGAGACAGGCTCGGAGACTGTGAGAACCCCTGCTGTCTACGG 3174
Qy 2161 TATATGTGGAACCGCTTACTGAGGAGCAGCATGAACACTTGTGTTGAAGGCTCAAAA 2220
Db 3175 TATATGTGGAACCGCTTACTGAGGAGCAGCATGAACACTTGTGTTGAAGGCTCAAAA 3234
Qy 2221 CAGAAGCAGACACTTCAAGACATACCGGCTGAGAAAGAACTATGCGCTCACTGGG 2280
Db 3235 CAGAAGCAGACACTTCAAGACATACCGGCTGAGAAAGAACTATGCGCTCACTGGG 3294
Qy 2281 AAGTGTACTTGGAGTTTGAAGCTTAAACGGCTGGAACCTATGAGGGGTGGCTGGCTCAC 2340
Db 3295 AAGTGTACTTGGAGTTTGAAGCTTAAACGGCTGGAACCTATGAGGGGTGGCTGGCTCAC 3354
Qy 2341 GCTGATATGCAACAGGAATGATGCTCGAGCAAGACAGAGAACTTGTGGCAATTTGATGT 2400
Db 3355 GCTGATATGCAACAGGAATGATGCTCGAGCAAGAGAGAACTTGTGGCAATTTGATGT 3414
Qy 2401 TACATGAGGAAAAAGTGTACAGCGGTACACTGAGTCTTTGGCAAGCAATGGCTGT 2460
Db 3415 TACATGAGGAAAAAGTGTACAGCGGTACACTGAGTCTTTGGCAAGCAATGGCTGT 3474
Qy 2461 GGTGAGTATGAGGGGGGTGCTCTAGATCTCAATTGATPAAGCAATAATTTCTGACTCAAT 2520
Db 3475 GGTGAGTATGAGGGGGGTGCTCTAGATCTCAATTGATPAAGCAATAATTTCTGACTCAAC 3534
Qy 2521 GGTGAGTATGAGTGAATGATGCTCTTGGCGAGAGACTACGTTTGTGATGTCCAGGGTAC 2580
Db 3535 GGTGAGTATGAGTGAATGATGCTCTTGGCGAGAGACTACGTTTGTGATGTCCAGGGTAC 3594
Qy 2581 AACCTTGTACAGCTTGCACACTTGGTGTGGGCAAAAAGCCAGGTTAAATATGTGCCAA 2640
Db 3595 AACCTTGTACAGCTTGCACAGCTTGTGTGGGCAAAAAGCCAGGTTAAATATGTGCCAG 3654
Qy 2641 GATGTGAATATCTGAAATATCTTCAACAATGTGTCTTCAAGAGGGAATGAACCAATT 2700
Db 3655 GATGTGAACAGTTGAAATATCTTCAACAATGTGTCTTCAAGAGGGAATGAACCAATT 3714
Qy 2701 TGGCTCAATATGAAGAGAGCTGACTCACTGGTACACCAAGGAGCAGCCGATCTTGCAG 2760
Db 3715 TGTGTCAATATGAAGAGAGCTGACTCACTGGTATATCTTAAGATCAGCCAACTTTCAG 3774
Qy 2761 AATACTGATGATGATGATCGACACCAAGATTTGATGTGACAGATACCAAGTGGTTGAT 2820
Db 3775 AATACTGATGATGATGATCGACACCAAGATTTGATGTGACCAAGTGGTTGATGAT 3834
Qy 2821 ACAACCTCCAGCTTCAAGATTTTCCCAACAACGTTGAGAGCGATGAGAAAGCTTACTGG 2880
Db 3835 ACAACCTCCAGCTTCAAGATTTTCCCAACAACGTTGAGAGCGATGAGAAAGCTTACTGG 3894
Qy 2881 GAGTTCCTAGCTCTCACTGCTGTATCTGCAATACAGATTCCTAATGAAGAGGCAATT 2940
Db 3895 GAGTTCCTAGCTCTCACTGCTGTATCTGCAATACAGATTCCTAATGAAGAGGCAATT 3000
Qy 2941 AAAAGCAGAGGTTGGGTGAATAATCAAGAACCTGTCAACAGATTCCTAATGAAGAGGCAATT 3000
Db 3955 AAAAGCAGAGGTTGGGTGAATAATCAAGAACCTGTCAACAGATTCCTAATGAAGAGGCAATT 4014
Qy 3001 G 3001
Db 4015 G 4015

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RESULT 3
US-10-668-767-1
/ Sequence 1, Application US/10668767
/ Publication No. US2004017114A1
/ GENERAL INFORMATION:
/ APPLICANT: Caspar, Timothy
/ APPLICANT: Cordova, Daniel
/ APPLICANT: Guttridge, Steven
/ APPLICANT: Rauh, James
/ APPLICANT: Smith, Rejane
/ APPLICANT: Tao, Yong
/ APPLICANT: Wu, Lihong
/ TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
/ FILE REFERENCE: B01533 US NA
/ CURRENT APPLICATION NUMBER: US/10/668,767
/ PRIORITY FILING DATE: 2003-09-23
/ PRIOR APPLICATION NUMBER: 60/412,795
/ PRIOR FILING DATE: 2002-09-23
/ PRIOR APPLICATION NUMBER: 60/427,324
/ PRIOR FILING DATE: 2002-11-18
/ NUMBER OF SEQ ID NOS: 149
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 15679
/ TYPE: DNA
/ ORGANISM: Heliothia virescens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (251)..(15676)
/ OTHER INFORMATION:
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (5515)
/ OTHER INFORMATION: n = c or g
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (13000)
/ OTHER INFORMATION: n = a or t
US-10-668-767-1

Query Match          94.9%; Score 2847.4; DB 7; Length 15679;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2905; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY      1  GTCATAGGCGCGCCCATCATCAATATGATGATCTCCACCGTCATTTGCGACATTCGAG 60
DB      1265  GTCATAGGCGCGCCCATCATCAATATGATGATCTCCACCGTCATTTGCGACATTCGAG 1324
QY      61  ACTGCGTGTGCTGCTTATAGCTTTACGAAGCGAAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB      1325  ACTGCGTGTGCTGCTTATAGCTTTACGAAGCGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1384
QY      121  GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB      1385  GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1444
QY      181  AGGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB      1445  AGGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1504
QY      241  ACTAAGTTATCAATAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB      1505  ACTAAGTTATCAATAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1564
QY      301  GCGTCAGTGAACCTGGGCGAGATGATGATGCTCGAGAGATCTCACTCACTCACTTCCGA 360
DB      1565  GCGTCAGTGAACCTGGGCGAGATGATGATGCTCGAGAGATCTCACTCACTCACTTCCGA 1624
QY      361  CAGCCCGATGAGAGATATGGAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB      1625  CAGCCCGATGAGAGATATGGAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1684
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QY      421  CGTCAGAGACTGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB      1685  CGTCAGAGACTGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1744
QY      481  ATCAAGTCATCAAGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB      1745  ATCAAGTCATCAAGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1804
QY      541  CAGAGCTGGAGAGAGATATGAGATATGAGATATGAGATATGAGATATGAGATATGAG 600
DB      1805  CAGAGCTGGAGAGAGATATGAGATATGAGATATGAGATATGAGATATGAGATATGAG 1864
QY      601  AACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB      1865  AACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1924
QY      661  CTGGGCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB      1925  CTGGGCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1984
QY      721  ATGAGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB      1985  ATGAGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2044
QY      781  CTATTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB      2045  CTATTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2104
QY      841  GGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB      2105  GGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2164
QY      901  AAGAACTGTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB      2165  AAGAACTGTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2224
QY      961  TTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB      2225  TTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2284
QY      1021  GACCAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
DB      2285  GACCAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2344
QY      1081  ACTGATATGCTCCATACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
DB      2345  ACTGATATGCTCCATACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2404
QY      1141  GACCTGATCTGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
DB      2405  GACCTGATCTGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2464
QY      1201  GTCAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
DB      2465  GTCAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2524
QY      1261  TTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
DB      2525  TTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2584
QY      1321  TTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB      2585  TTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2644
QY      1381  AGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
DB      2645  AGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2704
QY      1441  TACTTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
DB      2705  TACTTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2764
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1501 TACTTGGGCAACCTGTGCAAGCGGCGCTTGGCTGGAACCTCGGTAGTACAGGACGATACG 1560
Db TACTTGGGCAACCTGTGCAAGCGGCGCTTGGCTGGAACCTCGGTAGTACAGGACGATACG 2824
1561 GCCTCGGCGCTGCAACCTGTGATATCTTACAGATTAATCTGCGCTGCAATGCTGCAAA 1620
Db GCCTCGGCGCTGCAACCTGTGATATCTTACAGATTAATCTGCGCTGCAATGCTGCAAA 2884
1621 ATTGAGATTAAGCTGATGAAATATACAGAAATGTGGGCTATGATTAAGTTCGAGCA 1680
Db ATCAGAGCAAGCTGATGAAATATACAGAAATGTGGGCTATGATTAAGTTCGAGCA 2944
1681 GCGTGAATGATGCGGCGACAGAGAGAAATCTTGCAAGATCCACCTCGCTGCTGCC 1740
Db GCGTGAATGATGCGGCGACAGAGAGAAATCTTGCAAGATCCACCTCGCTGCTGCC 3004
1741 TTGCGAGCGATCCGCTGCTGAGAAAGATACGATACGATCAATGCTGCTGCAAGCACTC 1800
Db TTGCGAGCGATCCGCTGCTGAGAAAGATACGATACGATCAATGCTGCTGCAAGCACTC 3064
1801 AAGACTATCTGCTGCTGCTGCTATACATCAGCTTATGATTAAGCTCCAGCAGCATCCGC 1860
Db AAGACTATCTGCTGCTGCTGCTATACATCAGCTTATGATTAAGCTCCAGCAGCATCCGC 3124
1861 AAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
Db AAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3184
1921 GACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
Db GACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3244
1981 AACACCCCAACCTTTGGGCGCAGGAGAGATACAGCAGGAGTGAATTATGACTTAT 2040
Db AACACCCCAACCTTTGGGCGCAGGAGAGATACAGCAGGAGTGAATTATGACTTAT 3304
2041 GAGGACTGCGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
Db GAGGACTGCGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3364
2101 ATCAAGAAAGCCAAAGGAGACAGCTCGGAGACGTGAGAGACCTGCTGCTGCTGCTGCTG 2160
Db ATCAAGAAAGCCAAAGGAGACAGCTCGGAGACGTGAGAGACCTGCTGCTGCTGCTGCTG 3424
2161 TATATGCTGACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
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2221 CAGAAAGCAAGACTTCAAGACATACCGCGCTGAGAAAGATATGCGCTGCTGCTGCTG 2280
Db CAGAAAGCAAGACTTCAAGACATACCGCGCTGAGAAAGATATGCGCTGCTGCTGCTGCTG 3544
2281 AAGTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2340
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2341 GCTGATATGCAACAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
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2401 TACAAATGAGAAAAAGTGTACAGCGGTAACTGAGTCTTTTGGAGCAATGCGCTGCT 2460
Db TACAAATGAGAAAAAGTGTACAGCGGTAACTGAGTCTTTTGGAGCAATGCGCTGCTGCT 3724
2461 GGTGACGTATGAGGGGGTGTCTTATATCTCATTTGATTAAGATTAAGTTTCTCACTCAAT 2520
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2521 GGTGAGTTGTTGATGATGCTCTTGGCGGAGAGACTAGCTTTGCTGATGCTCCAGGGGTAC 2580
Db GGTGAGTTGTTGATGATGCTCTTGGCGGAGAGACTAGCTTTGCTGATGCTCCAGGGGTAC 3844
2581 AACTTTGTACGAGCTTGACACTTGTGTGGGCAAAAAAGCCAGGTAACTATGCGCAA 2640

3845 AACTTTGTACGAGCTTGACACTTGTGTGGGCAAAAAAGCCAGGTAACTATGCGTACG 3904
Gy GATGGAATATCTGGAATATCTTCAACAATGTGTCTTCAAGAGGATATGAACATTT 2700
Db GATGGAATATCTGGAATATCTTCAACAATGTGTCTTCAAGAGGATATGAACATTT 3964
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Db TGCGTCAATATGAAGAGAGAGCTGACTGCTGTAACAAGAGCAAGCCGATTTTGAG 4024
2761 AATCTGATGATGATGCTGCAACCAAGATTAATGTAACAGGATACCAAGCTGCTGAT 2820
Db AATCTGATGATGATGCTGCAACCAAGATTAATGTAACAGGATACCAAGCTGCTGAT 4084
2821 ACACCTCATGCTGCAAGATTTCCCAACAACGTTGAGAGATGAGAGAAAGCTTACG 2880
Db ACACCTCATGCTGCAAGATTTCCCAACAACGTTGAGAGATGAGAGAAAGCTTACG 4144
2881 GAGTTCTTACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2940
Db GAGTTCTTACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4204
2941 AAACCGAGGCTTGGGTGAGAAATCAAGACCTGTAACAAGATCTTAATGAAGAGAGCT 3000
Db AAACCGAGGCTTGGGTGAGAAATCAAGACCTGTAACAAGATCTTAATGAAGAGAGCT 4264
3001 G 3001
Gy 3001 G 3001
Db 4265 G 4265

RESULT 4
US-10-668-767-129
; Sequence 129, Application US/10668767
; Publication No. US2004017114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Guttridge, Steven
; APPLICANT: Raub, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, LiHong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: B1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 15405
; TYPE: DNA
; ORGANISM: Heliothis virescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(15402)
; OTHER INFORMATION:
; FEATURE:
; OTHER INFORMATION: pXL-HV2
US-10-668-767-129
Query Match 94.7%; Score 2841; DB 7; Length 15405;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 2901; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
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Db GTCTAAGCGCGCCATCATCAATATATGATGATGATGCTGCAACCGCTCATTTGAGCATTTCCGAG 1059

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QY 121 GAAAGAGAGAGAGAGTCTTCCAGAGAGAGAGAGAGTGGTCTTCCAGTCTTCC 180
DB 1120 GAAAGAGAGAGAGAGTCTTCCAGAGAGAGAGAGAGTGGTCTTCCAGTCTTCC 1179
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DB 1180 AGTCAAGAGAGAGAGAGTCTTCCAGAGAGAGAGAGAGTGGTCTTCCAGTCTTCC 1239
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QY 421 GGTGAGTGAACCTTGGGAGAGAGTGGTCTTCCAGAGAGAGAGAGTGGTCTTCC 480
DB 1420 GGTGAGTGAACCTTGGGAGAGAGTGGTCTTCCAGAGAGAGAGAGTGGTCTTCC 1479
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DB 1480 ATCAAGTGAACCTTGGGAGAGAGTGGTCTTCCAGAGAGAGAGAGTGGTCTTCC 1539
QY 541 GAGAGTGGAGAGATTTGGAACAGAGAGAGAGAGAGTGGTCTTCCAGTCTTCC 600
DB 1540 GAGAGTGGAGAGATTTGGAACAGAGAGAGAGAGAGTGGTCTTCCAGTCTTCC 1599
QY 601 AACCAACAGAGAGTGGGAGAGTGGGAGAGAGTGGGAGAGAGTGGGAGAGAGTGGG 660
DB 1600 AACCAACAGAGAGTGGGAGAGTGGGAGAGAGTGGGAGAGAGTGGGAGAGAGTGGG 1659
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DB 1660 CTGGGCTGGAGAGCTTGGGAGAGAGTGGGAGAGAGTGGGAGAGAGTGGGAGAG 1719
QY 721 ATAGAGTGGGAGAGCTTCAATATATATATATATATATATATATATATATATAT 780
DB 1720 ATAGAGTGGGAGAGCTTCAATATATATATATATATATATATATATATATATAT 1779
QY 781 CTATATAG 840
DB 1780 CTATATAG 1839
QY 841 GGTAAAG 900
DB 1840 GGTAAAG 1899
QY 901 AAGAACTGTGTCTGCAACCTGGGCTCTGCAACAGAGAGAGAGAGAGAGAGAGAG 960
DB 1900 AAGAACTGTGTCTGCAACCTGGGCTCTGCAACAGAGAGAGAGAGAGAGAGAGAG 1959
QY 961 TTGAGTGGGAG 1020
DB 1960 TTGAGTGGGAG 2019
QY 1021 GAGCAATAG 1080
DB 2020 GAGCAATAG 2079
QY 1081 ACTGTTAT 1140
DB 2080 ACTGTTAT 2139

QY 1141 GAGCTGTATCTGTATCGGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
DB 2140 GAGCTGTATCTGTATCGGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2199
QY 1201 GTTATATAG 1260
DB 2200 GTTATATAG 2259
QY 1261 TTGAGCTGAG 1320
DB 2260 TTGAGCTGAG 2319
QY 1321 TTGAGCACTTCAATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 2320 TTGAGCACTTCAATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2379
QY 1381 AGTGTGAGTGTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
DB 2380 AGTGTGAGTGTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2439
QY 1441 TACTCTCCCTTGTGAG 1500
DB 2440 TACTCTCCCTTGTGAG 2499
QY 1501 TACTCTCCCTTGTGAG 1560
DB 2500 TACTCTCCCTTGTGAG 2559
QY 1561 GCTTGTGAG 1620
DB 2560 GCTTGTGAG 2619
QY 1621 ATTAGAGATAG 1680
DB 2620 ATTAGAGATAG 2679
QY 1681 GGTGAGTGAAG 1740
DB 2680 GGTGAGTGAAG 2739
QY 1741 TTGAG 1800
DB 2740 TTGAG 2799
QY 1801 AAGAGTATCTGAG 1860
DB 2800 AAGAGTATCTGAG 2859
QY 1861 AACGTTGCTGTGAG 1920
DB 2860 AACGTTGCTGTGAG 2919
QY 1921 GAGCTGAGTGTGAG 1980
DB 2920 GAGCTGAGTGTGAG 2979
QY 1981 AACAGCCAG 2040
DB 2980 AACAGCCAG 3039
QY 2041 GAGAGCTGAG 2100
DB 3040 GAGAGCTGAG 3099
QY 2101 ATCAAG 2160
DB 3100 ATCAAG 3159
QY 2161 TATATGCTGAG 2220
DB 3160 TATATGCTGAG 3219
QY 2221 CAG 2280

Db	3220	CAGAGCAAGCCGACTTTCAGAACATACCGCGCTGGAGAAACTATGCCCTGACCTCTGGG	3279
OY	2281	AAAGTGATCTTCGAGTTTGAGATCTTAAACGGCTGGACCTATGAGGGTCCGCTGGACTAC	2340
Db	3280	AAAGTGATCTTCGAGTTTGAGATCTTAAACGGCTGGACCTATGAGGGTCCGCTGGACTAC	3339
OY	2341	GCTGATATGGCAACAGAAATGATGCTCGACCAAGCAAGAACTCTTGGGCAATTTGATGCT	2400
Db	3340	GCTGATATGGCAACAGAAATGATGCTCGACCAAGCAAGAACTCTTGGGCAATTTGATGCT	3399
OY	2401	TACAAATGAGAAAAAGTGTACAGCGGGTAAACACTGATCTTTCCGCAAGCAATGGGCTGT	2460
Db	3400	TACAAATGAGAAAAAGTGTACAGCGGGTAAACACTGATCTTTCCGCAAGCAATGGGCTGT	3459
OY	2461	GGTGACGTAGTGGGGGTGTTCTTAATCTCAATTGATTAAGATTAAGTTTCTCACTCAAT	2520
Db	3460	GGTGACGTAGTGGGGGTGTTCTTAATCTCAATTGATTAAGATTAAGTTTCTCACTCAAC	3519
OY	2521	GGTGAGTTGTTGATGATGATGCTCTTGGCGAGAGACTACGTTTGCTGATGTCAGGGTGAC	2580
Db	3520	GGTGAGTTGTTGATGATGATGCTCTTGGCGAGAGACTACGTTTGCTGATGTCAGGGTGAC	3579
OY	2581	AACTTTGATCCAGCTTGGCACTTGGTGTGGGCCAAAAGCCAGTTTAACATATGGCCAA	2640
Db	3580	AACTTTGATCCAGCTTGGCACTTGGTGTGGGCCAAAAGCCAGTTTAACATATGGCCAG	3639
OY	2641	GATGATGAATACCTCTGAATATCTTCAACATATGTTGCTTTCAGAGGGGATATGAACATTT	2700
Db	3640	GATGATGAATACCTCTGAATATCTTCAACATATGTTGCTTTCAGAGGGGATATGAACATTT	3699
OY	2701	TGCGTCAATATGAAGAGAGACGTGACTCACTGGTACCAAGACCAAGCCGATCTTGAG	2760
Db	3700	TGCGTCAATATGAAGAGAGACGTGACTCACTGGTACCAAGACCAAGCCGATCTTGAG	3759
OY	2761	AATACTGATGAGATGATGATGCAACACAGGATTTGATGTGACCAAGATACCAGCTGGTTCAAT	2820
Db	3760	AATACTGATGAGATGATGATGCAACACAGGATTTGATGTGACCAAGATACCAGCTGGTTCAAT	3819
OY	2821	AACCTCCATGCGCTCAAGATTTCCCAACACAGTTTGAGAGAGATGAGAAAGCTAACCTGG	2880
Db	3820	AACCTCCATGCGCTCAAGATTTCCCAACACAGTTTGAGAGAGATGAGAAAGCTAACCTGG	3879
OY	2881	GAGTTCTTACGCTCTCACTGCGCTGTTATCTGCAATTAAGATTCATTTGACGAGGCAAA	2940
Db	3880	GAGTTCTTACGCTCTCACTGCGCTGTTATCTGCAATTAAGATTCATTTGACGAGGCAAA	3939
OY	2941	AAAGCCAGACGTTGGGTGAGAAATCAAGGACCGTCAACGATCTTAATGAAGAGGCAGTT	3000
Db	3940	AAAGCCAGACGTTGGGTGAGAAATCAAGGACCGGCAACGATCTTAATGAAGAGGCAGTT	3999
OY	3001	G 3001	
Db	4000	G 4000	

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RESULT 5
US-10-668-767-143
; Sequence 143, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Guteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: Bn1513 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795

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? PRIOR FILING DATE: 2002-09-23
? PRIOR APPLICATION NUMBER: 60/427,324
? PRIOR FILING DATE: 2002-11-18
? NUMBER OF SEQ ID NOS: 149
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 143
? LENGTH: 15429
? TYPE: DNA
? ORGANISM: Helicobacter pylori
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)..(15429)
? OTHER INFORMATION:
? FEATURE:
? OTHER INFORMATION: PXL-HV3
US-10-668-767-143

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Query Match	94.6%	Score 2839.4	DB 7	Length 15429
Best Local Similarity	96.6%	Pred. No. 0		
Matches 2900; Conservative	0	Mismatches 101	Indels 0	Gaps 0

OY	1	GTCAATAGCGCGCCCATCATCAAAATATAGGTACATCAACCGCATTTGGCAGACATCCGAG	60
Db	1015	GTCAATAGCGCGCCCATCATCAAAATAGGTACATCAACCGCATTTGGCAGACATCCGAG	1074
OY	61	ACTGGCTTGTGGCTGTCTTATTAAGTCTTACGAAACGAAGAAAGAGTGGTAAAGTA	120
Db	1075	ACTGGCTTGTGGCTGTCTTATTAAGTCTTACGAAACGAAGAAAGAGTGGTAAAGTA	1134
OY	121	GAAGAAGAACGAGGATTTCTCCACGAGAAAGCAAGATGACGATGGCTTGACATTCTCC	180
Db	1135	GAAGAAGAACGAGGATTTCTCCACGAGAAAGCAAGATGACGACGGCTTGACATTCTCC	1194
OY	181	AGGTCAACGAGAGAAAGATCTAGGACTGCTCGAGTTATCAGAAAGTGTCTTCGCTGTTCC	240
Db	1195	AGGTCAACGAGAGAGAAATCTAGGACTGCTCGAGTTATCAGAAAGTGTCTTCGCTGTTCC	1255
OY	241	ACTAAGTTTATCAATGGCTTGGAAACTCTACAGAGAACCGTCTGCTCACTCGATGTTCTTC	300
Db	1255	ACTAAGTTTATCAATGGCTTGGAAACTCTACAGAGAACCGTCTGCTCACTCGATGTTCTTC	1314
OY	301	GCGTCACTGAACTCTGGGCGAGATGTGTATGTGCTCGAGGATCTCATCTAATTAATTGCGCA	360
Db	1315	GCGTCACTGAACTCTGGGCGAGATGTGTATGTGCTCGAGGATCTCATCTAATTAATTGCGCA	1374
OY	361	CAGCCCGATGAGATATGGAACAAGAAAGAAAAGAAATTCGCGGGCACTCCGAAC	420
Db	1375	CAGCCCGATGAGATATGGAACAAGAAAGAAAAGAAACAAATTCGCGGCCCTCCGAAC	1433
OY	421	CGTCAGGACCTGTTCCAAGAGAAAGGATATCTGAACCTGATCTTCGAAGCTATAGACAAG	480
Db	1435	CGTCAGGACCTGTTCCAAGAGAAAGGATATCTGAACCTGATCTTCGAAGCTATAGCTCAAG	1494
OY	481	ATCAACGTCAATCACGTCCACAGGGGTTCTCGCTGGAATTCCTGGCGGAGACGAATCTGGA	540
Db	1495	ATCAACGTCAATCACGTCTCAGGGGGTTCCTGGCTGGTTTCTGGCGGAGACGAATCTGGA	1554
OY	541	CAGAGCTGGGAAAAATATCTGGAATATTTGATCAAGTTCGCGGGGGCAATAATAAGGGC	600
Db	1555	CAGAGCTGGGAAAAATATCTGGAATATTTGATCAAGTGTGGGGGCAATAATAAAGGGC	1614
OY	601	AACCAACAAGAACTGCGCGCAGATTGCGGCACTCGAACCGGCTCAACTGGCTGTTCTCGCGC	660
Db	1615	AACCAACAAGAACTGCGCGCAGATTGCGGCACTCGAACCGGCTGAATGGCTGTTCTCGCGC	1674
OY	661	CTCGGCTTCGAGGCTCTCGGGGAGAGGCAACGGCAATGCTCGACGTGCTGCACTGCGTCTT	720
Db	1675	CTCGGCTTCGAGGCTCTCGGGGAGAGGCACTGCAATGCTCGACGTGCTGCACTGCGTCTT	1734
OY	721	ATTGACCTCGCTGAAGCTCTCAATATGATAGAGGACGAACAATAAAGATATATCTCT	780
Db	1735	ATTGACCTCGCTGAAGGCTTGAATATATAGAGGACGAACAATAAAGATATATCTCT	1794

OY	781	CTATTAGAAAAGCAGGGCGCGAACCTTAAAGTACTAAGTGTGCTATGTTCCGTGTGCGTC	840
Db	1795	CTATTAGAAAAGCAGGGCGCGAACCTTAAAGTACTAAGTGTGCTATGTTCCGTGTGCGTC	1854
OY	841	GGTAAACGGCGTCGCGGTGCGCTCTGTCAAGAAACAATCTGTGACTATCTTACTGCGCGGC	900
Db	1855	GGTAAACGGCGTCGCGGTGCGCTCTGTGTCAAGAAACAACAATCTGTGACTATCTTGTGCGCGGC	1914
OY	901	AAGAACTGTGTGTGCAAACTGCGCTGTGTGATCAAGTATCTAGTGTCCGTCCGAAATCT	960
Db	1915	AAGAACTGTGTGTGCTGCAAACTGTGCTGTGTGATCAAGTATCTAGTGTCCGTCCGAAATCT	1974
OY	961	TTCCGTGGGTCCAGTGTGAAGGGGTCCGGCACTGTATCCGCAAAATGTGTACTTGTGAGTGACTATG	1020
Db	1975	TTCCGTGGGTCCAGTGTGAAGGGGTCCGGCAAGTATCCGCAAAATGTGTACTTGTGAGTGACTATG	2034
OY	1021	GACCCACATAGAGAAAGACCACTATGTGATGCCATCTTACGATATGTGATGTGGGCCAACAT	1080
Db	2035	GACCCACATAGAGAAAGACCACTATGTGATGCCATCTTACGATATGTGATGTGGGCCAACAT	2094
OY	1081	ACTGGTTATGTCCCACTACCCCGGCGGTGGCGAAGAAATGGGAGGTAAACGCGGTGGAGAT	1140
Db	2095	ACTGGCTATGTCCCACTACCCCGGGTGTGTGTGAAAATGGGGAGGTAAACGCGGTGGAGAT	2154
OY	1141	GACCTGTACTGTATGACGGTTGGAACGGCGCTTACTCTGTGTCCGGGGGAGAGAACTTCC	1200
Db	2155	GACCTGTACTGTATGACGGGTTCGACGGCGCTTACTCTGTGTCCGGGGGAGAGAACTTCC	2214
OY	1201	GTCAATAGAGACTCAGTGTGAAGAGCGCTTATTTTGAAGAAAGGTGAACGTATGTGTGCGCA	1260
Db	2215	GTCAATAGAGACTCAGTGTGAAGAGCGCTTATTTTGAAGAAAGGTGAACGTATGTGTGTGCGG	2274
OY	1261	TTGGACCTGACGGTACCCCATATCAATCTTCACTGTCAACGAGTGTGGGTGACGGGATCC	1320
Db	2275	TTAGACCTGACGGTACCCCATCATCAATCTTCACTGTTCACGAGTGTGGGTGACGGGATCC	2334
OY	1321	TTCAACCACTTCAATCTGGAAGAGCATGTTCTTCCCGGTCAATCAAGTGTCTTATGTAAGCTG	1380
Db	2335	TTCAACCACTTCAATCTGGAAGAGCATGTTCTTCCCGGTCAATCAAGTGTCTTATGTAATG	2394
OY	1381	AGTTGTGGGTCTGTGTGTGGGGGAGAAACAAGTGTGTCTTCCGGTACAGCTGTCTTATGTAAGCTG	1440
Db	2395	AGTTGTGGGTCTGTGTGTGGGGGAGAAACATGTGTGATCTTCCGACAGCGGCTTCCAGAAAGC	2454
OY	1441	TACTCTCCGCTTGTGTGAGTCTCTCTGTGCGAGACGATCTCTCAGGCTGTGAACCGTGTTC	1500
Db	2455	TACTCTCCGCTGTGTGTGAGTCTCTCTGTGCGAGACGATCTCTCAGGCTGTGAGCCTTGTCTTC	2514
OY	1501	TACTTCGGCAACTGTGTCCAGCGGGCTTGTGTGTGACTCTCCGCTATGTACAGAACGATACG	1560
Db	2515	TACTTCGGCAACTGTGTCCAGCGGGCCCTGTGTGTGACCCCGGCTATGTACAGAACGATACG	2574
OY	1561	GCCTTCGTGTGCTTACACTGTGTGATTAATCTTACAGATTACTCTGTCTTACATATGTGAAACAA	1620
Db	2575	GCCTTGTGTGCTTACACTGTGTGACACTTTCACAGATTACTCTGTCTTACATATGTGAAACAA	2634
OY	1621	ATTAGAGTAAAGCTAGCTGAAATAATTAACGAAATGTGGGTATGAATTAATGTGAAGCA	1680
Db	2635	ATTAGAGACAAAGCTAGCTGAAATAATTAACGAAATGTGGGTATGAATTAATGTGAAGCA	2694
OY	1681	GGCTGTGATGTACGGCGAACACAGAGAGAACTTGTGACAAATCCCACTGCTGTGTGCC	1740
Db	2695	GGCTGTGATGTACGGGGAATCAAGAGAGAAACTTGTGACAAATCCCACTGCTGTGTGCC	2754
OY	1741	TTCCAGACGACTTCCCACTGTGTGAGAAACGATTAACAATACAATCTGTGTGTGACACTCTC	1800
Db	2755	TTCCAGACCTTCCCACTGCGGCTGTGAGAAACGATTAACAATACAATCTGTGTGTGACACTCTC	2814
OY	1801	AAGAATATCTGTGCTGTGGGCTATCAATCACTGAGCTTAAAGTAAAGCTTCCAGACGCAATCCGC	1860
Db	2815	AAGAATATCTGTGCTTGTGGGCTATCAATCACTGAGCTTAAAGTAAAGCTTCCAGACGCAATCCGC	2874
OY	1861	AACGTGTGTGTGCCAAGCACTTTTCAATGACGTCCAACGGCTCAAGCCGACCACTCTC	1920

Db	2875	AAAGTTCCGTTCCCAAGCAACCTTTCAATGCAAGTCCAAAGCCGCTTAAAGCCAGCAACATC	2934
Oy	1921	GACCTGAGTGCCTGTCAACCTGTGACACCCCAAGATGAGTGAAGTACGACGCTGCTGAG	1980
Db	2935	GACCTGGGGTGTCTCACTCTGACACCCAGATGAGATGACTGTATACCAAGCTGGCTGAG	2994
Oy	1981	AAACCCCAACACCTTTGGGCGCAGGAGAGGATACAGCAGGATGACTTATGCACTTTAAT	2040
Db	2995	AAACCCCAACACTTTGGGCGCAGGAGAGGATACAGCAGGATGACTTATGCACTTTAAT	3054
Oy	2041	GAGGACTGGACATGCAATGTTTCCCGGCACTGTGGCCATACCCGAAAGGTTGACATGCC	2100
Db	3055	GAGGACTGGACATGCAATGTTTCCCGGCACTGTGGCCATACCCGAAAGGTTGACATGCC	3114
Oy	2101	ATCAAGAAAGGCCAAGGGGACACAGCCTTGGAGACTGTGAGAACCTGTGCTGCTACGG	2160
Db	3115	ATCAAGAAAGGCCAAGGGGACACAGCCTTGGAGACTGTGAGAACCTGTGCTGCTACGG	3174
Oy	2161	TATATGCTGGACCCGCTTACTGGGGAGCAGATGAAGCACTTGTGTGGAAGGTCAAA	2220
Db	3175	TATATGCTGGACCCGCTTACTGGGGAGCAGATGAAGCACTTGTGTGGAAGGTCAAA	3234
Oy	2221	CAGAGCAGCAGACTTCAAGACATACCGGCTGAGAGAACTATAGCCGTCACTTGGG	2280
Db	3225	CAGAGCAGCAGACTTCAAGACATACCGGCTGAGAGAACTATAGCCGTCACTTGGG	3294
Oy	2281	AAAGTGTCTTCCAGCTTTGAGATCTTAAACGGCTGACCTATGAGGGTCCGCTGGCTCAC	2340
Db	3285	AAAGTGTCTTCCAGCTTTGAGATCTTAAACGGCTGACCTATGAGGGTCCGCTGGCTCAC	3354
Oy	2341	GCTGATATGGCACACGAAATGATGCTCGGACAAACAGAACTTTGGCATTTGATGCT	2400
Db	3355	GCTGATATGGCACACGAAATGATGCTCGGACAAACAGAACTTTGGCATTTGATGCT	3414
Oy	2401	TACATGAGGAAAAAGTGTACAGCCGTACACTGAGCTTTTGGCAAGCATGGGCTGTT	2460
Db	3415	TACATGAGGAAAAAGTGTACAGCCGTACACTGAGCTTTTGGCAAGCATGGGCTGTT	3474
Oy	2461	GGTGCAGATGGGGGGTGTCTCAATCTCATTTGATAGACATAGATTCTCACTCAAT	2520
Db	3475	GGTGCAGATGGGGGGTGTCTCAATCTCAATTTGATAGACATAGATTCTCACTCAAT	3534
Oy	2521	GATGAGTTGATGATGATGCTCTTGGCGGAGAGACTACCTTGTGATGTCCAGGGTGAC	2580
Db	3535	GATGAGTTGATGATGATGCTCTTGGCGGAGAGACTACCTTGTGATGTCCAGGGTGAC	3594
Oy	2581	AACTTTGTACACGCTTGTGACACTTGTGTGGCCAAAAAGCAGGTTAATATATGGCCAA	2640
Db	3595	AACTTTGTACACGCTTGTGACACTTGTGTGGCCAAAAAGCAGGTTAATATATGGCCAA	3654
Oy	2641	GATGAGATACCTTGAATAATCTTCAACAATGTGGCTTTCAGAGAGGATATGAACAATTT	2700
Db	3655	GATGAGATACCTTGAATAATCTTCAACAATGTGGCTTTCAGAGAGGATATGAACAATTT	3714
Oy	2701	TGCGTCAATATGAGAGAGAGCTGTACTGTGTACACCAAGAACCGGCACTTTCGAG	2760
Db	3715	TGCGTCAATATGAGAGAGAGCTGTACTGTGTACACCAAGAACCGGCACTTTCGAG	3774
Oy	2761	AATATCTGATGATGATGACACACAGAAATTGATGTGACCAAGATACCAAGCTGGTTCAAT	2820
Db	3775	AATATCTGATGATGATGACACACAGAAATTGATGTGACCAAGATACCAAGCTGGTTCAAT	3834
Oy	2821	ACACTCTCATGCTTCAAGATTTCCCAACAACAGTTCCGAGACATGAGAAACCTAATCTGG	2880
Db	3835	ACACTCTCATGCTTCAAGATTTCCCAACAACAGTTTCGAGACATGAGAAACCTAATCTGG	3894
Oy	2881	GAGTTCTTAACGCTCTCACTGCTGTATTTCTGCAATTAACGATTCATTTGACAGGCGAGA	2940
Db	3895	GAGTTCTTAACGCTCTCACTGCTGTATTTCTGCAATTAACGATTCATTTGACAGGCGAGA	3954
Oy	2941	AAAGCAGACGTTGGGTGAAATCAAGAACGCTCAACAGATCTTATGAAAGGCACTTT	3000

Db 3955 AAGCCAGCGCTGGGTGAGAAATCAAGACCGCCCAACAGATCTTAATGAAGAGCGAGTT 4014
Qy 3001 G 3001
Db 4015 G 4015

RESULT 6
US-11-097-143-22562
; Sequence 22562, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: C1000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22562
; LENGTH: 15606
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-22562

Query Match 54.0%; Score 1620.4; DB 10; Length 15606;
Best Local Similarity 71.5%; Pred. No. 0;
Matches 2147; Conservative 0; Mismatches 851; Indels 6; Gaps 1;

Qy 1 GTCATAGCGCGCCCATCATCAATATATGTGATCTCCACCGTCATTTGTCAGCATTCGAG 60
Db 937 GTGATCGGCTCGCCGATCATCAAGTACCGGCACTACCGTCATGTTCAACACTGCGAG 996
Qy 61 ACTGGCTTGTGCGCTCTTAATAGCTTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGT 120
Db 997 ACTGACTTGTGCTCAAGCTACAGAGTATGAGAGAAAGAAAGAAAGAAAGAAAGT 1056
Qy 121 GAAAGAAAGCAAGCATCTCCCAAGAGAAAGCAAGATGAGCATGCGCTGCACTTCTCC 180
Db 1057 GAGAGAAAGCAAGCATCTCTGCAAGAGAGGCAAGATGAGCATGCTGCACTTCTCG 1116
Qy 181 AGGTCAAGAGAAAGAAATCTAGACTCTCGAGTTATCAGAAAGTCTTCCGCTGTT 240
Db 1117 CGTCCCGAGAGAGAGTCCAGACAGCTCGTGCATCCGCAAGTGCAGAGCGCTTTC 1176
Qy 241 ACTAAGTTTATCAATGCTGTGAATCTTACAGAGAAACGCTGCTCATCTGATGTTCTTC 300
Db 1177 ACCCAAGTTTATTAAGCTTGAACACTGCAAGTCAAAATCCCGCACTTCATTTTCTTC 1236
Qy 301 GCGTCAGTGAACCTGGGAGAGTGGTATGTGCTCGAGATCTCATCAACTTATGCA 360
Db 1237 CAAAAGCTCAACCTCAAGAGATGTCATGTGCTTGGAGACTTATTAATTAATTTTCG 1236
Qy 361 CAGCCCATGAGATATGAGAACAGAGAAAAAACAATTCCTCGGCACTCCGAAC 420

Db 1297 CAACCCAGAGACGATATATGAGCAAGAGAGAAACGAATTCCTGCTCCGCAAC 1356
Qy 421 CGTCAGGACCTGTTCCAAGAGAGGCAATCTGAACCTGATCCTCGAAGCTATAGACAAG 480
Db 1357 CGACAGATCTGTTCCAGAGAGAGGCGCTGCTCAATCTGATCTCGAGGCCATTTGACAG 1416
Qy 481 ATCAACGTCATCAGTCCAGAGGGTCTCGCTGAATTCCTGCGGAGACGAATCTGGA 540
Db 1417 ATCAACATTAATCACTCGAGAGGCTTCTTACGACGCTTCCTGCGGAGACGAGAC 1476
Qy 541 CAGAGCTGGAGAAAGATCTGATATTTTGTATAGTTGCTGCGGCAATTAATAAGGC 600
Db 1477 CAGAGCTGGAGATCTCATCTCCACTATTGTACCACTTTGGCGGCATCATCAAGGC 1536
Qy 601 AACCAAGAACTGCGGCGAGTTGCGCAATCGAACCGGCTCACTGAGCTGTTCTCGGC 660
Db 1537 AACCAAGAACTGCGGCGAGTTGCGCAATCGAACGATCACTGAGCTATTTCTCCGC 1596
Qy 661 CTGCGCTCGAGGCTCGGCGAGAGGCAACGCAATGCTCAAGTCTGCACTGCGTCTT 720
Db 1597 CTGCGTTCCAGAGGCTCCAGAGAGGTTCCGGCATGTTGACGTACTTCACTGCGTCTG 1656
Qy 721 ATGACTCGCTGAAGCTCTCAATATATGATGAGGACGAACATTAAGATTAATCTCT 780
Db 1657 ATGACTCGCTGAAGGCACTTAATATGATGAGGATAGACATCAAGTGTATCATCTCC 1716
Qy 781 CTATTAGAAAAAGCATGGGCGGACCTTAAGTATCTAATGTCATGTCGCTGCGTC 840
Db 1717 CTGCTGAGAGAGCAACGCGAGAGGACCGAAGTCTTAAGCTTCTGTGTTCTTGTGCTG 1776
Qy 841 GGTAAACGCGTGGGAGTGGCTGCTCTCAAGAACAACTGTGATCTTAATCTGACCGGC 900
Db 1777 GGTAAAGAGTGGGAGTGGCTGCTCTCAAGAACAACTGTGATCTTAATCTGACCGGC 1836
Qy 901 AAGAACTGTTGCTGCAAACTGCGCTGTGATACGATATCTAATGTCCTGCGCAATC 960
Db 1837 AAGAACTGTTGCTGCAAGAGCTCTGTGTGACATGTGCGCAATCCGACCAACATC 1896
Qy 961 TTGCTGGAGTGAAGTGAAGAGGTGCGAGTGAACCGCAATGATCTTCAAGTGAATATG 1020
Db 1897 TTGCTGGAGTGAAGTGAAGAGGTGCGAGTGAACCGCAATGATCTTCAAGTGAATATG 1080
Qy 1021 GACCAATATGAGAGAGACCAATATATGATGATGATGATGATGATGATGATGATGATG 1080
Db 1957 GATCAATATGAGAGAGACCAATATATGATGATGATGATGATGATGATGATGATGATG 1080
Qy 1081 ACTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
Db 2017 TCCGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2076
Qy 1141 GACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
Db 2077 GACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2136
Qy 1201 GTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
Db 2137 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2196
Qy 1261 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
Db 2197 ATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2256
Qy 1321 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
Db 2257 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2316
Qy 1381 AGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
Db 2317 AGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2376
Qy 1441 TACTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500

Oy 1 GTCATAGCGGCCCATCATCAATAATGCTGATCTCACCGTCATTTGTGACATTCCGAG 60
Db GTGATCGGCTCGCCCATCATCAAGTACGCGACACTACCGTCATGTCAGACATCGCAG 1056
Oy 61 ACTGCGTTGTGCTGTCTTATTAAGCTTACGAAAGGAAAGAGAGGAGTGGTAAATA 120
Db ACTACCTGTGTGCTGAGCTACACGAGTTATAGACGAAAGAAAGAGCGTATGAAAGGTG 1116
Oy 121 GAAGAGAACCAAGCGATTCTCCACGAGGAAAGGCAAGATGAGAGATGAGCTCGACTTC 180
Db GAGAGAAAGCAAGCGATCTCTGACGAGAGGCAAGATGAGAGATGCTCGACTTCG 1176
Oy 181 AGGTCAAGAGAGAGAAATCTAGACTGTCTGAGTTATCAGAAAGTCTTCCGTCTTC 240
Db CGCTCCAGAGAGAGAGATCCAAAGCGCTCGTGCATCCGCAATGACGAGCGCTCTTC 1236
Oy 241 ACTAGTTTATCAATAGTCTGAGAACTCTACAGAGAAACCGTGCATCTGATGTTCTTC 300
Db ACCCGTTTATTAAGCGCTTGAAACACTGCAGTCAAAATCCCGACACTCCATTTCTTC 1236
Oy 301 GCGTCACTGAACTCTGAGGAGATGCTGATGCTCTGAGGATCTCATCACTACTTCGCA 360
Db CAAGAGTCAACTCTGAGAGATGCTCATGCTCTTGAAGACTTGAATCACTTTCTTC 1356
Oy 361 CAGCCGATGAGGATATGGAACAAGAGAAAAAAATAATCCGAGCACTCCGAAAC 420
Db CAACCCGAAAGCATATGAGACAGAGAGAAACAGAAACCAATTCCTGCGCCGCGCAAC 1416
Oy 421 CGTACGAGCTGTTTCAAGAGAGAGAGCAATCAAGACCTGATCCTCGAAGCTATAGACAG 480
Db CGACAGATCTGTTTCAAGAGAGAGGCGTCTCAATCTGATCTGGAAGCGCAATGACAG 1476
Oy 481 ATCAAGTCACTACGCTCCAGAGGATCTCTGCTGAGATCTGAGGAGAGAGAACTTGA 540
Db GTCAACATATCACTCTCGAGGGCTTCTTAGCAGCTTCTGCGCGGAGAGAGAGCGGC 1536
Oy 541 CAGAGCTGGAAATGATATCTGGAATTTGTATCACTGCTGCGGCAATATAAGGAGC 600
Db CAGAGCTGGAGTCTCATCTCCACTATTTGTATCAACTCTTGCGCGCATATCAAGGAGC 1536
Oy 601 AACCAAGAACTGGCGGCACTTGGCGGAATCGAACCCGCTCAACTGCTGTCTCGGCG 660
Db AACCAAGAACTGGCGGCACTGAGTTCGGAACAGTAAACCACTGCTATTTCTCGGCG 1596
Oy 661 CTGCGCTGCAAGGCTCTGAGGAGAGGAGCAAGGAGTCTGAGAGTCTGCACTGCGTCT 720
Db CTGCGTCTCAAGGCTCTCAAGGAGGAGTCTCGGCAATTTGAGAGTCTTCACTGCGTCTG 1716
Oy 721 ATGAGCTGCGCTGAAGCTCTCAATATGATGAGGAGAGAAACATTAAGTATATCTCT 780
Db ATGAGTTCGCAAGGCACTAAACATATGCGGAGTGAAGCAATCAAGTGGTATCTCC 1776
Oy 781 CTATTTAGAAAGCATGAGGCGGAGCCCTTAAGTACTAGTGTGCTATGTTCCGTGTGCTC 840
Db CTGCTGAGAAAGCAAGGAGGAGCCGAAAGTCTTGAAGCTTGTGTGTTCTTGTGCGTGTG 1836
Oy 841 GGTAAAGGCGCTCGCGGTGCGCTGCTGACAGAAACAATCTGTGACTATTTACTGCGCGGC 900
Db GGTAAAGGAGTGGCGGTGCGATCTTCCAGAAACAATTTGCGACTTTTGTGCTACCGGCG 1896
Oy 901 AAGAACTGTGTGCTGAACATGCGCTCGTGAATCAAGTATCTAGTGCCTCGCAACATC 960
Db AAGAACTGTGTGCTGAACATGCGCTCGTGTGACATGTGCGCAAGCATCCGACCGAAATC 1956
Oy 961 TTCTGTGGGTGAGTGAAGAGGTGCGGAGTGAACCGCAATGTAATTTGAGGTGACTATG 1020
Db TTCTGTGGGTGCGGTGAGGTTCTTCAATGACAGAAAGTGTACTTCTGAGGTGACATG 2016
Oy 1021 GACCAATATGAGAGAGACACATATGATGCAATTAAGCATATGAGTGGAGGCAACAT 1080
Db GATCAATATGAGAGACACAGACATGATGCGCCACTGCGCATTTGGGCTTGAATATCT 2076

Oy 1081 ACTGTTATGCTCCATACCCGCGCGGTGCGAGAAATGGGAGAGTAAACGCGTGGAGAT 1140
Db TCCGGTATATGATCCGTATCCCGAGAGCGGAGAAAGATGGGGTGGCAATGAGTGGCGAT 2136
Oy 1141 GACCTGATCTGTAGGAGGATTCAGAGGCGCTACCTGTGATCGGAGGAGAGAGACTCC 1200
Db GACCTGATCTCTTGGATTTGATGATGCTCTTCTTTGGAGGAGAGGTTCGAAACAATA 2196
Oy 1201 GTCAATAGAACTCATGTGTAAGAGCCTTATATTAAGAAAGGTGAAGTATGATGCGCA 1260
Db GTGTGAGACGCGCTCCGAGAGAGCCTTATACGTAAAGGCGATGTTATGCGGTGCC 2256
Oy 1261 TTGAGACTGAGAGGATCCCATATTAATCACTCATGTTCAACGAGAGTGGCGGTGAC 1320
Db ATTACCTCTTCTGTGCCCATCATCAAGTTTACTTTTAAACGAGTAAAGTGGCGGTAGC 2316
Oy 1321 TTGACCAACTCAATCTGAAAGGAGATGTTCTCCGAGTCAATCAGCTGCTCATGTAAGCTG 1380
Db TTTAGGAGCTTTAAGCTGAGAGAGATTTCTTCCGTGATGATGCTCATCAAAACTA 2376
Oy 1381 AGTTGTGCGTTCTGTGAGGAGAGAACAGGTCGTCTCGGTACGCGGCTCCAGAAAGC 1440
Db AGCTGTGCGTTCTTTCGAGAGGTATCATGTCGTTTAAAGTTTGCCTCCGCTCATGGGA 2436
Oy 1441 TACTCTCCCTTGTGTGAGTCTCTCTGCGGAGAGATCTTCAAGCTTGAAGCTGCTTC 1500
Db TTTCTCTCCCTCTGTGAGTGTCTATGCTCAGAGATCTTCACTGAGTGTGATCTTGTCTTC 2496
Oy 1501 TACTTGGGCAACTGTCCAGAGCGGCTTGGAGTGAACCTCGGTAATGACAGAGATAGC 1560
Db TACTTGTATATCTTGGCAAGATGTTTGTGCGGAGCAATGCTTATGAGAGAGACAT 2556
Oy 1561 GCTTGTGCTTACACTGTGATCTTAAAGATTACTCTGCTACATATGTTGAACAA 1620
Db GCTTGTGCTGAAGCCGTTGATACCAAGGAGTGAATGTCAGAGTTCGTGAGACAA 2616
Oy 1621 ATTGAAGATAGCTGCTGAAATATATACAGAAATGTTGGCTATGATTAAGATGAAAGCA 1680
Db ATCAAGAGAGAGCTGCGGAGAAATATCAGAGATGTTGGCTCTTAAACAAATGAAAGCG 2676
Oy 1681 GGCTGATATGAGCGGAGCAAGAGAGAGACTTGCAGAAATCCAGCCCTGCTGTCGCC 1740
Db GGCTGTGTGAGGAGAGCAACGAGATGATCAACCGCATCATCTTGTCTCAACCAT 2736
Oy 1741 TTGAGGAGACTCCCACTGTGTAAGAAAGATACGATACCACTCGCTGTGACAGACTC 1800
Db TTGAGAGAGCTTCCGCGGAGGAGAAAGCATATGAGACATATAGCTGTGCAAAACCTG 2796
Oy 1801 AAGACTATCTGTGCTGTGAGTACTATCATGCTTGAATAGCTTCAAGACGATTCGC 1860
Db AAGACGATTTATCTGCTGAGATATCTATCATTAACATGAGCAAGGCAAGGACGATTCGC 2856
Oy 1861 AAGGTGTGCTGCCCAAGCAACTTATGATGACGATCCAAAGGCTTCAAGGCAAGCACTC 1920
Db CAGTGTGCTGCCCAAGCAAGATCTTATGATGAGGAGCATGCTTCAAGGCTTCACTT 2916
Oy 1921 GACCTGAGTGTGCTCACTTGAACAACCAAGATGATGATGATGACAGCTGCTGAG 1980
Db GACCTTAAGCGCGGTGACATCAACCCCAATGTGAGAGGCTTGTGAGCAAGCTGCGGAG 2976
Oy 1981 AACACCAACAACCTTTGGCGAGGAGAGATACAGAGAGATGAGACTTATGACTTAAT 2040
Db AACACTCACAATTTGTGAGGAGAGGAGCGGATCAGAGAGGATGAGACTTATGCTTAAAC 3036
Oy 2041 GAGGACTCGGACATGATGATGTTCCCGGCACTGCTGATTAACCGAAGGTTGACGATGCC 2100
Db GAGGATGATGAAACCAAGAGATGTCACACTTGTGTCATATGCAAGAGAGAGGCT 3096
Oy 2101 ATCAAGAGGCAACAGGAGCAACAGCTCGAGACTGTGAGAGCCCTGTGTGTACTAGGG 2160
Db ATCAAGAGGCAACAGGAGCAACAGCTCGAGAGAGTGGAAAGCTCTGTGTGTACTAGGA 3156
Oy 2161 TATATGTGAGACCGGCTTACTGTGAGAGAGCATGAAAGCACTTTGTGAAAGCTCAAA 2220

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Db      3157 TATGCTTGGATCTCCGACGGGCGAAGGACGGAGGCACTTCTGCCCCAGCACAGCG 3216
Qy      2221 CAGAGCAAGACGACCTTGAGAACATACCGCGCTGAGAAACATATGCGCGTCTGCGG 2280
Db      3217 CTCAGATTGCGCGGATTCGGACCTTACAGGGTGGAGCGGACCTACGCCCTGACATCGGC 3276
Qy      2281 AAGTGTACTTGCAGTTTGAGATCTTAAACGGCTGACCTATGAGGGTCCGCTGCGCTAC 2340
Db      3277 AAGTGTACTTGCAGTTTGAGATCTTAAACGGCTGACCTATGAGGGTCCGCTGCGCTAC 2340
Qy      2341 GCTGATATGGACACAGGAATGATGCTCGGACAAAGACGAACTCTTGGGCAATTTGATGTT 2400
Db      3337 GCCGATTGCTATCCGGAGCCGATGCTGGGCGACGAGACACAGATGGGCTTTCATGGA 3396
Qy      2401 TACATGAGGAAAAAGTGTACAGCGGTAAACATGATCTTTCGGCAAGCATGGGCTGTT 2460
Db      3397 CACAAATGTACCAAAATGACCGCCGATCATTGAGCACTTTCGAGTCCGATATAGGCT 3456
Qy      2461 GGTGACGTAGTGGGGGTCTTCTAGATCTCATTTGATTAAGACATAGTTTCTCACTCAT 2520
Db      3457 GCGATGTGATTTGTTTCTTCAATGATGTCAGAGGCAAAACATAGCTTCTCGTTGAA 3516
Qy      2521 GGTGAGTTGTTGATGAGATCTTTCGGGAGAGACTACGTTTGTGATGT-----CCAG 2574
Db      3517 GGAGAACTCTGATGAGACGCGCTGGGCGGAGACGACCTTTGGCGACGTAACCGCGGAG 3576
Qy      2575 GGTGACAACTTTGACACAGCTTTCACATTTGTGGGCGAAAAGCCAGGTTAACAT 2634
Db      3577 GGGGTGGGCTTGTGCGCCCGCTGACCTGGAGATGGGCGCAAGAGCGCGCTCATCTAC 3636
Qy      2635 GGCACAGATGTAATCTCTGAATATCTTCAACAATGTGTCTTCAAGAGGATATGAA 2694
Db      3637 GGCACAGATGTAATCTCTGAATATCTTCAACAATGTGTCTTCAAGAGGATATGAA 3696
Qy      2695 CCATTTTGGCTAATATGAAAGAGACGTGACTCACTGGTACACCAAGGACCAAGCGGATC 2754
Db      3697 CGGTCTGGGTAAACATGCGCGCGCGGTAAACCACTGGTACACCAAGGACCAAGCGGATC 2754
Qy      2755 TTGCGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2814
Db      3757 TTGCGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3816
Qy      2815 TCAGATACACTCTCATGCTCAAGATTTTCCCAACAAGCTTTCGAGACGATGAGAAAGCT 2874
Db      3817 GCGGACACCCCGCGGACCTTAAAGATCTGCAACACCTTTCGAGACGATGAGAAAGCT 3876
Qy      2875 AACTGGAGTTTCACTGCTCTCACTGCTGATCTGCTGATCTGCTGATCTGCTGATCTGCTGAT 2934
Db      3877 AACTGGAGTTTCACTGCTCTCACTGCTGATCTGCTGATCTGCTGATCTGCTGATCTGCTGAT 2934
Qy      2935 GCAAGAAAAAGCAGACGTTGGGTAAATCAAGACCGTCAACAGATCTTATGAAAGG 2994
Db      3937 CAGGAGAAAGCCAGACGCTGGGACGATTAAGAACCGGACGATTAAGGCTAATGCGCGAG 3996
Qy      2995 GCAG 2998
Db      3997 GCGG 4000

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RESULT 8

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US-10-668-767-7
/ Sequence 7, Application US/10668767
/ Publication No. US20040171114A1
/ GENERAL INFORMATION:
/ APPLICANT: Caspar, Timothy
/ APPLICANT: Cordova, Daniel
/ APPLICANT: Guttridge, Steven
/ APPLICANT: Rauh, James
/ APPLICANT: Smith, Rejane
/ APPLICANT: Tao, Yong
/ APPLICANT: Wu, Lihong
/ TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors

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/ FILE REFERENCE: BBI533 US NA
/ CURRENT APPLICATION NUMBER: US/10/668,767
/ CURRENT FILING DATE: 2003-09-23
/ PRIOR APPLICATION NUMBER: 60/412,795
/ PRIOR FILING DATE: 2002-09-23
/ PRIOR APPLICATION NUMBER: 60/427,324
/ PRIOR FILING DATE: 2002-11-18
/ NUMBER OF SEQ ID NOS: 149
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 7
/ LENGTH: 15413
/ TYPE: DNA
/ ORGANISM: Peregrinus maidis
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: (1265)
/ OTHER INFORMATION: n = a,c,g, or t
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (17)..(15397)
/ OTHER INFORMATION:
/ US-10-668-767-7

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Query Match      51.4% Score 1542.2; DB 7; Length 15413;
Best Local Similarity 70.1% Pred. No. 0;
Matches 2101; Conservative 1; Mismatches 890; Indels 6; Gaps 2;

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Qy      1 GTGATAGGCGGCGCCATCATCAAAATATGTGATCTCACCGTCAATGTGACAGATTCCGAG 60
Db      1013 GTATAGGTGACCAAAATATCAAGTATGATGATGATGATGATGATGATGATGATGATGAT 1072
Qy      61 ACTGCTTGTGCTGTCTTATATAGCTTATACGAAACGAAAGAGAGAGTGGTAAAGTA 120
Db      1073 ACTGCTTGTGCTGTCTTATATAGCTTATACGAAACGAAAGAGAGTGGTAAAGTA 1132
Qy      121 GAAGGAAGCAAGCATTTCTCCACAGAGAGGCAAGATGACAGATGGCTGACTTCTCC 180
Db      1133 GAAGGAAGCAAGCATTTCTCCACAGAGAGGCAAGATGACAGATGGCTGACTTCTCC 1192
Qy      181 AGGTACAGGAGGAAGATCTAGACCTGCTGAGTTATCAGGAAGTCTTCCGCTGCTC 240
Db      1193 GCACTCAAGAGGAAGATCGGATCGGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 1252
Qy      241 ACTAAGTTATCAATAGTCTGGAACCTTACAGAGAACCGTCTCACTGATGTTCTTC 300
Db      1253 ACTAAGTTATCAATAGTCTGGAACCTTACAGAGAACCGTCTCACTGATGTTCTTC 1312
Qy      301 GCGTCACTGAACCTGGGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
Db      1313 GCACTGGAATTTGAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1372
Qy      361 CAGCCCGATGAGATATGAGAACAGAAAGAAACAAATTCGCGGCACTCCGAAC 420
Db      1373 CAGCCCGATGAGATATGAGAACAGAAAGAAACAAATTCGCGGCACTCCGAAC 1432
Qy      421 GGTGAGACCTGTTCCAGAGGAGGACATGAACTGATCTCTGAAAGCTTATAGCAAG 480
Db      1433 GGTGAGACCTGTTCCAGAGGAGGACATGAACTGATCTCTGAAAGCTTATAGCAAG 1492
Qy      481 ATCAAGCTATCAAGTCCGAGGGTCTCTGCTGATCTCTGCGGAGACGATCTGGA 540
Db      1493 ATCAAGCTATCAAGTCCGAGGGTCTCTGCTGATCTCTGCGGAGACGATCTGGA 1549
Qy      541 CAGAGCTGGGAAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Db      1550 CAGAGCTGGGAAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1609
Qy      601 AACCAAGAACTGGGCGGAGTTCCGCAACTGAAACCGCTCACTGCTGTTCTCGGC 660
Db      1610 AACCAAGAACTGGGCGGAGTTCCGCAACTGAAACCGCTCACTGCTGTTCTCGGC 1669
Qy      661 CTGGCTGCGAGGCTTGGGCGAGGCAACCGGACGCTGCAAGTGTGCACTGCTGCTT 720

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Db 1670 CTGGGCTACAGACATCAAGTGAAGGACGAGAAATCTTGATGTATTGCTGTCTC 1725
Oy ATAGACTCGCTGAAGCTCTCAATATGATGAGAGCAACAATATAAGTAAATCTCT 780
Db 1720 ATGATTCGCTGAGCGGTGAATATGATGAGGATGAGCATATAAAGTTATATATCT 1789
Oy 781 CTATTAGAAAAGCATGGGCGGACCTTAAGTACTAGATGTCTATGTTCCGTGCGTC 840
Db 1730 CTTCCTGAGAAACATGGAAGGATCCGAAAGTTTGATGTCTCTGTTCACTGTGTGTG 1849
Oy 841 GGTACGCGGTGCGGCTGCTGCTCAAGAACATCTGATCTACTGCTGCGCGC 900
Db 1850 GGTAAATGATGTCTGCTGTCTGATCTCAAAACAAATTTGATTTCTTTACTCTGA 1909
Oy 901 AAGAAGCTGTGCTCAAACTGCGCTGATGATCACTATGATGTCTGCTGCAACATC 960
Db 1910 AAAATCTTCTTCTTCAAAACGAACTAATGATGATGATGATGATGATGATGATGAT 1969
Oy 961 TTCTGCGGTGAGTGAAGGATGCGGATGATGCGCAATGATGATGATGATGATGATG 1020
Db 1970 TTTGTTGGGCGGT 2029
Oy 1021 GACCAATAGAGAGACACATATGATGATGATGATGATGATGATGATGATGATGATG 1080
Db 2030 GATCACTATGAGACACACATGATGATGATGATGATGATGATGATGATGATGATGAT 2089
Oy 1081 ACTGTTATGTCTTCAATACCGGCGGTGCGGAGAAATGAGGATGATGATGATGATG 1140
Db 2090 AGTGAATATGTGCTTATCTGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2149
Oy 1141 GACCTGTACTGATGAGGTTGAGCGGCTTACTCTGTGTGCGGCGGAGAGAGATCTCC 1200
Db 2150 GATCTTATTTCTTATGAGGTTGATGATGATGATGATGATGATGATGATGATGATG 2209
Oy 1201 GTCATATAGAGATCATGCTGAGAGGCTTATATAGAAAGGATGATGATGATGATG 1260
Db 2210 GT--CTACCGATGACATGATGATGATGATGATGATGATGATGATGATGATGATG 2266
Oy 1261 TTGACCTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
Db 2267 CTAGATTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2326
Oy 1321 TTACCAACTTCAATCTGAGAGGATGATGATGATGATGATGATGATGATGATGATG 1380
Db 2327 TTCAAGATTTCAATCTGAGAGGATGATGATGATGATGATGATGATGATGATGATG 2386
Oy 1381 AGTGTGAGTCTGCTGCGGCGGAGACACGATGATGATGATGATGATGATGATGATG 1440
Db 2387 AGTGTGAGTCTGCTGCGGCGGAGACACGATGATGATGATGATGATGATGATGATG 2446
Oy 1441 TACTCTCCCTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
Db 2447 TTCTCTCACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2506
Oy 1501 TACTCTCGCAACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
Db 2507 TACTCTCGCAACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2566
Oy 1561 GCTTCTGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
Db 2567 GATTTGTTCCAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2626
Oy 1621 ATTAGAGATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
Db 2627 ATTAGAGATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2686
Oy 1681 GAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
Db 2687 GAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2746
Oy 1741 TTGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
Db 2747 TTGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2806

Oy 1801 AAGAATATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1860
Db 2807 AAGAATATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2866
Oy 1861 AAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1920
Db 2867 AAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2926
Oy 1921 GACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1980
Db 2927 GATCTACGCGCATATCTTAAACCGAATGATGATGATGATGATGATGATGATGATG 2986
Oy 1981 AACAACCAACCTTTGCGGCGGAGAGATGATGATGATGATGATGATGATGATGATG 2040
Db 2987 AATACATATATCTATGCGGCGGAGAGATGATGATGATGATGATGATGATGATGATG 3046
Oy 2041 GAGGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2100
Db 3047 GAGGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3106
Oy 2101 ATCAAGAGGCGCAACAGGAGACAGCTGAGAGATGATGATGATGATGATGATGATGATG 2160
Db 3107 ATCAAGAGGCGCAACAGGAGACAGCTGAGAGATGATGATGATGATGATGATGATGATG 3166
Oy 2161 TATATGCTGACCGGCTTCTGAGGAGACAGATGATGATGATGATGATGATGATGATG 2220
Db 3167 TATATGCTGACCGGCTTCTGAGGAGACAGATGATGATGATGATGATGATGATGATG 3226
Oy 2221 CAGAGAGAGAGATCTTCAAGACATACCGGCTGAGAGATGATGATGATGATGATGATG 2280
Db 3227 TTAAGAGAGAGATCTTCAAGACATACCGGCTGAGAGATGATGATGATGATGATGATG 3286
Oy 2281 AAGTGTACTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2340
Db 3287 AAGTGTACTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3346
Oy 2341 GCTGATATGAGACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2400
Db 3347 TCAATATGCTGCGGCGGAGATGATGATGATGATGATGATGATGATGATGATGATG 3406
Oy 2401 TCAATATGCTGCGGCGGAGATGATGATGATGATGATGATGATGATGATGATGATG 2460
Db 3407 TTCAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3466
Oy 2461 GGTGACGTAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2520
Db 3467 GGTGACGTAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3526
Oy 2521 GGTGACGTAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2580
Db 3527 GGTGACGTAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3586
Oy 2581 AACTTTGATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCT 2640
Db 3587 AACTTTGATCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCT 3646
Oy 2641 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2700
Db 3647 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3706
Oy 2701 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2760
Db 3707 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3766
Oy 2761 AATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2820
Db 3767 AATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3826
Oy 2821 AACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2880
Db 3827 AACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3886

Qy 2881 GAGTCTTACGCTCTCACTGCTGTATCTGCAATACGAGTTCAATGACAGGACAG 2940
Db 3887 GAATTCCTCAGACTCTCACTCCAGATTATTTGCCACTCATCTTATCGAAGAGGTGA 3946
Qy 2941 AAAGCCAGACGTTGGGTGGAATCAAGACCGTCAACGATCTTATGAAAGAGCAG 2998
Db 3947 AAATTGAACGTTGGCAGAGATTAAGAAATCCGTGACATAGACTGTAGTGAAGCTG 4004

RESULT 9

US-10-668-767-5
Sequence 5, Application US/10668767
Publication No. US2004017111A1
GENERAL INFORMATION:
APPLICANT: Caspar, Timothy
APPLICANT: Cordova, Daniel
APPLICANT: Gutierrez, Steven
APPLICANT: Rauh, James
APPLICANT: Smith, ReJane
APPLICANT: Tao, Yong
APPLICANT: Mu, LiHong
TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
FILE REFERENCE: B01533 US NA
CURRENT APPLICATION NUMBER: US/10/668,767
PRIOR FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: 60/412,795
PRIOR FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 60/427,324
PRIOR FILING DATE: 2002-11-18
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 15315
TYPE: DNA
ORGANISM: Periplaneta americana
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(15312)
OTHER INFORMATION:
US-10-668-767-5

Query Match 44.5%; Score 1335.4; DB 7; Length 15315;
Beeb Local Similarity 66.2%; Pred. No. 0;
Matches 1988; Conservative 0; Mismatches 1001; Indels 12; Gaps 4;

Qy 1 GTCAATAGCGCGCCCATCATCAATATGTGTGCTCACCGTCAATGTGCAAGATTCGAG 60
Db 1000 GTAAATGAGCACTTATTAATTAAGTGTGACAGTACGCTATTAATCAACATTCGAT 1059
Qy 61 ACTGCTGTGCTCTCTTATTAAGCTTAACGAAGAAAGAAAGAGAGGAGTGGTAAAGTA 120
Db 1060 ACAAGTTATGTGTAAACATACAGAGCTTATGAAACAAAGAGAGAGGAGTGGTAAAGTA 1119
Qy 121 GAAGAGAGCAAGCATCTCTCAGCAGAGAGAGCAAGATGAGAGATGAGCTCGACTTCTCC 180
Db 1120 GAAGAGAGCAAGCATCTCTCAGCAGAGAGAGCAAGATGAGAGATGAGCTCGACTTCTCC 1179
Qy 181 AGGTCAAGAGAGAGATCTAGAGCTGCTGAGATTATCAGAGATGTTCTTCTGCTGTT 240
Db 1180 AGGATCTAAGAGAGAGATCTAGAGCTGCTGAGATTATCAGAGATGTTCTTCTGCTGTT 1239
Qy 241 ACTAAGTTATTAATGAGTCTGAGAACTCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db 1240 ACAAGTTATTAATGAGTCTGAGAACTCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1299
Qy 301 GCGTCAATGAG 360
Db 1300 TCATTCCTGTTATCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1359
Qy 361 CAGCCGATGAG 420
Db 1360 CAACCTGAG 1419

Qy 421 CGTACAGACCTGTTCCAG 480
Db 1420 AGAGAGAGTTATTTCAAG 1479
Qy 481 ATCAAGCATCAAGTCCAG 540
Db 1480 GTTAATATTAATGAGTCAAG 1536
Qy 541 CAGAGCTGGAATATGATATCTGATATTTGATGATGATGATGATGATGATGATGATGATG 600
Db 1537 CAAGTTGGAGTGTGATTTCTGATATTTATTAATGATGATGATGATGATGATGATGATG 1596
Qy 601 AACCAAG 660
Db 1597 AATCATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1656
Qy 661 CTGCGCTGAG 720
Db 1657 TTAGAGATCTAAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1716
Qy 721 ATAGACTGCGTGAAGCTCTCAATATGATGATGATGATGATGATGATGATGATGATGAT 780
Db 1717 ATGATTTCTCCGAGAGCTTTAAATATGATGATGATGATGATGATGATGATGATGATGAT 1776
Qy 781 CTATTAAG 840
Db 1777 CTTTGGAG 1836
Qy 841 GGTAAAG 900
Db 1837 GGTAAAG 1896
Qy 901 AAGAACTGCTGCTGCAAG 960
Db 1897 AAAAATTTACTTCTTCAAG 1956
Qy 961 TTGCTGAGTCAAGTGAAG 1020
Db 1957 TTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2016
Qy 1021 GACCATTAAG 1080
Db 2017 GATCATGATGAAG 2076
Qy 1081 ACTGTTATATGCTCAATACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Db 2077 GCAGGTTATGTTCCGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2136
Qy 1141 GACCTGATCTGATCGAG 1200
Db 2137 GATTTATATTTCTTCCGATTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2196
Qy 1201 GTCAATAGAGATGATGAG 1260
Db 2197 GT---GATGCTGAGTCAAG 2253
Qy 1261 TTGAGACCTGAG 1320
Db 2254 TTAGATTTAATCTAATCTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTT 2313
Qy 1321 TTCAACCACTCAATCTGAG 1380
Db 2314 TTCAAGAGATTTCAATTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2373
Qy 1381 AGTTGCTGTTCTGCTGAG 1440
Db 2374 GCGTGTGTTTATTTATGAG 2493
Qy 1441 TACTCTCCTTGTGAG 1500
Db 2434 TTTTCTCTCTCAATTTGAAG 2493
Qy 1501 TACTTCGCAACTGTCCAG 1560

Db 2494 TATTTGGAAATCTTAATGCTACTACGGGACCGTGTATGTTGAAGATGATACA 2553
Qy 1561 GCCTTCGTGCTACACCTGTGATCTTACAGATTTACTGCTACATATGTGGACAA 1620
Db 2554 GCATTTGTTCCAAATCCAGTTGATACATCATGCTTCTTAACCTAGTTACATGAAAT 2613
Qy 1621 ATTAAGATTAAGCTAGCTGAAATATACAGAAATGTGGCTATGAAATAGATCGAACA 1680
Db 2614 ATTAAGATTAATTAAGAGAAATATCATGAAATGTGGCAATGAAATTAATTAAGACT 2673
Qy 1681 GGCCTGATGTAACGGGACCAAGAGAACTTGCAACAGATCCACCCCTGCTGTGCC 1740
Db 2674 GGTGGCAATATGATGATTAAGAAATATATCTAGGAAATATCAATCCATGTTTAATAG 2733
Qy 1741 TTCAGCAGACTCCCACTGCTGAGAAAGATACGATACATACACTGCTGTGACAGACTC 1800
Db 2734 TTTGACAGTTGCTCCCGACCGAGAGAGCTTATGATTTCTCAATTAAGCTGTGCAACGCTT 2793
Qy 1801 AAGACTATCTGGCTCTGGGCTACTACATCACTAGCTTAAGAACTCCAGACGATCCGC 1860
Db 2794 AAAACGTTATGCGTGGATATCAATATCCATCATATCCACCGTCCGATTAATAA 2853
Qy 1861 AACGTTGCTGCGCCCAAGAACTTTCAATGAGTCCACCGGCTCAACCCGACCACTC 1920
Db 2854 ACGTACCGTTGCCCAAGAACATTTATGCAATCCAAATGATTAACCAACGACCACTA 2913
Qy 1921 GACCTGAGTGTCTGACCTCTGACACCCAGATGATGATGATGATGATGATGATGATG 1980
Db 2914 GATTATCTGCAATTAATTTGTCAGGGAAATGAAAGATTAATTAAGACATTAAGCTGAG 2973
Qy 1981 AACACCCACAACTTTGGGCGAGGAGATACAGAGGATGATGATGATGATGATGATG 2040
Db 2974 AATACACATTAATTAATGCGCAAAAGAAATACAAAGATGATGATGATGATGATG 3033
Qy 2041 GAGACTCGGACATGATCTGTTCCCGGACCTGGGCTATCCGAGGTTGAAGATGCC 2100
Db 3034 GAAAGATTAACAAATGTTAGCGATCTCTATTAGTACGTAACGAAAGTATGATGATG 3093
Qy 2101 ATCAAGAGGCGCAACAGGACACAGCTCGAGACTGAGAGACCTGCTGTCTACAGCG 2160
Db 3094 ATTAAAAAGCTAATAGAGATACAGAGATGAAACATGCTGCGCATTTATAGTATAGT 3153
Qy 2161 TATATGCTGACCCGCTTACTGGGAGACAGATGAA--CACTTGTGGAAGCTCA 2217
Db 3154 TACAACCTTAGACCCACCTGAGGAAACAAACAGGACATCTTAACAGAGAAAC 3213
Qy 2218 AAAAGAGAGAGAGACTTGAACATACCGGCTGAGAGAACTATGCTGCTGAGCT 2277
Db 3214 ACTAATGATATCTGACGTTGAGAACATATGCTGTAAGAAACATATGCTGTGCAAGT 3273
Qy 2278 GGAAGTGTACTTCAAGTTGAGATCTTAACGCTGAGACTTATGAGGCTGCTGAGCT 2337
Db 3274 GGAAGTGTATTTGAGTTGAGATATGACAAACGCGCCATGCGAGTTGATGAGGCT 3333
Qy 2338 CACGCTATATGACCAAGAAATGATGCTCGACAAAGAGAACTTTGGGCAATTTGAT 2397
Db 3334 AGTTTACATGTTCTCCGGGTTATCAATCGTGTAGTACGAAATTTCTGGGCAATTTGAT 3393
Qy 2398 GGTTCATATGAGAGAAAGTATACAGCGGTTACATGAGCTTTTCCGACAGCATAGGCT 2457
Db 3394 GGTTCATATGAGAGAAAGTATATATGAGGACAGCCGATATTTGGAGGCACTGCA 3453
Qy 2458 GTTGTGACGTAAGTGGGCTGTTCTAGATCTCAATGATAGAGATTAAGTTCTCACTC 2517
Db 3454 GTTGTGATGTCGTGGAGGCTTTTATGACTTAATGATCATATTAAGTTTTCGTG 3513
Qy 2518 AATGCTATGTTGATGATGATGCTTGGCGAGAGACTACGTTTGTGATGTCAGAGCT 2577
Db 3514 AATGAGAAATTAATGATGATGATGAGGAGAACTACGTTTCTGAAGTTCAAGGA 3573
Qy 2578 GACAACTTTGATCAAGCTTGACACTTGTGTGGCCAAAGGCAAGTTAACTATGGC 2637

Db 3574 GAAAGATTTGATCTGCTGATTTACTCTGCGACATAGACAAAGCAAAATTAATTTGCT 3633
Qy 2638 CAAGATGTAATATCTGAAATATCTTCAACAATGCTGCTTCAAGAGGATATGAAACA 2697
Db 3634 CAAGAGTAAATCTATGAAATATCTTCAACAATGCTGCTTCAAGAGGATATGAAACA 3693
Qy 2698 TTTTGGCTCAATATGAAAGAGAGAGCTGATCTGATGATCAACAGAGACAGCGATCTTC 2757
Db 3694 TTTTGGCTCAATATGAAAGAGAGAGCTGATCTGATGATCAACAGAGATCTTC 3753
Qy 2758 GAGATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2817
Db 3754 GAAATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3810
Qy 2818 GATACCTCCTACATGCTTCAAGATTTCCCAACAAGCTTCCAGAGATGAGAAAGCTAAC 2877
Db 3811 GATACCTCCTACATGCTTCAAGATTTCCCAACAAGCTTCCAGAGATGAGAAAGCTAAC 3870
Qy 2878 TGGAGTTCTTACGCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 2937
Db 3871 TGGAGTTCTTACGCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 3930
Qy 2938 GAAAG 2997
Db 3931 GAAAG 3990
Qy 2998 G 2998
Db 3991 G 3991

RESULT 10
US-10-668-767-3
; Sequence 3, Application US/10668767
; Publication No. US2004017114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutierrez, Steven
; APPLICANT: Rauch, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: B1513 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 15845
; TYPE: DNA
; ORGANISM: *Myzus persicae*
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (36)-(37)
; OTHER INFORMATION: n = A, C, G, or T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5807)
; OTHER INFORMATION: n = a or c
US-10-668-767-3

Query Match 44.0%; Score 1319; DB 7; Length 15845;
Best Local Similarity 66.0%; Pred. No. 0;
Matches 1974; Conservative 0; Mismatches 1005; Indels 12; Gaps 4;
Qy 1 GTGATAGCGCGCCATCATCAATATGATGATGATGATGATGATGATGATGATGATGATG 60

Db	1276	GTAAATGGTGCACCTTAATTAAGTATGGTGAACAGACAGTGTAAAGTGAACATTCGTAT	1335
Oy	61	ACTGGCTTGCGCTGCTCTTATTAAGTCTTACGAAAGAAAGAAAGAGTGGGTAAAGTA	120
Db	1336	ACAGGTTATGGTTAACTATAAGCTTATGAACAAAAAAGGAGTGGTAAAGTA	1395
Oy	121	GAAGGAAGCAAGCAATCTTCCAAGAGAAAGCAAGATGAGCGATGGCTCGACTTCTCC	180
Db	1396	GAAGAAAAACAACAGAGTATTACACAMAAAGTAAAGAGGACGATGGGTTTGACTTTAAGT	1455
Oy	181	AGGTCAAGAGGAAGAAATCTAGACCTGCTCGAGTTATCAGAAAGTGTCTTCGCTGTTT	240
Db	1456	AGAGGTCAAGAAAGAAAGTCAAGAACTGCTAGAGTTAAACGCAATGCTCTTCAATATTC	1515
Oy	241	ACTAAATTATCAATAGTCTGAGAACTCTACAGAGAAACGTCGTCACTGATGTTCTTC	300
Db	1516	ACACAGTTTATTTCTGAGATGGAGAACTTACAAAGTAAACAGGCGTTGCTCATTTATTTGT	1575
Oy	301	CGGTAGTGAACCTGGGCGAGATGGTGAATGTCCTCGAGATCTCACTCACTTCGCA	360
Db	1576	TCAATTCGTTAACTTAAATGAATGGTCAATGTCATGAAGAAATTAATTAATTAATCTTGGCT	1635
Oy	361	CAGCCCGATGAGGATATGGAACAAGAAAGAAAACAAATTCGCGGCACTCCGAAC	420
Db	1636	CAACTGAAAGAGAAATGAGACAGAAAGAAAAACAAACCGATTTAGAGCACTTAAGAAAT	1695
Oy	421	CGTCAGAGACTGTTTCCAAAGAGAGAGCACTAGAACCTGATCTTGAAGCTATAGACAG	480
Db	1696	AGACAGAAATTAATTTCAAGAAAGAAATTAATTAATTAATCTTAAGAGCCATTTGATTA	1755
Oy	481	ATCAACGTCACTACGTCCTCAAGGGGTTCTCGCTGATTCCTGGCGGAGACGAATCTGGA	540
Db	1756	GTAAACATTAATCACTCTCAGGGATCAATGTCAGTT--TAGCGGAGTGAAGAGCTGGA	1812
Oy	541	CAGAGCTGGGAAATGAATATCTGGATTAATTTGTAATCAGTTGCTGGCGGCAATTAATAAGGGC	600
Db	1813	CAAAATGAGAGTATATTTCTGGTTATTTATTAACAGTTGTAAGCTGCACATTAATTAAGGA	1872
Oy	601	AACCAACGAACCTGGCGGCAATTCGCGAATCGAACCCGCTCACTGGCTGTTCTCGCGC	660
Db	1873	AATCATACCACTGTGCTCAATTTGCTAATATCTAACCGATTAATATGGTTATTCAGCCGT	1932
Oy	661	CTGGGCTCGCAGGCTCTGGGCGAGGGCACCGGCATGCTCGACGTGCTGCATCGCTGCTT	720
Db	1933	TTAGGATCTCAAGCATCCAGTGAAAGAACTGGTATGTTAGATGTGCTCATTTGTGTTCTC	1992
Oy	721	ATAAGCTGCGCTGAAGCTCTCAATATGATGAGGAGCAACACATTAAGTGAATATCTCT	780
Db	1993	ATCGATTTCTCAAGAGCTTTAAATATGATGAAGAGCAACATTTAAAGTTATTAATATCA	2052
Oy	781	CTATTAGAAAGCATGGGCGGACCCCTAAAGTACATGATGTGCTATGTTCCGTGTCGCTC	840
Db	2053	CTTTTGAAGAAACATGCTGTGATTCAAAAGTGTGGATGTTTATATGTTCTCTGTGTGTT	2112
Oy	841	GGTAAACGCGCTGCGGTGCGCTGCTCAAGAACCAATCTGTGACTTAATCTGCGCGC	900
Db	2113	GGTAAACGGTGTGCTGTAAAGAGTTCCGAAATTAATATATGATGATTTCTTATTAAGGA	2172
Oy	901	AAGAACTGTTGCTGCAAACTGCGCTCGTGATCACTGATCTAGTGTCCGTCCAAACTC	960
Db	2173	AAAAATTAATCTTCCAAACCTTAACTTGTGTGACAGTGAAGCGGTACGTCCCAATATTT	2232
Oy	961	TTGATGGGTGAGTGAAGAGGTGCGCAGTGTACCGCAATAGGTACTTGAAGGTGACTATG	1020
Db	2233	TTTGTGTTGATCATGTAAAGTGAATCTGTGTTTATAGAAATGTGATTTATGAACTGGCAATA	2292
Oy	1021	GAACCATTAAGAGAACCAACATATGATGCCACTTACGATAGATGGGCAAACT	1080
Db	2293	GATCATGTAGAACAAACTACTATTTAAATCCGCACTTCGCAATGGATGGGCAAAATCA	2352
Oy	1081	ACTGTTATGTCTCCATACCCGGGCGGTGCGAGAAATGGGAGGTAAACGGCTGGGAAT	1140
Db	2353	GCTGGTTATGTTCATATCTGTGTGTGAGAAAAATGGGCGGAAACGAGTTGGGAT	2412

[illegible]

2218 AAACGAGACAGACAGACTTCGAAACATACCGCGCTGAGAGAACTATCCGCTGACTCT 2277
Db TCTATATAGATATTTGACGTTGAGAAACATATCGTGGGAAAAAAGCTATGCGTTCTAGT 3549
Qy 2278 GGAAGTGTCTCTGAGTTGAGATCTTAACGGCTGACCTAAGAGGTGCGCTGGCT 2337
Db 3550 GGAATATGTACTTGAATTTGAGTACTGACAAAGTGAACCTATGCGGTTGAGTGGCC 3609
Qy 2338 CACGCTGATATGACACAGAAATGATGCTCGGACAAAGACGAACTTTGGCATTTGAT 2397
Db 3610 AGTTTCAATGTTCCCGGTTATGAAATCCGCAATGATGAAATCTTTGGCATTTGAT 3669
Qy 2398 GGTATCAATGAGAAAAAGTGTACACCGGTAACTGAGTCTTTGCGAAGCATGGGCT 2457
Db 3670 GGTATTAAGAAAGAAAAATTTACATGGGACACCGCAATCATTTGGTAGACAGTGGCAA 3729
Qy 2458 GTTGTGACGTATGTTGGGGTGTCTCTAATCTCATTTGATTAAGCAATTAAGTTCTCACTC 2517
Db 3730 GTTGGAGATGTCGTGGAGGTGTTTTTAATTAAGACCAATACATTAAGCTTTTCGATG 3789
Qy 2518 AATGTGAGTTGTTGATGAGATGCTCTTGCGGAGAGACATACGTTTGTGATGCCAGGCT 2577
Db 3790 AAGGAGAAATTAATAATGATACGTTAAGAGGAGAAACATTTCTGAAAGTCCAGGA 3849
Qy 2578 GACAACTTTGTACACGCTTGCACTTGTGTGGCCAAAAAGCCAGGTTAATCATATGCG 2637
Db 3850 GAAAGATTTGTACCTGCTTTACGCTGGAATGAGCAAAAAAGCAATTTGATTTGCT 3909
Qy 2638 CAAGTGTGAATCTCTGAAATATCTTCAACAAATGTTGCTTCAAGAGGATATGACCA 2697
Db 3910 CAAGACGTTAATCTCAATTAATAATCTTCAAGATTTGACCTTCAAGAAAGATATGACCA 3969
Qy 2698 TTTTTCGCTCAATATGAGAGAGACGCTGACTGCTGTTACCAAGAGACAGCCGATCTTC 2757
Db 3970 TTTCTGTAAATATTAAGAGGCGCTGTGCTTATTTGTTATCTAAGATCAACCAATTTT 4029
Qy 2758 GAGAACTAGTATGAGATATGACACAGATTAATGATGACACAGATTAACAGCTGTTCA 2817
Db 4030 GAGAACTAGTATGAGATATGACACAGATTAATGATTAAGATTAAGATTAAGATTAAG 4086
Qy 2818 GATACACTCTCACTGCTCAAGATTTCCCAACAGCTTCAAGACATGAGAGAAAGCTAAC 2877
Db 4087 GATACACACCTTGTCTAAAGATTAAGTATTAATTAATTAATTAATTAATTAATTAAT 4146
Qy 2878 TGGAGTCTTACGCTCTCACTGCTGTTATCTGCAATTAAGAGATTAATTAAGAGGCA 2937
Db 4147 TGGAGATTTTACGCTCTCACTGCTGTTATCTGCAATTAAGAGATTAATTAAGAGGCA 4206
Qy 2938 GAAAAAGCCAGACGTTGGGTAGAAATCAAGACCGTCAACAGATCTTAATG 2988
Db 4207 GAAAAAGCCAGATGCGCAAGAAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 4257

RESULT 11
US-11-097-143-22561/c
; Sequence 22561, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: C1000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769

; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22561
; LENGTH: 24236
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-22561

Query Match 38.3%; Score 1150; DB 10; Length 24236;
Beet Local Similarity 67.7%; Pred. No. 0;
Matches 1749; Conservative 0; Mismatches 660; Indels 173; Gaps 3;

1 GTCATAGGCGCGCCCATCATCAATATATGATGATCCACCGTCATTTGACAGATTCGAG 60
Db 21229 GTATCGGCTGCGCGATCATCATGATACGCGACACTACCTCATCTTCAGCACTCGAG 21170
Qy 61 ACTGCTTGTGTGCTGCTTATTAAGTCTTACGAAACGAAAGAGAGAGTGGTAAATA 120
Db 21169 ACTAGCTTGTGTGCTGCTTATTAAGTCTTACGAAACGAAAGAGAGAGTGGTAAATA 21110
Qy 121 GAAGAGAGAGAGAGATTCCTCCACGAGAAAGCAATGATGATGATGATGATGATGATGAT 180
Db 21109 GAGAGAGAGAGAGATTCCTCCACGAGAAAGCAATGATGATGATGATGATGATGATGAT 21050
Qy 181 AGTCAAGAGAGAGAGATTCCTCCACGAGAAAGCAATGATGATGATGATGATGATGATGAT 240
Db 21049 CGCTCCAGAGAGAGAGATTCCTCCACGAGAAAGCAATGATGATGATGATGATGATGAT 20990
Qy 241 ACTAAGTTTA----- 250
Db 20989 ACCAGTTTATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 20930
Qy 251 -----TCAATGCTGTGAAACCTTAACAGAAACGCTGCTCATCTGATGTTCTTCG 301
Db 20929 AACTCATTTTCAAGCTTGTGAAACCTTAACAGAAACGCTGCTCATCTGATGTTCTTCG 20870
Qy 302 CGTCAAGAACTGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 361
Db 20869 AAAAGTCAACCTTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 20810
Qy 362 AGCCGATGAGATATG----- 378
Db 20809 AACCGAAGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 20750
Qy 379 -----GACACGAAAGAAACAAATTCGCGGCACTCGAAACCG 422
Db 20749 CTATTAATTAATTTTCAAGACAGAGAAACGAAACGAAATTCGCGGCAACCG 20690
Qy 423 TCAGGACCTGTTCCAAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 482
Db 20689 ACAGGATGTTTCAAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 20630
Qy 483 CAAGCTCATACGTCACGAGGCTTCTGCTGATTCCTGCGGAGACGAAATCTGAGCA 542
Db 20629 CAATATTAATCACTCGAGGCTTCTGCTGATTCCTGCGGAGACGAAATCTGAGCA 20570
Qy 543 GAGCTGGAATATATCTGATATTTGATTCAGTTGCTGCGGCAATTAATTAAGGCA 602
Db 20569 GAGCTGGAATATATCTGATATTTGATTCAGTTGCTGCGGCAATTAATTAAGGCA 20510
Qy 603 CCAAGAGAACTGCGGAGATTCGGAATGATGATGATGATGATGATGATGATGATGATGAT 662
Db 20509 CCAAGAGAACTGCGGAGATTCGGAATGATGATGATGATGATGATGATGATGATGATGAT 20450

663 CGGCTCGAGGCGCTCGGGCGAGGCGACCGGCACTGCTCGACGCTGCTGCACTGCGTCTTAT 722
Db CGGTTCCAGGCGCTCGAGGAGGATTCGGGCAATGTTGAGCGTACTTCACTGCGTCTGAT 20390
Qy 723 AGACTCGGCTGAAGCTCTCAATATATGAGGGAGCGAACACATATAAGTATATCTCT 782
Db CGATTGCGCAGAGGCGCATTAACATATATGAGGATGAGCAGTCAAGGATATATCTCCCT 20330
Qy 783 ATTAAAAAGCATGAGGCGGAGACCTTAAGTACTAGATGCTATGCTGCTGCTGCTGCG 842
Db GCTGAGAAAGCAGCGAGGAGACCCGAAAGTCTTAAGCGTTCTGTGTTCTTGTGAGG 20270
Qy 843 TAAACGCGCTCGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 902
Db TAAATGAGTGGGCGGATCTCTCCAGAACAACTTTGCGACTTTTGTCTACCGGGCA 20210
Qy 903 GAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 962
Db GAATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 20209
Qy 963 CGTGGGTGAGTGAAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1022
Db CGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 20149
Qy 1023 CCACTAAGAGAGACCACTATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1082
Db TCACTTCAAGAGAGACCACTATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 20089
Qy 1083 TGGTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1142
Db CGGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 20029
Qy 1143 CTTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1202
Db CTTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19969
Qy 1203 CAATAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1262
Db GGTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19909
Qy 1263 GGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1322
Db TGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19849
Qy 1323 CACCACTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1382
Db TAGGAGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19789
Qy 1383 TTTGAGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1442
Db CTTGAGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19729
Qy 1443 CTTGAGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1502
Db CTTGAGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19669
Qy 1503 CTTGAGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1562
Db CTTGAGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19609
Qy 1563 CTTGAGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1622
Db TTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19549
Qy 1623 TAGAGATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1682
Db CAGAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19489
Qy 1683 CTGAGATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1742
Db CTGAGATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19429
Qy 1743 CGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1802

19369 CGAGAGCTTCCGCGCGGAGAGAGCGATAGCAATCACTAGCTGCAAGCGCTGAA 19310
Qy 1803 -----GACTA 1807
Db 19309 GTAAAGCTTCACTTAAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 19250
Qy 1808 TCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1867
Db TTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19249
Qy 1868 GTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1927
Db GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19189
Qy 1928 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1987
Db GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19129
Qy 1988 ACAAGCTTGGGCGAGAGAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2047
Db ACAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19069
Qy 2048 CGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2107
Db GTGAG 19009
Qy 2108 AGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2167
Db AGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 18949
Qy 2168 TGAAGCTTGGGCGAG 2227
Db TGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 18889
Qy 2228 AAGCAGCTTGAAG 2287
Db TGGCGAG 18829
Qy 2288 ACTTGAAGTGAAG 2347
Db ACTTGAAGTGAAG 18769
Qy 2348 TGGCAG 2407
Db GGTATCCGAG 18709
Qy 2408 AG 2409
Db 18649 TG 18648

RESULT 12
US-10-305-720-1154
; Sequence 1154, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Yang, Janice K.; Sellhauer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1154
; LENGTH: 4078
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g1526977

US-10-305-720-1154

Query Match 22.3%; Score 668; DB 6; Length 4078;
Beeb Local Similarity 55.4%; Pred. No. 1.6e-205;
Matches 1590; Conservative 0; Mismatches 1225; Indels 57; Gaps 13;

QY 1 GTCATAGCGCGCCCATCATCAATATATGCTGCTACCGCTCATTTGCGAGATTCGAG 60
DB 1163 GGCATAGGGAACATCTGAATAATAAATACGCTGCTCATGATCTATATCAACATGTAAAC 1222
QY 61 ACTGCGCTGTGGCTGTCTTATTAAGCTTAAGCAAGAAAGAGAAAGAGAGAGAGTA 120
DB 1223 AAGGCTATAGGCTTACTTACAGTCTGTGAGCTGAATCCGTAGAAATGGAATCTATA 1282
QY 121 GAAGAGAGCAAGCCATCTCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTA 180
DB 1283 CAAGCTAAG---GCATATATGATATGAAGGCCCATGAGATGATAGATTAAGTTGTCG 1339
QY 181 AGGTCAAG 240
DB 1340 AGATCCGAGATGAG 1399
QY 241 ACTAAGTTATCAATAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 1400 AATGATTTATTAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1459
QY 301 GCGTCAAGTGAACCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 1460 TTGCTATAGAGTCCG-----TAAGCTAAGTGTGAGAGAGAGAGAGAGAGAG 1513
QY 361 CAGCCCGATGAG 420
DB 1514 CCCCCAGATGAG 1573
QY 421 CGTCAAG 480
DB 1574 CCGCAAAATCTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1633
QY 481 ATCAAGCTCATCAGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 1634 TTGCAAGCTCATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1690
QY 541 CAGAGCTGGAG 600
DB 1691 GAGCTTGAAGATCCATCTGAATCTCTGATGAGAGAGAGAGAGAGAGAGAG 1750
QY 601 AACCAAG 660
DB 1751 AATGCTGAAG 1798
QY 661 CTGCGCTCGAG 720
DB 1799 AGCAGATTTGAG 1858
QY 721 ATGAGCTGCGTGAAGCTCTCAATATGATGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 1859 GTAGAAAGTCCAG 1918
QY 781 CTATTAG 840
DB 1919 CTTTATGAG 1978
QY 841 GGTAG 900
DB 1979 TGCCAG 2038
QY 901 AAGAGCTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB 2039 AGAGACTTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2098
QY 961 TTCTGGGTGAG 1020
DB 2099 TTCTGGGTGAG 2158

QY 1021 GACCACATAGAG---AAGACCAACATATGATGCCATCTACGATAGAGAGAGAGAG 1077
DB 2159 GACCACAG 2218
QY 1078 ACTATGAG 1137
DB 2219 ACTGAG 2278
QY 1138 GATGAG 1197
DB 2279 GATGAG 2338
QY 1198 CCGCTCAATAG 1257
DB 2339 ACTGAG 2392
QY 1258 GATGAG 1317
DB 2393 TGTATGAG 2452
QY 1318 TCCCTGAG 1377
DB 2453 ATGTTGAG 2512
QY 1378 CTGAGTGTGAG 1437
DB 2513 ATAAAGATGAG 2572
QY 1438 GGTATGAG 1497
DB 2573 GGTATGAG 2632
QY 1498 -----TTTCACTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1551
DB 2633 GAGAGATGAG 2692
QY 1552 GAGATGAG 1611
DB 2693 AGCAG 2752
QY 1612 GTGAG 1671
DB 2753 CTAG 2812
QY 1672 ATGAG 1731
DB 2813 ATGAG 2872
QY 1732 CTGAG 1791
DB 2873 CTGAG 2932
QY 1792 CAG 1848
DB 2933 GAG 2992
QY 1849 GAG 1908
DB 2993 GAG 3052
QY 1909 CAG 1968
DB 3053 CTGAG 3112
QY 1969 CAG 2028
DB 3113 AAGTGGAG 3172
QY 2029 TATGAG 2088
DB 3173 TATGAG 3232

2089 GTTACGATGCGCATCAAGAGGCGCAACAGGAGCACAGCCTCGAGAGCTGTGAGACCTTG 2148
 Db CTGATGACCGGAACCGAAGAAATCCAAAGAGGACAGCCTCCGAGGCTGTGCGACGCTG 3292
 2149 CTGTCTACGGGTATATGTGTGACCCGCTACTGGGAGACAGATGAAAGCACTCTTTG 2208
 Db CTGGGGATCGGCTACCACTTGGAGACAC-----AGATCAAGATCATGACACCGAGCC 3346
 2209 GAGGCTCAAAACAGAGGAGACAGACTTCAGAACTAACCGGCTGAGAGAACTATGCGC 2268
 Db GAGGTGTGACGCGGACCGCGGAGAAAGTTCCGAACTTCCTGCGAGAGAGCTATGCA 3406
 2269 GTCACTCTGGAGAGTGTACTTCAGATTGAGATCTTAAACGCTGAGACTATGAGGCTC 2328
 Db GTGAAGCCGAGCGGTGTATTTGAAATTGAGACGGTCACTGTGAGAGACATGAGGGTT 3466
 2329 GCGTGGGCTCAGCTGATATGCGACCAAGATGATGCTGCGACAAAGACAGAACTTTG 2388
 Db GGTGGAAGTGTCTGTGTGTGCAACCGATCAGAGCTTGGCTCAGATGAGACGTGCTTT 3526
 2389 GCATTGATGTTTAAATGAGGAAAGGTAACAGCGGTAACTGAGTCTTCCGCAAG 2448
 Db GCTTTGATGCTTTCAAGGCCAGCGGTGCGCATGAGG---CAATGAACATATGAGGCGC 3583
 2449 CAATGGGCTGTGTGACGTAGTGGGGGTGTTCTTATCTCATTTGATTAAGCAATAGT 2508
 Db TCTTGGCAAGCAGGGGATGTGCTGGGGGTGTATGTGACATGAAGAACACACATATG 3643
 2509 TTCTCATCATATGTGATGTTGTTGATGATGCTCTTGGCGGAGAGACTACGTTTCTGAT 2568
 Db TTCAACATGAAATGAGGAAATCTTCTTGAATGATTCAGGCTCAGAACTGGCTTTCAAGAC 3703
 2569 GTCCAGGGTGAACA---CTTTGACAGCTGCAACACTTGTGTTGGGCGCAAAAGCGCAGG 2625
 Db TTGATGTTGGAGATTCATACCTGTGTGTAGCTTGGAGTGTCTCAATGTGGTATG 3763
 2626 TTACATATGCGCAGATGTGATATCTGAAATATCTTCAACATGTGTCTTCAGAG 2685
 Db ATGAATTTGAAAGATGTGACACTTGAATATTTTCAACATGTGTCTTACAGAG 3823
 2686 GGAATGAAACATTTTGGCTCAATATGAAAGAGACGTGACTCACTGTTCAACAGAC 2745
 Db GGCATGAAACATTTGGCTTAAATCAACAGGATATTTACATGTGTGCGTGAAGAGG 3883
 2746 CAGCGGATCTCGAGATATCTGATGATGATGACACAGAGTTGATGTGCGAGATA 2805
 Db CTTCCTCAGTT--TCTTCAAGTTCATCAACCATTAACATATGAGGTGAACAGATA 3940
 2806 CCAGCTGTTGATATCACTCCATGCTCAGATTTTCCCAACAGACGTTG 2857
 Db GACGCAACCATATGACATTTCCCAATGTTTAAAGTCACTCAGAACTTTT 3992

RESULT 13
 US-10-276-774-552
 / Sequence 552, Application US/10276774
 / Publication No. US20040053245A1
 / GENERAL INFORMATION:
 / APPLICANT: Hybeq, Inc.
 / APPLICANT: Tang, Y, Tom et al
 / TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
 / FILE REFERENCE: 21372-030
 / CURRENT APPLICATION NUMBER: US/10/276,774
 / PRIOR FILING DATE: 2002-11-18
 / PRIOR APPLICATION NUMBER: 09/560,875
 / PRIOR FILING DATE: 2000-04-27
 / PRIOR APPLICATION NUMBER: 09/496,914
 / NUMBER OF SEQ ID NOS: 2700
 / SOFTWARE: Custom
 / SEQ ID NO 552
 / LENGTH: 14302
 / TYPE: DNA

; ORGANISM: Homo sapiens
 US-10-276-774-552
 Query Match 22.3%; Score 668; DB 7; Length 14302;
 Beel Local Similarity 55.4%; Pred. No. 3.4e-205;
 Matches 1590; Conservative 0; Mismatches 1225; Indels 57; Gaps 13;

1 GTCATAGGCGCGCCCATCATCAATATGTGATCTCCACCGTCAATGTGACAGATTCGCG 60
 Db GGCATGGAACATCTGAATTAATAATAGGTGATCTAGATCTATATCAACATGTAC 1222
 61 ACTGCTGTGCTGTCTTATATAGCTTTACGAAACGAAAGAAAGGAGTGGTAAATA 120
 Db ACAGGCTTATGCTTATCTTACAGCTGTGACGTGAATCCGTGAGATGGATCTTATA 1282
 121 GAAGAGAAAGAGGATCTCCAGAGAGGAGCAAGATGAGAGATGAGCTGACTTCC 180
 Db CAGCTAAG--GCTATATGATCATATGAGGCAATGATGATGATGATGATGATGATG 1339
 1283 AGTCAAGAGAGAAATCTAGACTGCTGAGATTCAGAGATGTTCTTCTGCTGCTTC 240
 Db AGATCCAGATGAAAGATTCAGACCGGAGTTATCCGAGACAGTCTTCTTCTTCT 1399
 241 ACTAAGTTATCATGTGTGAAATCTTACAGAAACCGTCTGACTGATGTTCTTC 300
 Db AATGATTTATAGGGGCTTGAATGCTTCAAGAAAGGAGGAGGCTTCCACAGTCAT 1459
 301 GCGTCAGGAACTGCGGAGATGTGTATGTCCTCGAGATTCATCACTCATTTCCG 360
 Db TTGCTTATAGATCGG-----TAAGCTTATGTCAGATCTCATTTGCTTCTTCTC 1513
 1460 CAGCCGATGAGATATGAGACAGAGAAACAAATTCGCGGCACTCCGAAAC 420
 Db CCCCAGATGAGATTTAGAGACATGAGACAAAGAAACATACAGAGCCCTGAAGAT 1573
 1514 CCGCAAAATCTTTCAGAGAGAGGAAATGATCAACTGCTGATGATGATGATGACGT 1633
 421 GGTCAAGACTGTTCCAGAGAGGAGCACTGAACTGATCTCGAACTATGAGCAAG 480
 Db CCGCAAAATCTTTCAGAGAGAGGAAATGATCAACTGCTGATGATGATGATGACGT 1633
 1574 TTGACAGTCAACGTCGCCAGGGGTCTCTCGTGTGATTCGCGGAGAGAGATTCGGA 540
 481 ATCAACGTCATCACTGCCAGGGGTCTCTCGTGTGATTCGCGGAGAGAGATTCGGA 540
 Db TTGACAGTCAACGTCGCCAGGGGTCTCTCGTGTGATTCGCGGAGAGAGATTCGGA 1690
 1634 CAGAGCTGGAAATGATATCTGATATTTGATCAGTTGCTGCGGCAATATAAGGCG 600
 541 GAGCTTGAATATCATTTCTGATATTTCTGTATGATGTTGCTGCGGCTTAAATGAGA 1750
 1631 AATGCTTGAATATCATTTCTGATATTTCTGTATGATGTTGCTGCGGCTTAAATGAGA 1750
 601 AACCAAGAACTGCGCGCAGTTGCGGAACTGAAACCGCTCAACTGCTGTCTCGCGC 660
 Db AATGCTTGAATATCATTTCTGATATTTCTGTGCTC-----CTCGACTGTGAT-----C 1798
 1751 CTGCGCTGCGAGGCTCGGCGGAGGAGCACCGGATGCTGACAGTGTGCACTGCTGCT 720
 661 AGCAGATTTGAGAAAGCTGGAAGCTTCTTCAAGGATTCGAGAGGTTTACACTGTGTTTA 1858
 1799 ATGAGCTGCGTGAAGCTTCAATATGATGAGGAGCAACATATAAGTATATCTCT 780
 721 GTTAAAGTCAAGAGCTTAAATATTTTAAAGAGACATATAATCTATATCTCA 1918
 1859 CTTTAAAGCAAAACATGAGAAATACACAGGTTGATGATGCTGCTGCTGCTGCT 1978
 1919 GTTAAAGCAAAACATGAGAAATACACAGGTTGATGATGCTGCTGCTGCTGCTGCT 1978
 841 GGTAAAGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 1979 TGCACGCGGGGTGAGTCCGTTTAAACAGATCTCACTGTGACAACTCTCTCAAGAA 2038
 841 AAGAACCTGTTGCTGCAAACTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 901 AGAGACTTGTATGCTGAGACAGCTTGTGTGAACATGTGACAGACATGAGCCCAATATT 2098
 2039 TTGCTGCTGAGTGAAGGCTGCGCAGTGTACCGCAATGATCTTGAAGTATGATG 1020

Db 2099 TTTCTGGGCGTCAGTGAAGGTTCTGCTCAGTATTAAGAAATGTACTATGATGATGCTG 2158
Qy 1021 GACCAATATAG--AGACCAACATATATGATGCCATCTTACGATAGATGGCCAA 1077
Db 2159 GACCAACAGAGCCCTTTGTGCACTGAGCACTCACCTGCGAGTGGCTGGCTTCC 2218
Qy 1078 ACTACTGTTTATGTCCTCAATCCCGGGCGGTGCGAAGAAATGGGGAGTAAACGCTGGGA 1137
Db 2219 ACTGAAGATATTTCTCCCTACCTTGAGAGGGCGCAAGAGTGGGGTGAATGGTGTGGA 2278
Qy 1138 GATGACTGTACTCTGCTACGGGTTGACGGGCTTACTCTGCTCGGGGGAGGAAGACT 1197
Db 2279 GATGATCTCTCTCTATGATTTGATGGCCCTTCACTCTGCTCAGGTTGATTCCTGCT 2338
Qy 1198 CCGCTCAATAGAGCTCATGCTGAGAGGCTTATATATTAAGAAAGGTGACGTATAGTTC 1257
Db 2339 ACTGTAAGCTCAACCAACC-----ACATCTGTTAAGAACGTGATGATGTCATGCTGC 2392
Qy 1258 GCATTTGACCTGACGGTACCCATATCACTTCACTTCAACCGAGTGGGGTGAACGGGA 1317
Db 2393 TGTTTAGATCTGAGTGGCCCAAGCATCTGTTCCGAATTAATGACCAACTGTTCAAGA 2452
Qy 1318 TCCTTACCAACTTTCATCTGGAAGGCAATGTTCTTCCGGTCACTGCTCAGTATAG 1377
Db 2453 ATGTTTGAAGATTTCACATGATGCTCTTCTTTCAGTCTGTTAGTTTCTCTGACGA 2512
Qy 1378 CTGATTTGCTGCTCTCTGCTGCGGAGAGAACAGGTGCTCTCCGTTACCGGCTTCAGAA 1437
Db 2513 ATAAAGATGACCTTCTGCTGAGAGGCGCATGGAAGAAATTCATATTTCTTCTCTCACT 2572
Qy 1438 GGTACTCTCCCTTGTGAGATCTCTCTGCGCGAGAGATCTTCAAGCTTGAAGCGTGC 1497
Db 2573 GGGTATGCTCTGTTATGAAGCTGTTCTGCCAAGAAAGTTGAAGTGAACACAGC 2632
Qy 1498 -----TTCTACTTCGCGAACCTGTCGAAGGCGGCTTGAGTGAACCTCGCTATGAC 1551
Db 2633 CGAGATTCAGAGCAAGAAAGAACTTACACGCGACCTGCGGCGCCACAGTTTCCCTG 2692
Qy 1552 GACGATACGCGCTTCTGTCGCTACACTGTTGATCTTTACAGATTACTCTGCTCAAT 1611
Db 2693 ACGCAAGTGCCTTCAACCCATCCCTGTGATACAGCGATCGTGTGCTCTCAT 2752
Qy 1612 GTGGAACAAATTAAGATTAAGCTAGCTGAATAATACAGAAATGTGGCTATGATTAAG 1671
Db 2753 CTAGAAAGATTAAGAGAAATCTGCGAGAGAAATTCATGAATCTGCGTTATGAATAA 2812
Qy 1672 ATCGAAGCAGGCTGATGTACGGCGAACAGAGAGACTTGCAAGATCCACCCGCG 1731
Db 2813 ATTGAGCTTGGCTGCAATGATGTCGGTTAGAGTGAACAAGAGACACACCCATGC 2872
Qy 1732 CTGCTGCCCTTCAAGCGACTCCCACTGCTGAGAAACGATACGATCACTGCTGTG 1791
Db 2873 CTGGTGGAGTTCTCCAGCTGCTGGAACAGAGGCGCATTTACATTAACAAATGCTGTT 2932
Qy 1792 CAGACACTCAAGACTATCTGGCTCTGGGCTATCAAT--CAGCTTATAGTACCTTCA 1848
Db 2933 GAGACCCCTGAAGACTTGTGTGCAATAGATGTCATGTGGTATATCAGATGAACAATCT 2992
Qy 1849 GCAGCGATCCGCAAGCTTCTGTCGCCCAAGAACCTTTCAATGAGTCAACGCTTACAG 1908
Db 2993 GAAGACAGGTGAAGAAATATAGCTTACCCAAAGATTAACAGCTGACAGTGGATACAG 3052
Qy 1909 CCAGCACCCTGACCTGAGTGTCTGCTGACCTGACACCCAGATGATGAGCTATGAGAC 1968
Db 3053 CTTGCCCTTATGAGCTGAGCTTATTAATCAATCCCATGCGAAGAGCAATGCTGAGC 3112
Qy 1969 CAGCTGGCTGAACAACCAACCTTTGGGCGAGGAGAGATACAGCAGGATGACT 2028
Db 3113 AAGTTGGCAGAAATGACATATATGTGGCGGGGATGCAATCCGCGAGGGCTGAGCT 3172
Qy 2029 TATGACCTTATGAGGACTCGGACATGATGTTCCCGGACCTGCTGGTGGCTATCCGAG 2088
Db 3173 TATGCACTCCACAGACGTTAAGAAACAGAAATCTCTGCTGTTGTTCCCTACACTCT 3232

Qy 2089 GTTACGATGCTATCAAGAAAGCCACAGGAGACAGCCTTCGAGACTGTGAGACCTCTG 2148
Db 3233 CTGATATACCGAACCAAGAAATCCACAGAGACAGCTCCGCGAGGCTGTGCGACCTG 3292
Qy 2149 CTGCTTACGGGTATATGCTGAGACCGGCTTACTGAGGAGAGACATGAGCACTTGTG 2208
Db 3293 CTGGGATACGGCTACACTTGAAGAC-----AGATCAAGTCAATGACCGACAGACC 3346
Qy 2209 GAAGCTCAAAACAGAAAGACAGACTTCAAGACATACCGCGCTGAGAAATATGCC 2268
Db 3347 GAAGTGTGACGGGCAACGGGGAAGAGTTCCGATCTTCCGTGCGAAGAACCTTATGCA 3406
Qy 2269 GTCACTCTGGAAATGTGATCTTGAATTGAGATCTTAAACGCTGGAACCTATAGGCTC 2328
Db 3407 GTGAAGCGCGAGCGGTGTATTTGATTTGAGACGCTCACTGCTGAGACATGAGGTT 3466
Qy 2329 GCGTGGCTCACCGTATATGAGCACCGAAGATATGTCGAGCAAGACGAGAACTTTGG 2388
Db 3467 GGTGAGTGTCTCTGTGTGTCAACCGAGTCAAGAGCTTGAGTGAACGTGCTTT 3526
Qy 2389 GCATTTGATGATTAACAATGAGAAAGATGTAACGCGTAACTGAGTCTTTCGCGAAG 2448
Db 3527 GCTTTATATGCTTCAAGGCCCGACCGGTGGCATCAGG---CAATGAACATATGGGCGC 3583
Qy 2449 CAATGGCTGTGTGACGATGAGTGGGGGTGTTCTTGAATCTCATTTGAATAAGCATTA 2508
Db 3584 TCTTGGCAACAGGCGATGTCGTGGGGTGTATGGTTGACATGAACGAACACCATGATG 3643
Qy 2509 TTCTCACTCAATGATGATGTTGTGATGATGATGCTCTTGGCGGAGACATAGCTTGTGAT 2568
Db 3644 TTCACTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3703
Qy 2569 GTCAGAGGTGACAA---CTTGTACAGCTTGTGACACTTGTGTGGGCAAAAAGCCAGG 2625
Db 3704 TTTGATTTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3763
Qy 2626 TTAACATATGCGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2685
Db 3764 ATGAACCTTGAAGAGATGACACACTTGAATAATTTACCACTGTGTGCTTACAGAG 3823
Qy 2686 GATATGAACATTTTGGCTGATATGATGATGATGATGATGATGATGATGATGATGATG 2745
Db 3824 GGTATGAACATTTTGGCTGATATGATGATGATGATGATGATGATGATGATGATGATG 3883
Qy 2746 CAGCCGATCTTCAAGATATGATGATGATGATGATGATGATGATGATGATGATGATG 2805
Db 3884 CTTCCTCAAT---TCTTCAAGTTCCATCAACATGAAATATGAGGTGACCAAGATA 3940
Qy 2806 CAGCTGTGTCAGATACACTCCATGCTTCAAGATTTCCCAACAGCTTGC 2857
Db 3941 GACGGCACCATACAGATGCTCCCATGTTTAAAGTCACTCAGAAATCTTTTG 3992

RESULT 14
US-10-687-553A-490
; Sequence 490, Application US/10887553A
; Publication No. US2005085436A1
; GENERAL INFORMATION:
; APPLICANT: Garza, Dan
; TITLE OF INVENTION: Method to treat conditions associated
; with insulin signalling dysregulation
; FILE REFERENCE: 4-33362
; CURRENT APPLICATION NUMBER: US/10/887,553A
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: 60/485,883
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 490
; LENGTH: 15731
; TYPE: DNA


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QY 2088 GTTGAAGATCCATCAAGAGCCCAACAGGACACAGCTCCGAGACTGTGAGACCTTG 2148
DB 3233 CTGGATGACCGAACCAGAAATCCAAACAGGACACGCTCCGAGGCTGTGCGACGCTG 3292
QY 2149 CTGGCTAAGGGGTATATGCTGGACCGGCTCACTGGGGAGACAGTAAAGCACTCTGTTG 2208
DB 3293 CTGGGGTACGGCTTCAACTTGGAGACAC-----AGATCAAGATCATGACCCAGAGCC 3346
QY 2209 GAAGCGTCAMAAACAGAGCAGACAGCTTCAGACATACCGCGCTGAGAGAACTATGCC 2268
DB 3347 GAAAGTGTGACGGGACCGGGGAAAGGTTCCGAACTCTCCGTCCGAGAAAGCTATATCA 3406
QY 2289 GTACGCTGGGAAAGTGTACTTCAAGTTTGAGATCTTAAAGGCTGACCTATGAGGGTCC 2328
DB 3407 GTGAAGCGCGGACCGGTGTATTTGATTTGAGACGCTCACTGCTGAGACATGAGGGTTC 3466
QY 2329 GGCTGGGCTCAGCGTATATGSCACAGGAATGATGCTCCGACAGAGAGAAACTTTGG 2388
DB 3467 GATTGAGTCGCTCGGTGTGTCAACCGATCCAGAGCTTGCTCAGATGAACGTGCCCTTT 3526
QY 2389 GCATTGTATGTATCAATGAGGAAAGATGTACAGCGGTAACTAGATCTTTCGCGAAG 2448
DB 3527 GCTTTGATGGCTTCAAGGCCAGGGGGTGGCATCAGGG---CAATGAACATATAGGGGCC 3583
QY 2449 CAATGGGCTGTTGGTACGATGAGTGGGGGTCTTCAATCTCATTTGATTAAGCATTAAT 2508
DB 3584 TCTTGGCAAGCAGCGATGTCTGGGGGTGTATGTTGACATGAACGAAACACACCATGATG 3643
QY 2509 TTCTCACTCAATGATGATGTTGATGATGATGCTCTTGGCGGAGAGACTAGCTTTGCTAT 2568
DB 3644 TTCACTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3703
QY 2569 GTCCAGGCTGACAA---CTTGTACCAAGCTTGCACATTTGGTGGGCCAAAGAGCCAGG 2625
DB 3704 TTTGATGTGGGAGATGATTAATCTGTGTGTACCTTGGAGTGGCTCAAGTGGGTAGG 3763
QY 2626 TTACATATGCGCAAGATGTGATATCTTGAATATCTTCAACATGTTGCTTTCAGAGAG 2685
DB 3764 ATGAACCTTGGAAAGATGTGACGACTTGAATATTTTCAACATCTGTGGCTTCAAGAG 3823
QY 2686 GGATATGAACCAATTTTGGGTCAATATGAAGAGACGATCACTGCTGATACCAAGAGAC 2745
DB 3824 GGCTATGAACCAATTTTGGGTCAATATGAAGAGATATTTACCATGTGGCTGAGCAAGAG 3883
QY 2746 CAGCGATCTTCAAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2805
DB 3884 CTTCCTCAGTT---TCTTCAAGTTCATCAACCAATGAACATATGAGGTGACAGATTA 3940
QY 2806 CCAAGCTGTTGATATCACTTCATGCTTCAAGATTTTCCACAAACAGCTTGC 2857
DB 3941 GACGCGCACCATGACAGTTCCTCCCATGTTTAAAGGTCACTCAGAAAGTCTTTTG 3992
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TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-500
Query Match 21.5% Score 646.6; DB 7; Length 15359;
Best Local Similarity 55.3%; Pred. No. 3.3e-198;
Matches 1537; Conservative 0; Mismatches 1184; Indels 60; Gaps 12;

QY 1 GTCTAGGCGGCGCCCATCATCAATATGATGATCTCCACCGTCAATGTGACAGCATTCGAG 60
DB 1124 GGATGGGCGCCCGCTGAGATCAAGTACGGGAGTCACTGTGCTTGTGAGCATGTGGCC 1183
QY 61 ACTGGCTTGGGCTGTCTTATAGTCTTAAAGAAAGAAAGAAAGGAGTGGTAAAGTA 120
DB 1184 TCAGAGCTGTGGCTCACTATGCGCTCCAGACCCCAAGGCCCTGCGCTCG---CGTG 1240
QY 121 GAAGAAGAGAGAGATCTCCACGAGAAAGGAGAAAGTGAAGATGAGCTGAGCTTCTCC 180
DB 1241 CTCAAGAAAGAGAGATCTGACACAGAGAGGCAATGAGAGCACTGTGCTGAC 1300
QY 181 AGGTCAAGAGAGAGAGATCTAGAGCTGCTCAAGTATCAGAAAGTGTCTTCCGCTGTC 240
DB 1301 CGTGCAGAGAGAGAGAGTCCAGGCGCGCGCATGATCCACAGACCAATGGCTATAC 1360
QY 241 ACTAAGTTTATCAATGCTCTGAGAACTCTTCAAGAGAAACGCTGTCACTGATGTTCTTC 300
DB 1361 AACCAATTCATCAAGAGCTTGAACAGCTTCAAGCGGAGAGCAAGGGCTCGGGGCCACC 1420
QY 301 G-----CGTCAAGAACCTGGGGGAGATGATGATGATGATGATGATGATGATGATGATGAT 354
DB 1421 GCTGGCAGGGGCGCTGCCATGAGGCGCTTATCTGAGCTTGGAGCTTCAATCATATAC 1480
QY 355 TTGCAAGGCGCATGAGAGATATGAAACAGAAAGAAAGAAAGAAAGAAAGTTCGAGGCACTC 414
DB 1481 TTGAGGCTCCTCCGAGAGCTTGCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1540
QY 415 CGAAACCTGACAGACTGTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 474
DB 1541 CGCAACCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1600
QY 475 GACAAAGTCAAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 534
DB 1601 GACGCGCTAAATGCTACACCACTGCTGCCACTTGTGAGT---TTGAGAGAGAGAGAG 1657
QY 535 TCTGACAGAGCTGGGAAATGATATCTGATATTTGATCAATGCTGCGGCAATATA 594
DB 1658 GACGCGAGAGCTGAGAAAGAGATGAGAACTTCTCATTAATCTTCAAGCTTCTTATAC 1717
QY 595 AAGGCAACCAACAGATGCGGAGAGTTCGCAACTGAAACGCTCAACTGGCTGTTC 654
DB 1718 CGTGGCAATGATGAGCAACTGTGCCCTCTT-----CTCCACAAACTTGGAGCTGGCTG 1771
QY 655 TCGGCGCTCGGCTCGAGGCGCTCGGCGAGAGGCAAGGCAAGTGTGCAAGCTGCTGCTGC 714
DB 1772 AGCAAGCTGATGAGG-----TGAAGGCTGTGTGGCACTTGAAGGCTGTGATGCTG 1825
QY 715 GTGCTTATAGACTGCTGAGAGCTTCAATATGATGAGGAGAGAGAGAGAGAGAGAGAGAG 774
DB 1826 GTCTCATTTAGAGTCCAGAGTTCGAGACATATCCAGAGAGATCACTCAAGTGCATC 1885
QY 775 ATCTCTATTAAGAAAGATGAGGCGGAGAGCTTAAAGTACTAGATGCTATGCTGCTG 834
DB 1886 ATCTCCTCTTGAAGAGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1945
QY 835 TGGGTGATTAAGGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 894
DB 1946 TGTGTGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2005
QY 895 CCGGCAAGAACTGTTGCTGCAACTGCGCTGCTGATCACTATCTAGTGTCCGCTCG 954
DB 2006 CTGGCGGAGAGTTCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2065
QY 955 AACATCTTGTGGTGAAGTGAAGAGGTGCGAGGTACCGCAATGTGATCTTGAAGGTG 1014
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Db 2066 AAACATCTTGTGGCCGAGCGGAGGCAACAAGCATACAGCAATGCTTGAAGGTG 2125
QY 1015 ACTATGAGCA---CATAGAGAAAGCAACATATGATGCCATCTACGATAGATGG 1071
Db 2126 ATGTGAGAGAGGTGATCTTCATTTCTGAGAGCTCAGGCCACCACTTGGGGTGGCTGG 2185
QY 1072 GCCAACACTACTGTATGTCCCATATCCGAGCGGTGGAGAAATGGAGGTAAAGC 1131
Db 2186 GCCCTCACGAGGGGTGACACCCCTACCTGGGGCGGAGGGGTGGGGCGGCAACGGG 2245
QY 1132 GTGGAGATGACCTGTACTCTGATCGAGGTTCAGCGCGCTTACTTGGTCCGGGGAGG 1191
Db 2246 GTGGCGATGACCTGTATCTCTACCGGCTTGTGATGATGATCTCTGAGCAGAGACGCTG 2305
QY 1192 AAGATCCCGTCAAATAGATCATGCTGAGAGCCTTATATGAAAAGGTGACGTGTAT 1251
Db 2306 GCACGCCAGT-----GACTTCCCGAGGGCAGCACCTTCGGCCCTGAAAGCATGTATC 2359
QY 1252 GATTGCGCATTTGACCTGACGGTACCCATATCACTTCAATGTTCAACGAGTGGGGTG 1311
Db 2360 AGCTGTCTGCTGATCTCAGCGTGGCTGCTCATCTCTTCCGATCAACGGCTGGCTGTG 2419
QY 1312 ACGGATCTTCAACCACTTCAATCTGAAAGGATGTTCTTCCGGTCAATCAGTGTCT 1371
Db 2420 CAGGGTGTCTTGAAGTCTTCAACCTGACGGGCTCTTCTTCCGTGTGTCAGCTTCTCG 2479
QY 1372 AGTAGCTGAGTGTGCTGCTGCTGCTGGCGGAGAACAGCGTGTCTCCGTAACCGGCT 1431
Db 2480 GCTGTGTCAAGTGGGTCTCTCTTGTGGCGCCATGTGAAATTCAGTTCCTGCGC 2539
QY 1432 CCAGAAAGGCTACTCTCCCTGGTGGAGTCTCTCTGCGCAGCAGATCCTCAGCTGAG 1491
Db 2540 CCACTGTGCTATGCTCCATGAGGTGTGCTCTCTGAGAGCATCTCATCTTGA 2599
QY 1492 CCGTGTCTTCTACTTGGGCAACCTGTCAAGCGGG-----CCTTGGCTGAGCTTCGCTA 1545
Db 2600 CCAATCAAGAGATATGACGGAGGGGCCCGGGGCTCCTCCTGTGGGCTCCAGTGC 2659
QY 1546 GTACAGAGCATACGGCTCTGCTGCTACACTGTGTATCTTTCATATCTTGTCT 1605
Db 2660 TGGCTCTGACACACGAGCTTGTGCTGCTGCTGTGAGCACTGTCAAGTGTCTGTGCG 2719
QY 1606 ACATATGTGGAACAATATAGATATAGCTAGCTGAAATATATACGAAATGTGGCTATG 1665
Db 2720 CCCCCTGTGAGCGCATTCGGAGAAAGCTGGCGAGAACTCAAGAGCTCTGGCGCTA 2779
QY 1666 AATAAGATCGAAGCAGCTGATGTATCGGCAACAGAGAAAGACTTGCACAAAGTCAAC 1725
Db 2780 ACCGCAATCGAGCAGGGGTGAGCTACCGGCCGGTTCGGATGACAAAGAGGCTGCAC 2839
QY 1726 CCGTGTCTGTGCTCTGAGGAGCTCCCATCTGTGAGAAAGATACATACATCTC 1785
Db 2840 CCGTGTCTGTGAGCTTCCACAGCCTTCCAGAGCCTTGAAGAGAACTTACAACTCTGAGATG 2899
QY 1786 GCTGTGCGAGCATGAAGCTATCTGTGCTTGGGCTACTATCAGCTT---AGATAG 1842
Db 2900 TCTGGGAGAGCGCTGAAGCTGTGCTGTGGCTGTGCACTGGGCTGAGGATGAG 2959
QY 1843 CCTCAGGACGATCCGCAACGTTGCTGTGCCCAAGCAACTTTCATGCACTCAACGAC 1902
Db 2960 AAGGCGAGAGCAACTGAGAAAGAAACAACATCCCAAGACGTATATGATGAGCAATGGG 3019
QY 1903 TACAAAGCAGACCACTGACCTGAGTGTCTGACCTCTGACACCCAAAGATGATGACTA 1962
Db 3020 TACAAAGCAGGCTCCGCTGAGCTTGAAGCACTGTGCGGCTGACCGCGCAGAACACCTG 3079
QY 1963 GTAGACAGCTGTGAGAAACCAACAACCTTGGGCGAGGAGAGATACAGAGGGA 2022
Db 3080 GTGAGCCGCTGTGAGAAATGGGCAACAAGTGTGGCCGAGACCGCGTGGGCCAGGGC 3139
QY 2023 TGAATTAATGAGACTTCGAGCATGCTTCCCGCACTGTGTGCATATC 2082

Db 3140 TGAAGCTACAGCGCATGTGACAGACATCCAGCGCGCCGAAACCTTCGGCTGTGCTTAC 3199
QY 2083 CCGAAGGTGAGCATGTCATCAAGAGGCAACAGGACACAGGCTCGAGACTGTAGG 2142
Db 3200 CGCCTGTGATGAGCCACCAAGCGAGCAACGGGACACACCTTGTGAGCGGCTGGC 3259
QY 2143 ACCGTGTGTCTACGGGTATATGCTGAGCCGCTTACTGGGAGCAGCATGAAGCACTC 2202
Db 3260 ACCCTCTGGGCTACGGCTACAAATCGAGCTCTCTGACAGAGCCAGTCAAGTGGAG 3319
QY 2203 TTGTGGAAGGCTCAAAACAGAACAGACACTTCAGAAATACCGGCTGAGAAAGAC 2262
Db 3320 AACCAAGTCTGTTGTGACCGGGTGC-----GCATCTTCCGGGCAAGAAATCC 3367
QY 2263 TATGCGCTCAGCTCTGGGAATGTGATCTTGAAGTTTGAATCTTAAAGCTGACCTATG 2322
Db 3368 TATACAGTGCAGAGCGCGCGTGTGATCTTGAAGTTTGAAGAGTCAACACAGGAGATG 3427
QY 2323 AAGGTCTGGGGTCAACGCTGATATGAGCACAGAAATGATGCTGAGCAAGACGAGAC 2382
Db 3428 CGCGTGGCTGGGCGAGGCGCAGAGCTGAGGCTGATGTAGAGCTGGAGCTGACGAGCTG 3487
QY 2383 TCTTGGCATTTGATGTGTTAATATGAGAAAGTGTACAGCGGTAACTGATCTTTC 2442
Db 3488 GCTATGTCTTCAATGTGGCACCGCGCCAGCGCTGGCACTTGGG---CAGTAAACATTT 3544
QY 2443 GGCAAGCAATGGGCTGTTGTGATGAGTGGGGGTCTCTAGATCTCATGTATGAGAG 2502
Db 3545 GGGCGCCCTGAGCGGCGGAGATGTGTTGGCTGTATGATGACCTACAGAGAACCC 3604
QY 2503 ATTAATTTCTCATCAATGTGATGATGTGTGATGATGCTCTTGGCGAGAGATACGTTT 2562
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QY 2563 GCTGATGTCCG---GTTGACAACTTTGTATCAGCTTGCACACTTGTGTGGGCCAAAA 2619
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Db 3845 AAAGGCTTGGCCCAAGTTGAG 3865

Search completed: April 14, 2006, 22:12:28
Job time : 2303 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: Apr11 14, 2006, 13:55:27 ; Search time 14479.5 Seconds
(without alignments)
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Title: US-10-668-767-127_COPY_1000_4000

Perfect score: 3001
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba:*
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4: gb_om:*
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13: gb_vi:*
14: gb_hcg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1620.4	54.0	15606	6	COS94804 Sequence
2	1150	38.3	24236	6	COS94803 Sequence
3	1150	38.3	168601	2	AC007471 Drosophila
4	1150	38.3	271696	2	AB003835 Drosophila
5	1138	37.9	100002	14	AC020372 Drosophila
6	1127	37.6	25680	2	DR09YRH
7	819.4	27.3	16879	2	AB051576 Hemikent
8	674.2	22.5	15378	4	SSCRCRNA
9	674.2	22.5	15378	4	PIGRYRN
10	671.4	22.4	14904	9	AF295105 Mus muscu
11	671	22.4	15378	6	A26812 MH mutant p
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14	668	22.3	15378	6	AR270591 Sequence
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ALIGNMENTS

RESULT 1
LOCUS COS94804 15606 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 22562 from Patent WO0171042.
ACCESSION COS94804
VERSION COS94804.1 GI:41651849
KEYWORDS

SOURCE Drosophila sp.
ORGANISM Drosophila sp.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 Venter, J.C., Adams, M., Li, P.W. and Myers, E.W.

TITLE Detection kits, such as nucleic acid arrays, for detecting the expression of 10,000 or more Drosophila genes and uses thereof
JOURNAL Patent: WO 0171042-A 22562 27-SEP-2001;
PB Corporation (NY) (US)

FEATURES
Location/Qualifiers

source

1..15606
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ORIGIN

Query Match 54.0%; Score 1620.4; DB 6; Length 15606;
Best Local Similarity 71.5%; Pred. No. 0;
Matches 2147; Conservative 0; Mismatches 851; Indels 6; Gaps 1;

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61 ACTGCTGTGCTGCTCTTATATGCTTACGAAAGGAAGGAGGAGTGGTAAAGTA 120
997 ACTGCTGTGCTGCTCTTATATGCTTACGAAAGGAAGGAGGAGTGGTAAAGTA 1056
121 GAAGGAAGCAAGCATCTTCCAGAGGAGGCAAGATGAGCATGCGCTGACTTCC 180
1057 GAGGAGGAAGCAAGCATCTTCCAGAGGAGGCAAGATGAGCATGCGCTGACTTCC 1116

181 AGGTCAAGAGAGAAAGATCTAGACCTGCTGAGTTATCAGAAAGTGTCTTCCGTGTC 240
Db CGCTCCAGAGAGAGAGATCCAAAGACAGTCTGTCTATCTCCGACATGAGACAGCTCTTTC 1176
Qy 241 ACTAGTTTATCAATGATGTGGAACCTGACAAAGAAACCGTGTGATCTGATGTTCTTC 300
Db 1177 ACCAGTTTATTAACGCTTGAACACTGCAAGTAAATGCGGCACTCCATTTTCTTC 1236
Qy 301 GCGTCAGTGAACCTGAGGCGAGATGATGATGCTGAGATCTGATCAATCTACTTCGCA 360
Db 1237 CAAGAGTCAACCTCAACGAGATGATGATGCTTGAAGACTTATTAATGACTTTTCG 1296
Qy 361 CAGCCCGATGAGATATGAGACAGCAAGAAACAAATTCGCGGCACTCCGAAC 420
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LOCUS COS94803 24236 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 22561 from Patent WO0171042.
ACCESSION COS94803
VERSION COS94803.1 GI:41651848

KEYWORDS
SOURCE
ORGANISM
Drosophila sp.
Drosophila sp.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
AUTHORS
TITLE
JOURNAL
Venter, J.C., Adams, M., Li, P.W. and Wrege, E.W.
Detection of 10,000 or more Drosophila genes and uses thereof
Patent: WO 0171042-A 22561 27-SEP-2001,
PE Corporation (NY) (US)
Location/Qualifiers

FEATURES
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ORIGIN

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QY 302 GGTCAATGAG 361
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QY 379 -----GAG 422
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RESULT 3
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 DEFINITION
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 BACR02C22, complete sequence.
 AC007471
 VERSION
 AC007471.4 GI:13129409
 KEYWORDS
 HTG.
 ORGANISM
 Drosophila melanogaster (fruit fly)
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
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 1 (bases 1 to 168601)
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 Unpublished
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 Rubin,G.M.

TITLE Direct Submission
JOURNAL Submitted (05-MAY-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Feb 27, 2001 this sequence version replaced gi:5670626.
COMMENT Sequence submitted by:
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720

This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive web site (<http://www.fruitfly.org/sequence/>) or send email to hdg@fruitfly.berkeley.edu.

FEATURES

Location/Qualifiers
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/mol_type="genomic DNA"
/strain="Y; cn bw sp"
/db_xref="taxon:7227"
/map="44F-45A"
/clone="BACR02C23 (D582)"
/clone_1b="RPCT-98 (Rowell) Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
pBAC3.6")

ORIGIN

Query Match 38.3%; Score 1150; DB 2; Length 168601;
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Matches 1749; Conservative 0; Mismatches 660; Indels 173; Gaps 3;

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Oy 61 ACTGCGTTGTGCTGCTTATTAAGTCTTACGAAACGAAAGAGAGAGTGGTAAAGTA 120
Db 60992 ACTAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 61051
Oy 121 GAAGAGAGAGAGAGAGAGATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db 61052 GAAGAGAGAGAGAGAGAGATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 61111
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Oy 241 ACTAAGTTA----- 250
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Oy 483 CAACGTCATCGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 542

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RESULT 4
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DEFINITION Drosophila melanogaster chromosome 2R, section 15 of 74 of the
complete sequence.
ACCESSION AE003835 AE002787 AE013599
VERSION AE003835.4 GI:23240369
KEYWORDS
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster

REFERENCE
AUTHORS

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pelegrinota;
Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 271696)
Adams,M.D., Celniker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D.,
Amanatides,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Galle,R.F.,
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Sutton,G.G., Wortman,J.R., Yandell,M.D., Zhang,Q., Chen,L.X.,
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Abbil,J.F., Aghayani,A., An,H.J., Andrews-Pfannkoch,C., Baldwin,D.,
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Burtis,K.C., Buam,D.A., Butler,H., Cadien,E., Center,A.,
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Dietz,S.M., Dodson,K., Doup,L.E., Downes,M., Dugan-Rocha,S.,
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Kravitz,S., Kulp,D., Lai,Z., Laeko,P., Lei,Y., Levitsky,A.A.,
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Science 287 (5461), 2185-2195 (2000)
10731132
TITLE
JOURNALS
PUBMED
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AUTHORS
2 (bases 1 to 271696)
Celniker,S.E., Wheeler,D.A., Kronmiller,B., Carlson,J.W.,
Halden,A., Patel,S., Adams,M., Champe,M., Dugan,S.P., Friese,E.,
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AUTHORS
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Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review
Genome Biol. 3 (12), RESEARCH0083 (2002)
12537572
TITLE
JOURNALS
PUBMED
REFERENCE
AUTHORS
4 (bases 1 to 271696)
Kaminker,J.S., Bergman,C.M., Kronmiller,B., Carlson,J.,
Svirskas,R., Patel,S., Friese,E., Wheeler,D.A., Lewis,S.B.,
Rubin,G.M., Ashburner,M. and Celniker,S.E.
The transposable elements of the Drosophila melanogaster

JOURNAL	euchromatin: a genomics perspective
PUBMED	Genome Biol. 3 (12), RESEARCH084 (2002)
AUTHORS	5 (bases 1 to 271696) Celniker,S., Carlson,J., Wan,K., Pfeiffer,B., Frise,E., George,R., Hoeklin,R., Stopleton,M., Patel,J., Park,S., Strychar,R., Smith,B., Yu,C. and Rubin,G.
CONSRMT	Berkeley Drosophila Genome Project
TITLE	Drosophila melanogaster release 4 sequence
REFERENCE	Unpublished
AUTHORS	6 (bases 1 to 271696)
JOURNAL	Adame,M.D., Celniker,S.E., Gbbbe,R.A., Rubin,G.M. and Venter,C.J.
REFERENCE	Direct Submission Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
AUTHORS	7 (bases 1 to 271696)
CONSRMT	FlyBase
TITLE	Direct Submission
JOURNAL	Submitted (22-JUL-2005) FlyBase, Harvard University, Biological Laboratories, 16 Divinity Ave, Cambridge, MA 02138, USA
COMMENT	On Sep 20, 2002 this sequence version replaced gi:2164554.
FEATURES	location/Qualifiers
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CDS	
gene	
mRNA	

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KEYWORDS HTG, HTGS_PHASE2
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ORGANISM Drosophila melanogaster
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 100002)
AUTHORS Adams, M. and Venter, J.C.
TITLE Direct Submission
JOURNAL Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
COMMENT This sequence was identified as CDM:10212949 by the submitter.
For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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Drosophila melanogaster
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (sites)
Takehima, H., Nishi, M., Iwabe, N., Miyata, T., Hosoya, T., Masai, I.
and Hotta, Y.
Isolation and characterization of a gene for a ryanodine
receptor/calcium release channel in Drosophila melanogaster
FEBS Lett. 337 (1), 81-87 (1994)
8276118
2 (bases 1 to 25680)
Takehima, H.
Unpublished
Submitted (09-Aug-1993) to DDBJ by:
Hitoshi Takehima
International Institute for
Advanced Studies
c/o Shimadzu Corporation N-80
1 Nishinokyo-Kuware-cho
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21592..21702,21760..22179,22248..22449,22513..25192) /note="p1-p8, p9, p10-p12, p13(12096-12248), p14-p26." /codon_start=1 /product="ryanodine receptor homologue" /protein_id="RAA04212.1" /db_xref="GI:2160478"	21592..21702,21760..22179,22248..22449,22513..25192) /note="p1-p8, p9, p10-p12, p13(12096-12248), p14-p26." /codon_start=1 /product="ryanodine receptor homologue" /protein_id="RAA04212.1" /db_xref="GI:2160478"
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Beet Local Similarity	67.7%; Pred. No. 1.5e-274;
Matches 1748; Conservative	0; Mismatches 660; Indels 175; Gaps 5;
QY	1 GTCTATGGCGGCCCATTCATCAATATGATGATCTCCACCCGTCATTTGCGACATTCGAG 60
DB	5255 GTGATCGGCTCGCGGATCATCAATATGATGATCTCCACCCGTCATTTGCGACATTCGAG 5314
QY	61 ACTGGCTTGCGCTGTCTTATAGCTTACGAAACGAAGAAGAGGAGTGGGTAAAGTA 120
DB	5315 ACTAGCTTGTGGCTCAGCTTACGAAGATTATAGACGAAAAAGAGGCGCTAGGAAGTG 5374
QY	121 GAAAGAAAGCAAGGATTTCTCACAAGGAAGGCAAGATGACGATGGCTTCGACTTCTC 180
DB	5375 GAGAGGAAGCAAGGATTTCTCACAAGGAAGGCAAGATGACGATTTGCTCGACTTCTCG 5434

QY 181 AGGTCAAGAGAGAGAAATCTAGGACTGCTGAGTTATCAGGAAGTGTCTTCGCTGTC 240
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RESULT 8
 SSCRNA 15253 bp mRNA linear MAM 17-FEB-1997
 LOCUS S.scirofa mRNA for calcium release channel (CRC).
 DEFINITION X62880
 ACCESSION X62880.1 GI:1936
 VERSION 1
 KEYWORDS calcium channel; CRC (Trp1) gene; ryanodine receptor; sarcoplasmic reticulum protein; transmembrane protein.
 SOURCE
 ORGANISM
 Sus scrofa (pig)
 Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buthera; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
 REFERENCE 1 (bases 1 to 15253)
 AUTHORS Harblitz,I., Kristensen,T., Bonnes,M., Kran,S. and Davies,W.
 TITLE DNA sequence of the skeletal muscle calcium release channel cDNA and verification of the Arg615---Cys615 mutation, associated with porcine malignant hyperthermia, in Norwegian Landrace pigs
 JOURNAL Anim. Genet. 23 (5), 395-402 (1992)
 PUBMED 1329581
 REFERENCE 2 (bases 1 to 15253)
 AUTHORS Harblitz,I.
 TITLE Direct Submission
 JOURNAL Submitted (28-OCT-1991) I. Harblitz, Norwegian College of Veterinary Medicine, Dept of Biochemistry, P.O. Box 8146 Dep, 0033 Oslo 1, NORWAY
 COMMENT
 FEATURES
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 Related sequence: M32501.
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1171 CGCTGTACGAGAGAGAGATCCAGAGCGGCCGCAATGATCTAAGACATGCTGAGCTCTAC 1230
241 ACTAAGTTATCAATGATGTCTGGAACCTCTACAGAGAAACCGTGTCACTGATGTTCT--- 297
1231 AACCACTTCAATCAAGAGGCTGAGACAGCTTCAAGCGAAGAACCGAGGCTCTGAGGACCCG 1290
298 ---TTGCGGTCAAGTAACCTGAGCGAGATGATGATGTGCTCTGAGAACTCTACATCACTAC 354
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DEFINITION AF295105
ACCESSION AF295105.1 GI:11321165
VERSION
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SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 14904)
AUTHORS Zhao, M., Li, P., Li, X., Zhang, L., Winkfein, R.J. and Chen, S.R.
TITLE Molecular identification of the ryanodine receptor pore-forming
segment
JOURNAL J. Biol. Chem. 274 (37), 25971-25974 (1999)
PUBMED 10473538
AUTHORS Chen, S.W.
TITLE Direct Submission
JOURNAL Submitted (10-AUG-2000) Physiology and Biophysics, University of
Calgary, 3330 Hospital drive N.W., Calgary, AB T2N 4N1, Canada
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 AUTHORS
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Best Local Similarity 55.6%; Pred. No. 8.7e-159;
Matches 1546; Conservative 0; Mismatches 1175; Indels 60; Gaps 11;
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OY 61 ACTGAGCTTGTGGCTGTCTTATTAAGCTTACGMAACGAAAGAAAGGAGTGGGTAAAGTA 120
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OY 241 ACTAAGTTTATCAATGTGTCTGMAACTCTCAAGAGAAACCGTCTCACTGATGTTTC--- 297
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Db		3262	ACCCTGCCTGGGGCTACCGGCTTACAACATCGAGCCGCCGACCAAGAGCCTCACAGTTGAG	3321
Oy		2203	TGTTTGGAAGCGGTCAAATAAGAAGCAAGACATTCAAGACATACCGGCTGAGAAAGAC	2262
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Query Match	22.4%	Score 671,	DB 6,	Length 15378,
Best Local Similarity	55.6%	Pred. No. 8.7e-159,		
Matches 1546; Conservative	0;	Mismatches 1175;	Indels 60;	Gaps 11,

QY 1 GTCATAGGCGCGCCCATCATCATATATGGTACTCCACCGTCATTTGTGCGAGATTTCCGAG 60
Db 1126 GGCATAGGCGCGCCCATCATCATATATGGTACTCCACCGTCATTTGTGCGAGATTTCCGAG 1185

OY	61	ACTGCGCTGTGGCTCTCTTTATTAAGTCTTATCGAAACGAAAGAGAGAGTGGGTAAAGTA	120
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OY	121	GAAGAGAAAGCAAGCGATCTCCACAGAGAAAGGACAGATGACAGTGGCCTCGACTTCTCC	180
Db	1243	CTCAAGAAAGAAAGCCATTCTGACCAAGAAAGGCCACATGAGCATGCACTGCACTGACC	1302
OY	181	AGGTCAACAGAGAAAGAACTTAGACCTGCTCGAGTTATCAGGAAGTGTTCCTTCGCTGTC	240
Db	1303	CGCTGTACAGAGAGAGATCCACAGCGCGCCGCAATCTATAGCACTGCGCCCTCTAC	1362
OY	241	ACTAAGTTTATCAATGATCTGGAACTGTACAAAGAAACCGTGTCACTCGATGTTCT---	297
Db	1363	AACCACTTCAATCAAGGCGCTGAGACGCTTCAAGCGAAAGCCAGGGGCTTGGGGCCCCG	1422
OY	238	---TTGCGGTCAAGTGAACCTGGGCGAGATGGTGTATGTGCTCGAGATCTCATCACTAC	354
Db	1423	GCTGGCAACAGGCTTACCCCTGAGGGCGGTCACTCTGAGCTGTGAGGACCTCATCGGCTTAC	1482
OY	335	TTTCGACAGCCCGATGAGATATGGAACAACGAAAGAAACAAACAAATTCCGGGCACTC	414
Db	1483	TTTGAAGCCGCCCTCGAAGAGCTGTGAGACAGAGAGAAAGACAGAGACCTGCGAGCTCG	1542
OY	415	CGAAACCGTCAAGACCTGTTCCAAAGAGAAAGCACTACTGAACCTGATCCTCGAAGCTAT	474
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OY	1015	ACTATGACCAACATAGAGAAAGAC---ACACATATGATGCAACATTAACGATAGATGG	1071
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 ORGANISM
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 Unclassified.
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 AUTHORS
 Au-Young, J. and Seilhamer, J. J.
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 Composition for the detection of signaling pathway gene expression
 JOURNAL
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ORIGIN

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2006, 13:59:54 ; Search time 11349.5 Seconds

(without alignment)
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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genomic survey sequence.
ACCESSION DQ052093
VERSION DQ052093.1 GI:66905537
KEYWORDS GSS.
SOURCE Homo sapiens (human)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 14832)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civeello,D.,
White,T.J., Sniensky,J.J., Adams,M.D. and Cargill,M.
White,T.J., Sniensky,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
JOURNAL PLOS Biol. 3 (6), E170 (2005)
PUBMED 15869325
AUTHORS 2 (bases 1 to 14832)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civeello,D.,
White,T.J., Sniensky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
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Matches 1423; Conservative 0; Mismatches 1298; Indels 60; Gaps 12;

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Homnidae; Pan.
REFERENCE 1 (bases 1 to 14736)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Clivello,D.,
White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
A scan for positively selected genes in the genomes of humans and
chimpanzees
(et) PLoS Biol. 3 (6), E170 (2005)
JOURNAL PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 14736)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Clivello,D.,
White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
TITLE JOURNAL
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them based on alignment. Translation starts at the beginning of alignment.
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Oy	1372	AGTAAGCTGAGTGTGGGTCCGTGCGGCGGAGAACACGGTGTCTCCGATACGGGCT	1431
Db	2080	GCTGTGTGACAGGTGGGTCTCTCTTGTGTGCGCGCATGTGAATTCAAAGTTCGTGCC	2139
Oy	1432	CCAGAAAGCTACTCTCCCTGTGTGAGTCTCTCTGCCGACAGAGATCTCAGCCTGAG	1491
Db	2140	CCACTGGCTATGTCTTCAGTGCATGAGGCTGTGCTCCTCGAGACGACCTCCATCTTGAA	2199
Oy	1492	CCGTGCTTCTACTTCGCGACCTGTCCAAGCGGG-----CCTTGGTGAACCTCCGCTA	1545
Db	2200	CCCATCAAGAGATATCGACGGGAGGGGCCCCGGGGCCTCACTGTGTGGGCCCCAGTGC	2255
Oy	1546	GTACAGACGATACGGCCTTGTGTGCTACACCTGTGTATCTTTACATTAATCTGTGCT	1605
Db	2260	TGCTCTGACACACCGACTGTGTGGCTGTGCCCTGTGTGACATGTTCMAATGTCTGTGCG	2319
Oy	1606	ACATATGTGGAACAATATTAGAGATAGCTAGCTGAATAATATACAGAAATGTGGCTATG	1665
Db	2320	CCCATCTGTGAGCGCATTCGGGAGAAAGCTGGCGGAGAACATCTCAGCAGACTCTGGCGCTA	2379
Oy	1666	AATAAGATCGAAGCAGGCTGATGTACGGCGACAGAGAGAAAGCTTGCACAAAGTTCAC	1735
Db	2380	ACCCGCATCGAGCAGGGCTGAGCTACACGGCCCCGANNNNNNNNNNNNNNNNNNNNNNNN	2439
Oy	1726	CCGTGCTGTGCCCTTTCGAGGGACTCCCACTGTGTGAGAAACATACGACTACACTC	1785
Db	2440	NN	2499
Oy	1786	GCTGTGACAGACACTCAGACTATCTCTGGCTGTGGCTACTACATCAGCTT---AGATTAAG	1842
Db	2500	NN	2555
Oy	1843	CCTCAGACGCGATCCGACGTTGTCTGTCCCAACGAACTTTCAATCAAGTCCACACGGC	1902
Db	2560	AAGCGGAGGACAACTTGAAAGAAACAAACCTCCCAAGAGTATATGATGAGCAATGGG	2619
Oy	1903	TACAAAGCAGCACTGACTGTGAGTGTGTCACTTGACACCCAAAGATGATGAGCTA	1962

Db	2620	TACAAAGCCGGCTCCGCTGAGACTGTAGCAATGTGCGGCTGAAACACGGGCGAAGACACTG	26719
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Db	2680	GTGACCGCTCTGGGAGAAATGGGCAACACGTGTGGGCTCCGAGACCGGTGTGGCCAGGGC	2739
QY	2023	TGACCTTATGGACTTAAATGAGGACTCGGAGCATGCAATGCTTCCCGCACTGGTGCATAC	20828
Db	2740	TGAGACTACAGCGAGTGCAGACATCCCAAGCCGCGCCGAAACCTTCGGCTGTGCTTAC	27999
QY	2083	CCGAGGTTGACGATGCGCATCAAGAGGCCAACAGGACACAGCCTCGGAGACTGTGAGG	2142
Db	2800	CGCCTGCTGAGCAGAAAGCCACCAAGCGACAGAACCGGGACAGCTCTCGCAGGCGTGCGC	2859
QY	2143	ACCTGCTGTCTTACGGGTATATCTGGACCCGCTTACTGGGGAGCAGATGAAGCACTC	2202
Db	2860	ACCTCTCTGGGCTTACGGGTACACATGAGCTTCTTACCAAGGAGCCAGTCAAGTGGAG	2919
QY	2203	TTGTTGGAAGGCTGAAAACAGAAACAGACAGACTTCAGAACATACACGCGCTGAGAAAGAC	2262
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QY	2263	TATCCGCTGACCTCTGGGAAGTGTACTTGTGAGTTTGATCTTAAACGCTGACCTATG	2322
Db	2968	TATACAGTGCAGAGCGGCGCGCTGGTACTGTGAGTTTGAAGACATCAACAAGGAGATG	3027
QY	2323	AGGCTCGGCTTGGGCTCACGCTGATATGCGACACAGAAATGATGCTTCGACAGACAGAAC	2382
Db	3028	CGAGTGGGCTTGGGCGAGGCGCCGACCTAGGCTGTATGATGAGCTGGGAGCTGACGAGCTG	3087
QY	2383	TCTTGGGCAATTGATGTTTACATGATGAGGAAABAAAGTATACAGCGGTAAACATGACTTTTC	2442
Db	3088	GCTATGCTTCAATGAGGACCGAGGCGACGCGCTGGCACTTGGG---CAGTGAACATTT	3144
QY	2443	GGCAAGCAATGGGCTGTGTGTGACGTAGTGGGGGTGTTCTTGAATCTCATTTGATTAAGCG	2502
Db	3145	GGGCGGCGCTTGGCAGCGGGCGAGTGTGTGGCTGTATGATGACCTTACAGAGAACCC	3204
QY	2503	ATTAAGTTTCTCACTCAATGCTGATGTTGTATGATGATGCTTGGCGGAGACATACGTTT	2562
Db	3205	ATTATCTTCAACCTCAATGCGGAGAGTCTCATGTCTGACTCAGGCTCCGAACAGCCTTC	3264
QY	2563	GCTATGTCAG---GCTGACAACTTTGTACCACTTGCACACTTGGTGTGGGCGAABAA	2619
Db	3265	CGGAGATGATGATTTGGGAGCGGCTTCCTGCGCCCTGACACTTGGGACCTGGCGAAGTG	3324
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Db	3385	CAGGAAAGCTTCGAGCCATTTTGCATCAATGACAGCGCCAGTACACACTGTGTTGAC	3444
QY	2740	AAGGACCAAGCCGATCTTCGAG	2760
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LOCUS D0034793			
DEFINITION Homo sapiens RYR3 gene, VIRTUAL TRANSCRIPT, partial sequence,			
ACCESSION D0034793			
VERSION D0034793.1			
KEYWORDS GI:66886002			
SOURCE GSS.			
ORGANISM Homo sapiens (human)			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
Hominidae; Homo.			
REFERENCE			
1 (bases 1 to 9562)			

AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civeello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees

JOURNAL (et) PLoS Biol. 3 (6), E170 (2005)

PUBMED 15869325

REFERENCE 2 (bases 1 to 9562)

AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civeello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.

FEATURES

source 1..9562

organism="Homo sapiens"

molecule="genomic DNA"

db_xref="taxon:9606"

chromosome="15"

gene <1..>9562

locus_tag="HC4229"

ORIGIN

Query Match 16.7%; Score 501.8; DB 11; Length 9562;

Best Local Similarity 51.1%; Pred. No. 4,1e-135;

Matches 1484; Conservative 0; Mismatches 1248; Indels 171; Gaps 12;

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427 GGCATGGAGATTCGAAATCAATGATGAGATTCGTCTGCTTTGTGACGATATAGCC 486

61 ACTGCTGTGCTGCTCTTATATGCTTATCGAAACGAAAGAGAGAGTGGTAAAGTA 120

487 AGTGTCTGTGGGTACCTACAAAGACACAGACGCAAACTCCGCGTGGACCTGTA 546

121 GAGAGAGACGATCTCTCAAGAGAGGCAAGATGAGAGTGGCTGACCTTCTCC 180

547 AAAAGAAAAG--GTCTATCTCATCAGAGAGGCGCATGATGATGATTAACACTGCA 603

181 AGGTCAAGAGAGAGATCTAGAGCTGCTGAGTTATCAGAGATGTTCTTGGCTTTC 240

604 AGATCCAGCGTGAAGAGTCCAGGCTGCTCGATCATCCGAAACATACAGCTTATTC 663

241 ACTAAGTTTATCAATGCTGTGAAACTCTACAGAGAACCGTCTCACTGATGTTCTTC 300

664 AGCCAGTTTGTCAAGTGAACA-----TGGACAGCTGCCCC 702

301 GCGTCAAGTGAACCTGGGCGAGATGATGATGCTGCGAGATCTCATCACTTCCGA 360

703 ATCAACCTGCTATGAAAGATCTCGCAGACCTTACAGACTTATGCTTATCCAG 762

361 CAGCCCGATGAGATGAGACAGAGAAACAAACAAATTCGCGGACCTCCGAAAC 420

763 CCCCAGAGAGAGATGAGATGAGACAGAGAAACAAACCTCCGCTCACTCAAAAAC 822

421 CGTCAAGAGCTGTTCCAGAGAGAGCATATGAACTGATCCTCGAAGCTTATAGAAC 480

823 AGACAAATCTTTTCAAGAGAGAGAGATGTTGGCTTGTCTTAAATTTGACCGC 882

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1894 CCAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1953

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Db 2194 GAGAAAGACTATTAACCTGCAATGTCACACTGAAACCTTAAA----- 2234
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Db 2235 ----- 2234
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Db 2235 --CTATATGATGTCCAGCGCTATAGCCAGCCCTTGGATTTGTCTGATGTGAAGTGT 2292
Qy 1942 AACCCAAAGATGATGAGCTATGATGACCAAGCTGCTGAAACACCACACACTTTGCGCC 2001
Db 2293 TTACTCTCTCAAGAAATTTTGTGATTAAGCTTCGAGAAATGCAACAATGTTTGGGCA 2352
Qy 2002 AGGAGAGATACGACGAGGATGACCTTATGGAAGCTTATGAGGACTCGGACATGATGAT 2061
Db 2353 AAGGACAGATTAAGCAAGATGACCTATGACATCCACAGATTTGAAAGCAAAAGA 2412
Qy 2062 TCCCGCAGCTGTGTCATACCCGAGGTGACATGATCCATCAAGAGCCCAACGAGGAC 2121
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LOCUS
DEFINITION
Pan troglodytes RYR3 gene, VIRUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
D0034794
VERSION
D0034794.1 GI:66866003
KEYWORDS
GSS.
SOURCE
Pan troglodytes (chimpanzee)
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Pan.
REFERENCE
1. (bases 1 to 9526)
Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civejlo, D.,
White, T.J., Snihsny, J.J., Adams, M.D. and Cargill, M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
(er) Plos Biol. 3 (6), E170 (2005)
JOURNAL
PUBMED
15869325
REFERENCE
2. (bases 1 to 9526)
Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civejlo, D.,
White, T.J., Snihsny, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
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Qy 61 ACTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 451 AGTGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 510
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Qy 181 AGGTCAAGAGAGAAAGATTTAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
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RESULT 5
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melanogaster cDNA clone EK253833 5, mRNA sequence.
ACCESSION CO307176
VERSION CO307176.1 GI:49229019
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 438)
Kopczynski, C., Platt, D., Campbell, J., Muzong, C., Laufer, A.,
Peterson, E. and Swimmer, C.
Exelixis FlyTag EST Project CK01 Library
Unpublished (2004)
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu
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/db_xref="taxon:7227"
/clone="EK253833"
/clone_lib="Exelixis FlyTag CK01 pCDNA-SK+"
/note="Organ: mixed stage embryos, imaginal disks, and
adult heads; Vector: pCDNA-SK+; Site_1: NotI; Site_2:
XhoI; Random primed, normalized library from mixed stage
embryos, imaginal disks, and adult heads."

ORIGIN

Query Match 9 0% Score 270.8; DB 7; Length 438;
Best Local Similarity 77.6%; Pred. No. 1,4e-67;
Matches 340; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

QY 472 ATAGACAGATCAAGTCACTACGTCACAGGGGTTCTCGCTGATCTCTGGCGGAGAC 531
DB 1 ATTGACCAAGTCAACATATACCTCGCAGGGCTTCCTAGCCAGCTTCTGGCGGAGAC 60
QY 532 GAATCTGACAGAGCTGGGAAATGATATCTGATATTTGTATCAATGCTCGCGGCAATA 591

DB 61 GAGACCGCCAGAGACTGGGAGTCTATCTCAACCTATTTGTACCAACTTTGGCCGCCATTC 120
QY 592 ATAAAGGCAACACACAGAACTGGCGGCAAGTTTCGCAACTGAACCGGCTCAACT-66CT 650
DB 121 ATCAAGGCAACACACAGAACTGGCGGCAAGTTTCGCAACTGAACCGGCTCAACT-180
QY 651 GTTCTCGGCTCGGCTCGCAAGGCTCGGCGGAGGAGCCGCGATGTCTGACGTCGCA 710
DB 181 ATTCTCCGCTCGGTTCCGAGGCTCGAGGAGGTTCCGCGATGTGTGACGTACTTCA 240
QY 711 CTGGGTCTTATACCTGCTGAAAGCTCTCAATATATGAGGAGCAACATATAAGT 770
DB 241 CTGGGTCTTATACCTGCTGAAAGCTCTCAATATATGAGGAGCAACATATAAGT 300
QY 771 GATATCTCTCTATTAAGAAAGCATGGGCGGAGCCCTAAAGTACTAGATGTCTATGTC 830
DB 301 GATCATCTCTCTGCTGAGAGAGACGCGAGAGGACCCGAAAGTCTTAACGTTCTGTGTC 360
QY 831 GCTGTGGCTCGGTAAACGCGCTCGGCTGCTCTCAAGAAACAATCTGTGACTACTT 890
DB 361 CTGTGGGTGGGTATATGAGATGGCGGTGCGATCTCTCCAGAAACAATTTGCACTTTT 420
QY 891 ACTGCGCGCAAGACT 908
DB 421 GCTACCGGCAAGATCT 438

RESULT 6
LOCUS B1510684 506 bp mRNA linear EST 08-APR-2002
DEFINITION B160003A20A12.5 Bee Brain Normalized Library. Bb16 Apis mellifera
cDNA clone B160003A20A12 5', mRNA sequence.
ACCESSION B1510684
VERSION B1510684.1 GI:15361058
KEYWORDS EST.
SOURCE Apis mellifera (honey bee)
ORGANISM Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
Apoidea; Apis.
1 (bases 1 to 506)
Whitfield, C.W., Band, M.R., Bonaldo, M.F., Kumar, C.G., Liu, L.,
Pardinas, J., Robertson, H.M., Soares, B. and Robinson, G.B.
Annotated expressed sequence tags and cDNA microarrays for studies
of brain and behavior in the honey bee
Genome Res. 12 (4), 555-566 (2002)
Contact: Gene E. Robinson
Department of Entomology
University of Illinois
505 S. Goodwin Ave., Urbana, IL 61801, USA
Tel: 217 265 0309
Fax: 217 244 3499

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
PUBMED
11932240
Contact: Gene E. Robinson
Department of Entomology
University of Illinois
505 S. Goodwin Ave., Urbana, IL 61801, USA
Tel: 217 265 0309
Fax: 217 244 3499
Email: gene@life.uiuc.edu
This research was funded by the University of Illinois Critical
Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
Award in Functional Genomics to G.B. Robinson and an NSF
Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
PCR Primers
FORWARD: TAAATGACCTCACTATAGG
BACKWARD: ATTAACCTCACTAAG
Plate: B160003A20 row: A column: 12
Seq primer: AGCGATACAAATTCACACAGGA
High quality sequence stop: 506.
Location/Qualifiers
1..506
/organism="Apis mellifera"
/mol_type="mRNA"
/strain="mixed strains of European bees, predominantly
A.m. ligustica"
/db_xref="taxon:7460"
/clone="B160003A20A12"

FEATURES

source

/sex="female"
/tissue_type="brain"
/dev_stage="adult worker honey bee"
/lab_host="DH108"
/clone_lib="Bee Brain Normalized Library, BBl6"
/note="Organ: brain; Vector: pT73-Pac; Site_1: EcORI;
Site_2: NotI; The BBl6 library was constructed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806. RNA was
prepared from dissected brains of adult worker bees of
various ages and various behavioral groups."

ORIGIN

Query Match 8.3%; Score 249.8; DB 3; Length 506;
Best Local Similarity 69.5%; Pred. No. 2.2e-61;
Matches 354; Conservative 0; Mismatches 152; Indels 3; Gaps 1;

1165 GGCGCTACCTCTGGTCCGGGGGAGAAAGTCCCGTCAATAGACTCATAGCTGAAAG 1224
1 GCGCGCTATCTGTGACGGGCGGTGAAAGACCAAGT---TGTCCAAAGTGAAGG 57

1225 CCTTATATTGAAAGAGTGAAGTGAAGTGGTGGCATTTGACCTGACGGTACCTAATC 1284
58 CCTTACATCAGGAAAGCGATCGGTGCGGTGGATCTCAGCATACCCATTAATC 117

1285 AACTCATGTTCAAGGAGTGGGGTGAACGGATCTTCAACCACTTCATCTGGAAGGC 1344
118 AGGTTCACCTTCAAGGAGCGGCCCATTTACAGGATGTTCCGAAATTTCACTGACGGA 177

1345 ATGTTCTTCCGGGATCATAGCTGTCTAGTAACTGAATGTCGGTTCCTGTCGGCGGA 1404
178 ATGTTCTTCCGGGATCATAGCTGTCTAGTAACTGAATGTCGGTTCCTGTCGGCGGA 237

1405 GAACACGGTGTCTCCGGTACGGGCTCCAGAAAGCTACTCTCTGGTGAAGTCTCTC 1464
238 GACCAACGGCGGCTCAAGTTCCAACTCCGAAAGAAATCTCACCGTTGGTGAAGAGCTG 297

1465 CTGCGGACGAAATCTCAGCTGAGCGGTCTTCTAATTGGGAACTGTGCCAAGCGG 1524
238 CTACCCCAACAAATTTTGTCTCTGATCCGTCTTCTACTTGGGAACTGAACAAAGTG 357

1525 GCGTTGGCTGAGACTCCGCTAGTACAGAGAGATTAAGCGCTTGTGCTACCTGTTGAT 1584
358 GTGCTGGCGCGCCCTCTGGTGTGAGAGACGACGCGCTTGTGCTGCGGCGCGGTGAC 417

1585 ACTTACAGATTACTGTGCTTCAATATGTGAACAAATTAAGATTAAGTGAAGTGAAT 1644
418 ACTTCCATGATCAATCTGCGTCTTACGTGAGCAAAATCAGGGAAGAGTGGCGGAAAC 477

1645 ATACACGAATGTGGGCTATGAATAAGAT 1673
478 ATCCACGAGATGTGGGCAATGAACAAAT 506

DB

RESULT 7
DN394725 741 bp mRNA linear EST 07-MAR-2005
LOCUS DN394725
DEFINITION LIB934-059-B1-K1-All LIB934 Canis familiaris cDNA clone
CLN12937360, mRNA sequence.
ACCESSION DN394725
VERSION DN394725.1 GI:60575946
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
1 (bases 1 to 741)
REFERENCE 1 (bases 1 to 741)
AUTHORS Staten,N.R.
TITLE Direct Submission (Staten,N.R.)
JOURNAL Unpublished (2005)
COMMENT Contact: Nick Staten

Tel: 636 247 6855
Email: nicholas.r.staten@pfizer.com.
Location/Qualifiers
1..741
source

/organism="Canis familiaris"
/mol_type="mRNA"
/strain="Beagle"
/db_xref="taxon:9615"
/clone="CLN12937360"
/tissue_type="brain"
/lab_host="DH108"
/clone_lib="LIB934"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; brain
from normal dog"

ORIGIN

Query Match 7.3%; Score 220.2; DB 8; Length 741;
Best Local Similarity 58.6%; Pred. No. 1.3e-52;
Matches 422; Conservative 0; Mismatches 289; Indels 9; Gaps 2;

777 CTCTTATTGAAAGCATGGGCGGACCTTAAGTACTAGATGTGCTATGTCGCTGTG 836
22 CTCCTCTGGAACAAGCATGGGAGAAACCAAGTGTGACGTCGTGTTCCTGTG 81

837 CGTCGGTAAACGCGTGGCGGTGCGCTGCTCAAGAACAACTGTGAATTAATCTTACTGCC 896
82 TGTGTGAATGTGTGGCGGTGGCGCTCCAAACCAAGATCTCATTAAGAACTTGTCTCC 141

897 CGGCAAGAACTGTGTGCTGCAAACTGGCGTGTGTGATCACTATCTAGTGTCCGCA 956
142 TGGCGGTGAGCTTGTGCTGCAAAACCTATCAATATGTCAACAGATCCGCCCA 201

957 CATCTGTGGGTGAGTGAAGAAAGGTGGCGAGTGAACGCAATGTACTTCAGAGTAC 1016
202 CATCTTGTGGCGGAGAGAGGCTCCAGCAATAGGCAAAATGTACTTGAAGTAT 261

1017 TATGACCAATAGAGAGAC---ACAATATGATGACATATACGATAGATGGGC 1073
262 GTTGAAGAGGTGGTCCATTCCTGACAGTCAAGGCCACCCACTGGCGGTGGCTGGGC 321

1074 CAACATAGTGTATGTCCATACCGGGGGGTGGCGAAGAAATGGGAGTAAACGGGT 1133
322 CCTCATGAGGGCTACAGCCCTTACCGAGGGGGCGGCGAGGGCGGCAATGGGT 381

1134 GGGAGATGACCTGACTGCTGACGGGTGACAGCGGCTTACTCTGTGTCGGGGGAGGAA 1193
382 CGGCGACGACCTTATTTCTACGGCTTTGATGGGCTGATCTTGGACAGACACGTGGC 441

1194 GACTCCGCTCAATAGACCTCATGTGTAAGACCTTATATTGAAAGGTGAAGTATAGG 1253
442 AAGCTGTG-----GACTTCCCAAGACAGACACTCTGACCCTGAGAGCGTCAAG 495

1254 TTGGGCAATGACCTGACGATACCCATATCACTTCAATGTTCAACGAGATGCGGTGAC 1313
496 CTGCTGCTGGAACCTCAGGTATCCGTCCATCTCTTCCGACATCAATGCTGTCTGTGCA 555

1314 GGATCTCTTCAACAACTTCAATCTGGAAGGAGATGTTCTTCCGGGATCAGCTGCTAG 1373
556 GGGGTCTTTGAGGCTTCAACCTGGAAGGAGCTTCTTCTCTGTGTGACCTTCTGACG 615

1374 TAACTGAGTGTGCGTCTGCTGGGCGGAGAACACCGGTGATCTCCGGTACCGGCTCC 1433
616 TGTGTCAAGGTGGCGTCTCTCTTGTGGGCGGCAATGTGAATTAAGTTCTCTCCCTCC 675

1434 AGAAGCTTACTCTCTCTTGTGAGTCTCTCTGCGGACGAGATCTCAAGCTGAGACC 1493
676 AACTGATATGATCCCATATGATGAGGCTGTCTCTCTGAGAGACGACTTCACTGAGACC 735

DB

RESULT 8
BB619828 686 bp mRNA linear EST 26-OCT-2001
LOCUS BB619828
DEFINITION BB619828 RIKEN full-length enriched, adult male thymus Mus musculus

LOCUS	AL919721	523 bp	mRNA	linear	EST 06-JUL-2006
DEFINITION	AL919721	PUR-Z1+z2	Danio rerio cDNA	clone 067-G09-2,	mRNA sequence
ACCESSION	AL919721				
VERSION	AL919721.1	GI:23185019			
KEYWORDS	EST.				
SOURCE	Danio rerio (zebrafish)				
ORGANISM	Danio rerio				
REFERENCE	Bukacynska; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.				
AUTHORS	Lo,J., Lee,S., Xu,M., Liu,F., Ruan,H., Eun,A., He,Y., Ma,W., Wang,W., Wen,Z. and Peng,U.				
TITLE	15000 unique zebrafish EST clusters and their future use in microarray for profiling gene expression patterns during embryogenesis				
JOURNAL	Genome Res. 13 (3), 455-466 (2003)				
PUBMED	12618376				
COMMENT	Contact: Peng J Lab of Functional Genomics Institute of Molecular and Cell Biology 30 Medical Drive, Singapore, 117609, Singapore Email: pengj@imcb.a-star.edu.sg Clone requests: info@openbiosystems.com Open Biosystems, 6705 Odysseey Drive, Huntsville, AL 35806. Location/Qualifiers				
FEATURES	source	1..523			
	/organism="Danio rerio"				
	/mol_type="mRNA"				
	/strain="local wildtype"				
	/db_xref="taxon:7955"				
	/clone="067-G09-2"				
	/tissue_type="whole embryo or fish"				
	/dev_stage="mixed stages"				
	/clone_idb="PUR-Z1+z2"				
ORIGIN					
Query Match	6.5%; Score 194.2; DB 1; Length 523;				
Best Local Similarity	63.7%; Pred. NO. 5.2e-45;				
Matches 328; Conservative	0; Mismatches 183; Indels 4; Gaps 2;				
Dn	651 GGCAATGCTCGACGCTCTGCACTGCGTCTTATAGCTCGCTGAAGCTCTCAATATGATG 750				
Dn	523 GGCAATTTTAAAGGTCTTCACATGATTCCTTAAACGAGTCCAGATCTCTGAACATCATTC 464				
Dn	751 AGGAGCGAACAACATAAAGTATATCTCTGATTAAGAAAAGCATGGGCGGACCTTAA 810				
Dn	463 CAGAGGCTCATCATTAATTCATTATTTCTCTGCTGATACAGACGGGCGCACTACAG 404				
Dn	811 GTACTAGATGTGCTATGTTCGTGTCGTCGCTGAACGGCGTCGCGTGCCTGTGCAG 870				
Dn	403 ATTCTGATGTTCTCTGTTCCCTTTGTGTGTGCAACGGGTATAGCTGTAGAGCAATCAG 344				
Dn	871 AACCAATCTGTGACTTACTTACTGCGCGGCAAGAACTGTGTGCTGCAACTGCGTCTG 930				
Dn	343 AATTTCATCTGTGACCACTGCTTCCAAAGAGAGACTGCTGCTTCAACAGACTGCTC 284				
Dn	931 GATCAGATCTAGTGTGTCGTCGCGCAACATCTTCGTGGGTCCAGATGAAAGGTCCGCA 990				
Dn	283 AGTAGTGTCCAAAGTATAGACCCAAACATCTTCCTGGGCAATGAGTGAAGGCTCTGCA 224				
Dn	991 TACCGCAATGTGATCTTCGAGGTGACTATGACCAATAGAGAAAGACACATATGATG 1050				
Dn	223 TATAGGAATGTGATCTTCGGGTGATATCATCATTAAGTAGACCATTTGTATACAGTAG 164				
Dn	1051 CCA---CATCTACGATAGATGGGCGCAACACTACTGTTATATGTCCTATACCCGGGCGGT 1107				
Dn	163 CCCACTCACCTTCGGGTGGTGGCGGCGACCACTAAAGGCTAGCGCCCGTATTC--CGCGGT 105				

Oy	1108	GGCGAGAAATGGGGAAGGTAAACGGGTGGGAGAATACCTGTACTCTGTACGGGTTCAGACGC	1167
Dd	104	GGGAGGGCCTGGGAGCAACGCGTTCGGAGATATCTTTACTCTACGCTTTTGATGACC	45
Oy	1168	GCCTAACCTCTGTCGCCGGGGAGGAAGACTCCGCT	1202
Dd	44	CTCATCTGTGGGAGGGCGAATCCCGCGGCCGT	10
RESULT 11			
BB251214			
LOCUS			
DEFINITION	BB251214 RIKEN full-length enriched, 7 days neonate cerebellum Mus musculus cDNA clone A730045E16.3, similar to U50465 Orcokollagus cuticulus cardiac ryanodine receptor (Ryr-2) mRNA, mRNA sequence.		
ACCESSION	BB251214		
VERSION	BB251214.2	GI:16355849	
KEYWORDS	EST,		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 652) Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,U., Komoto,H., Kouda,M., Koya,S., Macnuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Saeki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sugabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toyota,T., Muramatsu,W. and Hayashizaki,Y. RIKEN Mouse ESTs (Arakawa,T., et al. 2001) Unpublished (2001)		
TITLE	On Jul 6, 2000 this sequence version replaced gi:8943960.		
JOURNAL	Contact: Yoshinobu Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Teurumi-Ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-9222 Fax: 81-45-503-9216		
COMMENT	Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Komoto,H., Okazaki,Y., Muramatsu,W. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujisake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matsuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Kita,A., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,W., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Kono H., Fukunishi,Y., Shihata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanake,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y. Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp/) for further details. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. location/Qualifiers 1..652		
FEATURES			
SOURCE			

Qy	424	CAGGACCTGTTTCCAGAGAGAAAGGCACTGAACCTGATTCCTCGAAGCTATAGACAAAGATC	483
Db	459	CAAGATCTTTTCCAGAGAAAGAGAAAGATTCTTAATATGATTTCTTGACACTATGCAAAATTC	518
Qy	484	AACGTCATCAGCTCCACAGGGGTTCTCGCTGGAATTCGCGCGGAGACGAATCTGACAG	543
Db	519	TCTCAATATGAGAGCGCTTCTGATTTTCGCTGATTAAT---CGGAGAAAGACTCATGNG	575
Qy	544	AGCTGGGAAATGATATCTGATATTTTGATTCAGTTGCTGGCGGCAATATTAAGGCAAC	603
Db	576	AAATGGGAGCAGATCTCTATCTGATCTTTTGATGCTGATGATTAAGGAAAT	635
Qy	604	CACACGAACTGGCGGCGAGTTGCG	626
Db	636	CATTATATTTGTCCTCAATTTGC	658
RESULT 13			
LOCUS	BJ104437	610 bp	mRNA linear EST 18-JAN-2002
DEFINITION	BJ104437 unpublished oligo-capped cDNA library, C. elegans l1 stage.		
ACCESSION	BJ104437		
VERSION	BJ104437.1	GI:18247107	
KEYWORDS	EST.		
SOURCE	Caenorhabditis elegans		
ORGANISM	Caenorhabditis elegans		
REFERENCE	A complementary view of the C. elegans genome		
AUTHORS	Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y. and Sugano, S.		
TITLE	Unpublished (2002)		
JOURNAL	Contact: Tadasu Shin-I		
COMMENT	Center For Genetic Resource Information		
	National Institute of Genetics		
	1111 Yatae, Mishima, Shizuoka 411-8540, Japan		
	Tel: 81-559-81-6856		
	Fax: 81-559-81-6855		
	Email: tshini@genes.nig.ac.jp.		
FEATURES	Location/Qualifiers		
SOURCE	1. 610		
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	/sex="hermaphrodite"		
	/tissue_type="whole animal"		
	/dev_stage="L1"		
	/clone_lib="unpublished oligo-capped cDNA library, C. elegans l1 stage"		
ORIGIN			
Query Match	6.2%	Score 186.2;	DB 3; Length 610;
Best Local Similarity	57.8%;	Pred. No. 1.3e-42;	
Matches	351;	Conservative 0;	Mismatches 253; Indels 3; Gaps 1;
Qy	14	CCATCATCAATATATGTGTGATCTCCACCGTCATTTGTGCACATTCGAGCTGGCTTGTGC	73
Db	7	CTACATATAGATATGAGAGAGCAATATGCTTTTATTCACACGTGAAACTCAGCTGTGT	66
Qy	74	TGTCCTTATTAAGCTTATACGAAACGAAAGAGAGAGGAGTGGTAAATGATGAAGAAACAAG	133
Db	67	TGTCTCTATCAAAACAATGATAGTTACAAAGAAAGAAAGACTTGGAAGGTGAAAGAGAAAGAG	126
Qy	134	CGATTTCTCCACGAGAGAGCAAGATGACGATGCGCTCGACTTCTCCAGGTCCACAGAGG	193
Db	127	CAGTTGCTCTGAAAGATGCGTCACATGATGATGACTGTTTACACTTTCTTTATGCGCTTAAAG	186
Qy	194	AAGAAATCTAGAGCTGCTCGAGTTATCAGAAAGTGTTCCTTCGCTGTTCCTAAAGTTATCA	253

Db	187	AAGATCCAAATCAGCTGAGTGCATTAGAAATGTTCAATCGGTTCTCAATAAATCTTGA	246
Oy	254	ATGCTTGGAAACCTCTACAAAGAAACCGTCCGTACTCGATGTTCTTCGGTCAATGAAC	313
Db	247	AAGAAATCGAATGCAATTGCAACTTGAAGGAAACCAATCAACGATTGGAAGAAGTGCATC	306
Oy	314	TGGCGAGATGATGATGTCCTCGAGAGATCATCAACTATTCGCACAGCCCGATGAGG	373
Db	307	TCAAATGAAGTTTAAATTTGATGGAAGATCTCATTTGAATCTTTTGACAACAACCAATGATG	366
Oy	374	ATATGAAACAGAAAGAAAAAACAATTCGGGCACTCCGAAACGCTCAGACCTGT	433
Db	367	AGCAAGACTTTGAGAGAAACAGAAATCACTTGAGAGCTCTTGATGTCGCAAGATCTTT	426
Oy	434	TCCAAAGGAAGGCATACTGAACTCGATCCCTGAACTATGACAAAGATCAACGTCA	493
Db	427	TCCAAAGAAAGGAGTTCTTAATATGATTTCTTGACATATGACAAATTTCTCAATAG	486
Oy	494	CGTCCCAAGGGGTTCCCTCGCTGATTCCTGGCGGAGACGAATCTGGAACAGACTGGGAA	553
Db	487	AGGGGCTTCCGATTTCCCTGGATTAA--CGAGAGAGAGCTCATGTGAATGGAGAC	543
Oy	554	TGATATTCGATATTTGTATCAATGTTCTGGCGGCATAATAAGGGCAACCAACGAAT	613
Db	544	AGATCTCACTTAATCTGTATCTTTTGGTAGCTGATATTAAGGAATCATTAAT	603
Oy	614	GGGGCA	620
Db	604	GTGCCCA	610

RESULT	14
BUSJ3121	
LOCUS	BUSJ3121
DEFINITION	692 bp mRNA linear EST 28-NOV-2001 603405553P1 CSECHN61 Gallus gallus CDNA clone CHEST309m9 5', mRNA sequence.
ACCESSION	BUSJ3121
VERSION	BUSJ3121.1 GI:25821122
KEYWORDS	EST.
SOURCE	Gallus gallus (chicken)
ORGANISM	Gallus gallus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
AUTHORS	Phasianinae; Gallus. 1 (bases 1 to 692)
TITLE	Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.
JOURNAL	Pong,M.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J. A Comprehensive Collection of Chicken cDNAs
COMMENT	Curr. Biol. 12 (22), 1965-1969 (2002) 12445392 Contact: Simon Hubbard Department of Biomolecular Sciences University of Manchester Institute of Science and Technology (UMIST) PO Box 88, Manchester, M60 1QD, UK Tel: 01612008930 Fax: 01612360409 Email: Simon.Hubbard@umist.ac.uk. Location/Qualifiers 1..692 /organism="Gallus gallus" /mol_type="mRNA" /strain="Compton Line 151" /db_xref="taxon:9031" /clone="CHEST309m9" /sex="Female" /dev_stage="adult" /lab_host="DH10B" /note="Organ: heart; Vector: pBluescript II KS(+); Site_1 EcoRI, Site_2 NotI. This normalized library was constructed from 1 million independent clones. CDNA synthesis was initiated using an oligo(dT) primer, using
FEATURES	
Source	

methyated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Query Match 6.2%; Score 186; DB 5; Length 692;
 Best Local Similarity 57.2%; Pred. No. 1.5e-42;
 Matches 380; Conservative 0; Mismatches 275; Indels 9; Gaps 2;

740 TCAATATGATGAGGAGCAACATMAAGATATCTCTATTAGAAAGCATGGGC 799
 22 TAAACATATTAGAGAGACATTTAATCATCATCTGCTTTGGACAACATGGAA 81
 800 GCGACCTTAAAGTACTAATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 859
 82 GAAACCATAGGTTTGGATGCTTATGCTTCTCTGCTGCTGCTGCTGCTGCTGCT 141
 860 GCTGCTGACAGAAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 919
 142 GCTGCTGACATCTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 201
 920 CTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 979
 202 CCGGCTTGTGACATGATGAGAGCATGCGACCTAATATTCTTGGAAATTAGTGAAG 261
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Db 676 TTGG 679

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 sequence.
 ACCESSION BU341628
 VERSION BU341628.1 GI:25849629
 KEYWORDS EST.

SOURCE

Gallus gallus (chicken)
 ORGANISM Gallus gallus

REFERENCE

1 (bases 1 to 777)
 Boardman, P.E., Sans-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.J., and Hubbard, S.J.

TITLE

A Comprehensive Collection of Chicken cDNAs

JOURNAL

Curr. Biol. 12 (22), 1965-1969 (2002)

COMMENT

Contact: Simon Hubbard
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 Tel: 0161208930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES

Location/Qualifiers

1..777

/organism="Gallus gallus"

/mol_type="mRNA"

/strain="White Leghorn, H1sex"

/db_xref="taxon:9031"

/clone="CHSST462f8"

/dev_stage="16 day embryo"

/lab_host="DH10B"

/clone_id="CSEQCHN67"

/note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
 EcoRI; Site_2: NotI; This normalized library was
 constructed from 1 million independent clones. cDNA
 synthesis was initiated using an oligo(dT) primer using
 methyated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was blunted, ligated to NotI adapters, digested with
 EcoRI, size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."

ORIGIN

Query Match 5.3%; Score 160; DB 5; Length 777;
 Best Local Similarity 55.2%; Pred. No. 7.1e-35;
 Matches 421; Conservative 0; Mismatches 325; Indels 16; Gaps 5;

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GenCore version 5.1.7
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Run on: April 14, 2006, 14:01:15 ; Search time 499.5 Seconds
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Scoring table: IDENTITY_NUC
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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	671	22.4	15378	3	US-08-785-420-1
2	668	22.3	4078	3	US-09-016-434-1154
3	597	19.9	15572	3	US-09-424-783-1
4	61.8	2.1	1050	2	US-08-480-481-4
5	60.2	2.0	1050	2	US-08-480-481-3
6	58	1.9	1598	3	US-08-785-420-3
7	46.2	1.5	900	2	US-08-480-481-6
8	43	1.4	7218	2	US-08-232-463-14
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20	36.4	1.2	650	3	US-09-533-553-306
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24	35.6	1.2	1398	3	US-09-252-991A-3757

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26	35.6	1.2	2490	3	US-10-104-047-65	Sequence 65, Appl
27	35.6	1.2	10528	3	US-09-902-540-945	Sequence 945, Appl
28	35.6	1.2	61913	3	US-09-949-016-15338	Sequence 15338, A
29	35.6	1.2	61922	3	US-09-949-016-11772	Sequence 11772, A
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ALIGNMENTS

RESULT 1
US-08-785-420-1
; Sequence 1, Application US/08785420
; Patent No. 6001976
; GENERAL INFORMATION:
; APPLICANT: MacLennan, David H
; APPLICANT: O'Brien, Peter J
; TITLE OF INVENTION: DIAGNOSIS FOR PORCINE MALIGNANT
; TITLE OF INVENTION: HYPERTHERMIA
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: P.O. Drawer 34009
; CITY: Charlotte,
; STATE: No. 6001976th Carolina 28234
; COUNTRY: U.S.A.
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,420
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,388
; FILING DATE:
; APPLICATION NUMBER: US 08/030,159
; FILING DATE: 15-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Layton, Jr., Samuel G.
; REGISTRATION NUMBER: 22807
; REFERENCE/DOCKET NUMBER: 3477-73
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 704-377-1561
; TELEFAX: 704-377-1561
; TELEX: 57-5102
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15378 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO

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; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: Porcine RYR1 Gene
; POSITION IN GENOME:
; UNITS: bp
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US-08-785-420-1

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QY	241	ACTAAGTTTATCAATGTGTCTGGAACTCTACAAAGAAACGGTGTCACTGATGTTCT---	297
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O	y	1015	ACTATGGAACCAATAGAGAAAGACC--ACACATATGATGCGACATCTACCGCATATGATGG	1071
D	b	2128	ATGTGTGACGAAAGTGGTTCCATTCTTGAGACAGCTCAAGGCCAACCACTCGCGGGTGGGCTGG	2187
O	y	1072	GCCAAACACTAGTGGTATATGTCCTCCATACCCGGGCGGTGGCAGAAATGGGGAGGTAAACGGC	1131
D	b	2188	GCCTTACCCGAAGGCTACAGCCCTTACCTCTGGGGGCGGCGAGAGGCTGGGGCGGCAACGGG	2247
O	y	1132	GTGGAGATGACCTGTATCTGTACGGGTTGACCGGCGCTTACCTTGTGTCGGGGGAGGG	1191
D	b	2248	GTGGGCGATGACCTTATTCCTTACGGCTTGAACGGGCTGCATCTGTGACAG-----GA	2301
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O	y	1252	GATTGGCGATTTGACCTGACGGTATACCAATATATCAATCTTATCTTCAACCGAGTGGCGGGT	1311
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O	y	1312	ACGGGATCTTTCACCACTTCAATCTGGAAGGATGTTCTTCCCGGTCAATCAAGTGTCT	1371
D	b	2422	CAGGGCGTCTTTCGAGGCTTCAACCTCAACGGGCTCTTCTCCCGGTGTCACGCTTCTCG	2481
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D	b	3022	TACAAGCAGCGCACTGACCTGAGACATGTGACATGACGCTGTGGCGAGACCAAGCTG	3081
O	y	1963	GTAAACCAAGTGGCTGAGAACCAACCAACCTTTGGGCCAGGGAGAGATACAGCAGGGA	2022
D	b	3082	GTGAACCGGTGGCGGAGAACGGGCAACAAGTGTGGGCCCGAACAAGAGTGGCCACGGGC	3141

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Oy	2680	CAGAGGGA	TATGAA	CCATTTT	GCTCAAT	TATGAA	GAGACGTG	CACTCATGTGATACCC 2739	
Db	3787	CAGGAAGG	TTTGAAC	CAATCG	CAATG	CAGAG	CGTCCG	CTCATTA	CGTGTTCAGC 3846
Oy	2740	AAGAGC	CAGCCG	ATCTT	CGAG	2760			
Db	3847	AAAAGC	CTTCCCA	CGATT	TGAG	3867			
RESULT 2									
US-09-016-434-1154									
Sequence 1154, Application US/09016434									
Patent No. 6500938									
GENERAL INFORMATION:									
APPLICANT: Janice Au-Young									
APPLICANT: Jeffrey J. Sellhamer									
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING									
TITLE OF INVENTION: PATHWAY GENE EXPRESSION									
NUMBER OF SEQUENCES: 1490									
CORRESPONDENCE ADDRESS:									
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.									
STREET: 3174 PORTER DRIVE									
CITY: PALO ALTO									
STATE: CALIFORNIA									
COUNTRY: USA									
ZIP: 94304									
COMPUTER READABLE FORM:									

```

? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/016,434
? FILING DATE: HEREMITH
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? CLASSIFICATION:
? ATTORNEY/AGENT INFORMATION:
? NAME: Zeller, Karen J.
? REGISTRATION NUMBER: 37,071
? REFERENCE/DOCKET NUMBER: PA-0002 US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (650) 855-0555
? TELEFAX: (650) 845-4166
? INFORMATION FOR SEQ ID NO: 1154:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 4078 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? LIBRARY: GENBANK
? CLONE: g1526977
? US-09-016-434-1154

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Query Match	22.3%	Score 668;	DB 3;	Length 4078;
Best Local Similarity	55.4%	Pred. No. 1.2e-184;		
Matches 1590;	Conservative 0;	Mismatches 1225;	Indels 57;	Gaps 13;

QY	1	GTCAATAGCGCGCCCATCATCAAAATATATGATGACCTACCGTCAATGTGCACATCTCCAG	60
Db	1163	GGCATTTGGGAACATCTGAAATTAATTAACGGTACCTCAGTACTATATACACATGTAGAC	1222
QY	61	ACTGGCTTGTGGCTGTCTTATATAGTCTTATCGAAACGAAGAAAGAGTGGTAAAGTA	120
Db	1223	ACAGGCCATATGGCTTATCTTACCAAGTCTGTGAGCGTGAATAACCGTGAAGATGGGATCTATA	1282
QY	121	GAAGAGAACGACGGATTTCTCCAGAGAAAGGCAGATGACGATGGCTTGACTTCTCC	180
Db	1283	CAAGCTAAG---GCTATATTATCATCATGAAAGCCACATGTGATGTGGCATTAAGTTTGTG	1339
QY	181	AGGTCCACGAGGAAGAACTTAAGACTGTGAGATTATCAGAAAGTGTCTTCCGTGCTTC	240
Db	1340	AGATTCACGACGTGAAGATTCACGCAACGCCGAGTATCCGAGACACAGTCTTCTTTTC	1399
QY	241	ACTAAGTTTATCAATATGCTCTGAAAACTTCAACAGAAACCGTCTGTCACTGATGTTCTTC	300
Db	1400	AATGATTTTATTAAGAGGGGCTTGATATGCTCTCAGCAAAAGAAAGGAGGCTTCCACAGTCAT	1455
QY	301	GGCTGACTGAACTGTGGGCGAGATGGTATGTGCTCCAGGATCTCATCACTTACCTTCGA	360
Db	1460	TTGCTTATAGAGTCCG-----TAAAGCTAAGTCTGCAGAGATCTCATTTGGCTACTTCCAC	1513
QY	361	CAGCCCGATGAGATATGGAACACGAAGAAACAAACAAATTCGGGGCACTCCGAAC	420
Db	1514	CCCCAGATGAGCAATTATGACATGAAACAAACGAACATACGAGCCCTGAAGAAAT	1573
QY	421	CGTCAGACCTGTTTCCAAGAGAAAGGCATCTGAACTGATCTTGAAGCTATAGACAAG	480
Db	1574	CGGCAAAATCTCTTCCAGGAAGAGGAATGATCAACCTCGTGTGATGTAGATAGACGCT	1633
QY	481	ATCAACGTCAACGTCCTCCAGGGGTTCTCGCTGGAATCTTGGCGGGAACGAATCTTGA	540
Db	1634	TTGCAACGCTCTACACAGTGCAGCACTTTGCTG---ATGTTGTGTGGCGAAGACAGA	1690
QY	541	CAGAGCTTGGGAAATGATATCTGGAATTTTGTATCAGTTGCTGGGGGCAATTAATAAGGGC	600
Db	1691	GAGTCTTGAATAATCCATTTCTGAATTTCTGTATGAGTGTGGCGGCTCTTAATTATGAGGA	1755

601 AACCAAGCACTGGCGGAGTTCCGGAATCGAACCGCTCAATGCGCTGTTCCGGC 660
Db 1751 AATCGTAAATCTGCTCAATTTCTGGCTC-----CCTGACCTGGTGTAT-----C 1798
Qy 661 CTGGGCTCGAGGCTCGGGCGAGGGCAACCGGATGCTCGAGCTGTGCACTGGGCTT 720
Db 1799 AGCAATTTGAAAAGACTGGAAGCTTCTTACGCAATTTGGAAGTTTATACCTGTGTTTA 1858
Qy 721 ATGAGCTGCGCTGAAGCTCTCAATATGATGAGGAGCAACATTAAGTGAATATCTT 780
Db 1859 GTAGAAAGTCCAGAGCTCTAATATATTAAGAAAGACATTTAAATCTATATCTCA 1918
Qy 781 CTATTTGAAAAGACTGAGGCGGCAACCTTAAGTACTAGATGCTATGTTCCGTGGCTC 840
Db 1919 CTTTATGACMAACATGGAAGAAATCAAGAGTTCTGGATGTCTTGCTGCTCACTGTGTAT 1978
Qy 841 GGTAAAGGCGTGGCGGCTGCTGCAAGAACATCTGTGACTATCTTACTGCGCGGC 900
Db 1979 TCCACGGGGTTGCAAGTCCGTTCTAACAGCACTCATCTGTGACAAATCTCTTACAGGA 2038
Qy 901 AAGAACTGTGCTGCAAACTGCGCTCGTGAATCAAGTATCTAATGTCCGTCGAATC 960
Db 2039 AGAGACTGTTATGCAAGCAAGTCTTGTGAACATGTGACAGATGAGACCAATATTT 2098
Qy 961 TTGCTGGGTCCAGTGAAGAGGTCGCGCAAGTACCCGAATGTACTTGAAGTGAATG 1020
Db 2099 TTTCTGGGGGTCAAGTGAAGGTTCTGCTCAGTATTAAGAAATGCTATGAATTAATGATG 2158
Qy 1021 GACCACTATGAG---AAGACCAACATATGATGCCATCTACGCAATGGAATGGGCAAC 1077
Db 2159 GACCAACAGAGCCCTTGTGTGACAGTGAAGCACTCACCTGCGAGTGGCTGGCTTCC 2218
Qy 1078 ACTACTGTTATGTCCTCAATACCGGGCGGTGGAGAAATGGGAGGTAAACGCGCTGGGA 1137
Db 2219 ACTGAAGGATATTTCCCTACCTGAGGGGGCGAAGATGGGGTGAATGTTGTGA 2278
Qy 1138 GATGACCTGTACTCGTACGGGTTGCAAGCGCGCTACTCTTGTGTCGGGGGAGAGAAACT 1197
Db 2279 GATGATCTCTTCTCTATGGAATTTGATGGCTTCACTCTGCTCAGTGTGATTTGCTGCT 2338
Qy 1198 CCGGCAATGAGCACTCATGCTGAAGAGCCTTATATTAGAAAGGTGAGCTGATGAGTTGC 1257
Db 2339 ACTGTAGCTACCAACC-----AATCTGTATTAAGATGATGATGTCACTGTTGC 2392
Qy 1258 GCATTTGACCTGACGGTACCCATTAATCAATTCATGTTCAACGAGTGGGGTGAACGGGA 1317
Db 2393 TGTTTAGATCTGAGGCCCAAGACATCGTTCGGAATTAAGCAACCTGTTCAAGGA 2452
Qy 1318 TCTTTCACCAACTTCAATCTGGAAGGCAATTTCTTCCGGTCAATGACTGCTCTAGTAA 1377
Db 2453 ATGTTTGAAGAAATTTCAACATCATGATGGCTTCTTCCAGTCCGTTAGTTTCTCTGCA 2512
Qy 1378 CTGAGTTGTGCGGTTCTGCTGGGGCGAAGAACAGCGTCCGTTACGGCGCTCAGAA 1437
Db 2513 ATTAAGTACGCTTTCTGCTTGAAGGCGACATGGAATTCAAATTTCTTCTCACCT 2572
Qy 1438 GGCATCTCTCCCTTGGTGAAGTCTCTCTGCGGACAGATCTTCAAGCTGGAAGCCGTC 1497
Db 2573 GGGTATGCTCCTTGTATGAGCTGTCTGCCAATAAGAAAGTTGAAGTGAACACAGC 2632
Qy 1498 -----TTCTACTTGGGCACTGTGTCACAGCGGGGCTTGGCTGCACTCCGTAATAC 1551
Db 2633 CGAGAGTCAAGCAAGAAAGAACTTAACAACGCGACCTGCTGGGGCCCAAGTTTCCCTG 2692
Qy 1552 GACGATACGGGCTTGTGCTACCTGTGTAATCTTTACAGATTAATCTGCTCAATAT 1611
Db 2693 AGCGAAGCTGCTTCAACCCATCTCTGTGATACAGCCAGATGTGTTGCTTCTCAT 2752
Qy 1612 GTGGAACAAATTAAGATGATGCTGAATAATATACAGAAATGTGGCTATGATTAAG 1671
Db 2753 CTAGAAAGATTAAGAAAGAAATGCGCAGAGATATTCATGAATCTGGGTTATGAATAA 2812
Qy 1672 ATCGAAGCAGGCTGATGTATCGGCGACCAAGAGAAAGCTTGCAAGATCCACCCCTGC 1731

2813 AATGAGCTTGGCTGCAATATGTCGCGTTAGATGACAAAGAGACCAACCCATGAC 2872
Qy 1732 CTGTCGCCCTTGAAGCACTCCCACTGCTGAGAAAGATACATACATCACTGCTGTG 1791
Db 2873 CTGGTGAAGTTCTCCAAAGCTGCTGGAACAGAGGCGCAATTAACATTAATGTGCTT 2932
Qy 1792 CAGACACTCAAGACTATCTTGGCTCTGGGCTACTAAT---CAGCTTATGATTAAGCTTCA 1848
Db 2933 GAGACCTGAAGACTTTGTTGGCATATGAGATGTCAATGGGATATATGATGAACATGCT 2992
Qy 1849 GCAGCACTCCGCAACGTTCCGTGCGCAAGAACCTTTATGCTGCTCAACGCTTACAG 1908
Db 2993 GAAGCAAGGTGAAGAAATGAAGCTAACCAAGATTAACAGCTGACAAAGTGAATACAG 3052
Qy 1909 CCAGACCAACTGACAGTGTGCTGACCCCTGACACCCAAATGATGATGATGATGATGAC 1968
Db 3053 CTTGCCCTTATGACCTGAGCTTATTAACATCAACCCCATGCGAAGAACATGTGAC 3112
Qy 1969 CAGCTGGCTGAAGAACCCCAACACTTTGGCGCAGGAGAGATACAGCAGGATGACT 2028
Db 3113 AAGTTGGCAAGAAATGACATTAATGTGTGGCGGGATCGAATCCGGCAGGGCTGACAT 3172
Qy 2029 TATGACCTTATGAGACTGCGAATATGATGCTTCCCGCACTGTGTGCCATACCCAG 2088
Db 3173 TATGCAATCCAAACAGAGCTTAAGAAACAGAAATCTTGCCTTGTCTTACATCTCT 3232
Qy 2089 GTTACAGATGCTCAAGAAAGGCCAAGGAGCAAGCCTGCGAGACTGTGAGGACCTTG 2148
Db 3233 CTGATATACCAACCAAGAAATCCAAAGAGCAGCTCCGCGAGGCTGTGCGACCTG 3292
Qy 2149 CTGCTTACCGGATATATGCTGAGCCGCTTACTGCGGAGCAGATGAAGCATCTTGTG 2208
Db 3293 CTGGGATACGGCTTCAACTTGAAGCAC-----AGATCAAGATCATGACGACAGACC 3346
Qy 2209 GAAAGCTTAAACAGAGCAAGCAAGCACTTCAAGACATACCGCGTGAAGAAATTAAGCC 2258
Db 3347 GAAATGTGACAGCGCACCGGGGAAAGGTTCCGAATCTTCCGTGCGAAGAACTTATGCA 3406
Qy 2269 GTCACTCTGAGAAAGTGTACTTCAAGTTTGAATCTTAACGGCTGACCTATGAGGATC 2328
Db 3407 GTGAAGCCCGGACCGTGTGATTTTGAATTTGAAGCGTCACTGCTGAGACATGAGGTT 3466
Qy 2329 GCGTGGCTCAAGCTGATATGCGACAGAAATGCTTGGGACAAAGCAGAACTTGTG 2388
Db 3467 GGTGAGATGCTGCTGTTGATCAACCGGATCAGAGGCTTGGCTCAATGAACGTGCTT 3526
Qy 2389 GCATTTGATGTTTCAATGAGAAAGGTGACAGCGGTAACTGAGTCTTTGGCAAG 2448
Db 3527 GCTTTTATGCTTCAAGGCGCCAGCGGTGCAATCAGGG---CAATGAACATATGCGCGC 3583
Qy 2449 CAATGGGCTGTGGTGAAGTATGAGGGGTTCTTATGATCTCAATGATTAAGACGATTAAG 2508
Db 3584 TCTTGGCAAGGCGAGATGTCGTGGGTGATATGTTGACATGAACGAACACATGATG 3643
Qy 2509 TTCTCACTCAATGTGAGTTGTGATGATGCTCTTGGCGAAGACTACGTTTGTGAT 2568
Db 3644 TTCACTGATGATGTAATCTTCTTATGATGATCAAGGCTCAGAACTGGCTTCAAGAC 3703
Qy 2569 GTCCAGGTTGCA---CTTGTACAGCTTGAACATTTGTGTGGGCGCAAAAAGCCAGG 2625
Db 3704 TTTGATGTTGGCGATGATTCATACCTGTGTGTAGCCTTGAAGTGGCTCAAGTGGTGG 3763
Qy 2626 TTAACATATGCGCAAGATGTAATATCTGAAATATCTTCAACAATGTGCTTCAAGAG 2685
Db 3764 ATGAATTTGAAAAGATGTCAGACCTTGAATATTTTCACTCTGTGCTTACAGAG 3823
Qy 2686 GGAATATGAACATTTTGGCTGCAATATGAGAGAGACGTGACTCATCTGTAACCAAGAC 2745
Db 3824 GGTATATGAACATTTGCGTTAATTAACAAGGGAATTAACATGTGGCTGAGCAAGAG 3883
Qy 2746 CAGCGATCTTCCAGAAATACTGATGAGATATGACACAGATTAATGTGATCCAGATA 2805

Db 2661 CCTAGAAAAGATCCGAGACAGACTAGCTGA AAAACATCCATGAGCTTTGGGGAATGAATA 2740
 Qy 1671 GATCGAAGCAGGCTGATGTAGTACGCGGACCAAGAGAGAAGACTTGCACAGATCCACCCCTG 1730
 Db 2741 AATAGAACTTGGCTGACCTTTCGGAAGATAGAGATGACATTAATAACAACACCCCTG 2800
 Qy 1731 CCTGTCCTTTCGAGCGACTCCACCTGCTGAGAAAGATACGACATACAACTCGCTGT 1790
 Db 2801 CCTGTGAGATTTCAGAACTCCCGAAGACTGAGAAAGATATTAACCTGCAAAATGTCAAC 2860
 Qy 1791 GAGAGCACTCAAGACTATCTCGGCTCTGCTGCTACTACATCACTGACTGATAAGC---CTCC 1847
 Db 2861 TGAACCTTAAACCTCTTGAACCTGAGTTGCCAATGCTCAATGTTAAACCCAGCTGC 2920
 Qy 1848 AGCAGCAGCTCCGCAAGCTTCTGCTGCCAAGAACCTTTCATGCACTGACCTCAACGCGTACAA 1907
 Db 2921 TGAGAGAGATCTCAAGAAAGTCAACCTGCCAAAACATATGATGATCCACGCGTATA 2980
 Qy 1908 GCCAGCAGCACTGCACTGAGTGTCTGCAACCTGACACCCGAAGATGATGAGTATGAGA 1967
 Db 2981 GCCAGCCCTTGTGATTTGTCTGATGTGAGCTGTTACTCTCCAGAAATTTTATGTGA 3040
 Qy 1968 CCAGCTGCTGAGAACACCCCAACCTTGGCCGAGAGAGATACAGCGAGATGAC 2027
 Db 3041 TAACTTGCAGAAATGACACAAATGTTGGCAAAAACAGAAATAAACAAGATGAC 3100
 Qy 2028 TTATGACTTATAGAGACTCGGACATGATGATCTCCCGACCTGCTGTCATACCCGAA 2087
 Db 3101 CTATGCACTCCACAGGATTTTGAAAGACAAAGAAATCCCGCTGTGCTGCTATGCAAT 3160
 Qy 2088 GGTGACGATGCCATCAAGAAAGCCACAGGACACAGCTTCGAGACTTGAAGACCT 2147
 Db 3161 ACTGATGAGGCTACCAAGAAATCAACAGGACAGCTGCGGAGCTGTCGCCACTTT 3220
 Qy 2148 GCTGCTCAAGGATATATCTGGAACCGCCCTACTGGGAGAGATGAAGACTCTGTT 2207
 Db 3221 TGTGTTTACGAGTATTAATTTGACCATCAACCAACAACTAGCTGCTGCTGGA 3280
 Qy 2208 GGAAGCGTCAAAACAGAACAGACAGACTTCAGAACATACCGCGCTGAGAAACTATGC 2267
 Db 3281 GAAGTCAAGATAGACAG-----ATCGATTTTCCGGGAGAGCATCTATCC 3331
 Qy 2268 GGTGACTCTGGGAAGTGTACTTGAAGTTGAGATCTTAAACGCTGACCTATGAGGT 2337
 Db 3332 AGTGAATCTGGAAGTGTATTTTGAAGTTGAAGTGTGACTGAGAGAGACATGCGAGT 3391
 Qy 2328 CGGCTGGCTCAACCTGATATGAGCAACAGAAATGATGCTCGGACAAAGCGAACTCTG 2387
 Db 3392 CGGCTGGCGAAGCCAGGCTGTCCAGCTGATGCTGAGCTGGGCGCCATGACCAAGCCTT 3451
 Qy 2388 GGCATTTGATGTTTACATAGAGAAAGATGTACAGCGGTAACTGAGTCTTTCGCAA 2447
 Db 3452 TGTGTTTGAAGGCAAGGGGCCAGCGCTGTGCAATCAAGGAAG---TGGGTATTTGGGCG 3508
 Qy 2448 GCAATGGGCTGTGTCAGTATGAGGAGTTCCTAGATCTCAATGATAAGCATGAG 2507
 Db 3509 TACCTGGCAGCAGGAGATGTCGATGATATTAACCTGATGATGCTTCAATGAT 3568
 Qy 2508 TTTCTCACTCAATGGTGTGATGATGATGCTCTTGGCGGAGAGACTAGTGTGCTGA 2567
 Db 3569 CTTCACATGAAATGGGAGCTGCTGATCAACAAAGGCTCTGAATCTTGCTTCGCTGA 3628
 Qy 2568 TGTCAGAGGTACAA---CTTGTACAGCTTGCACCTTGTGTGGCCAAAAGCAG 2624
 Db 3629 CTAGAGATTTGAGATGCTTCTGTCATCTGCTGTGGGTCTATCTCAGATCGGCG 3688
 Qy 2625 GTTAACTATGCGCAAGATGTGAATCTCTGAATACTTCAACAATGTGCTTTCAGGA 2684
 Db 3689 CATGAATCTCGGACAGATGCAAGTACTTCAAGTTTATACATATGTCGGTCTCCAGA 3748
 Qy 2685 GGGATATGAACATTTTGCCTCAATATGAAGAGACTGACTCACTGCTACACCAAGA 2744
 Db 3749 GGGCTTGAAGCTTTTCTCTCAACATGAACAGAGATGTCTATGTGCTTCAACCAAGCG 3808

Qy 2745 CCAGCCGATCTTCGAGATATCTGATGATGATGACACCGAGATTGATGTGACCAAGAT 2804
 Db 3809 CTTCCGACGTTTGTCA---CGGCCAAAGATATCAACATATAGGCTCATGAGAT 3865
 Qy 2805 ACCAGCTGTTCAATACCTTCATCTCCATGATTTCCCAACAACGTTTCAGACAT 2864
 Db 3866 TGATGGACCATGACAGCCCTCGTCTCAAGGTGACGATTAAGCAATTTGACACCA 3925
 Qy 2865 GGAGA 2869
 Db 3926 GAATA 3930
 RESULT 4
 US-08-480-481-4
 ; Sequence 4, Application US/08480481
 ; Patent No. 5639614
 ; GENERAL INFORMATION:
 ; APPLICANT: Sen, Luyi
 ; APPLICANT: Philipson, Kenneth D.
 ; APPLICANT: Luisis, Aldons J.
 ; TITLE OF INVENTION: GENE MUTATION IN PATIENTS WITH IDIOPATHIC DILATED CARD
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Knobbe, Martens, Olson & Bear
 ; STREET: 620 Newport Center Drive 16th Floor
 ; CITY: Newport Beach
 ; STATE: CA
 ; COUNTRY: U.S.A.
 ; ZIP: 92660
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/480,481
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Altman, Daniel E.
 ; REGISTRATION NUMBER: 34,115
 ; REFERENCE/DOCKET NUMBER: UCLA012.001A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 714-760-0404
 ; TELEFAX: 714-760-9502
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1050 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Genomic DNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE:
 ; ORIGINAL SOURCE:
 ; FEATURE:
 ; NAME/KEY: Other
 ; LOCATION: 380...380
 ; OTHER INFORMATION: Position distinguishes idiopathic
 ; OTHER INFORMATION: dilated cardiomyopathy
 ; NAME/KEY: Other
 ; LOCATION: 776...776
 ; OTHER INFORMATION: Position distinguishes idiopathic
 ; OTHER INFORMATION: dilated cardiomyopathy
 ; NAME/KEY: Other
 ; LOCATION: 1...1

OTHER INFORMATION: Position 1 corresponds to
OTHER INFORMATION: 7987 of the rabbit cDNA homolog
US-08-480-481-4

Query Match 2.1%; Score 61.8; DB 2; Length 1050;
Best Local Similarity 47.7%; Pred. No. 2.2e-07;
Matches 235; Conservative 0; Mismatches 237; Indels 21; Gaps 1;

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QY 1563 CTTCGCTGCTACCTGTTGATTTACGATTTACTGCTGCTACCTGATGTAACAAT 1622
DB 117 CTTTACCCACAACTGTTGATTTACTCTCAATTTTAACTTCTGAGAGTTGAACTT 176
QY 1623 TAGAGATAGCTAGCTGAAATATACAGAAATGCGCTAGTAATAGATGAAAGAG 1682
DB 177 CATTAACAATATGAGAAATCTTCATGACAAATGTCATATGACAAAGTTAGCAATG 236
QY 1683 CTGATGTAAGCGGACGACGAGAAAGATTGCAAGATCCACCCCTGCTGTCCTT 1742
DB 237 ATGATTTATGAGAAATATATTCAGACTCTCCAGATTCACCTTGATGAAACATA 296
QY 1743 CGAGGACTCCCACTGCTGAGAAAGATAGACATACAACTCGCTGTCAGACATCA 1802
DB 297 TAACTATTATTTGAAAGAAAGAAATTTATGCTGCGCAATCAAGAAATCTCTCA 356
QY 1803 GACTATCTGCTGCTGCTGCTACTACAT-----CAGCTTAGATTA 1841
DB 357 AACTATGTTGCTTGGGGTTGGAAGATTGAAAGAACCCAGAAAGACAGATGGCCT 416
QY 1842 GCTTCAGACGACATCCGACAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1901
DB 417 TTATTAACCGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 476
QY 1902 CTACAGGACGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1961
DB 477 TTATGTTCCCGAGCATTTGACATGACATGTTACATCTACAGACCTGCTGCTAT 536
QY 1962 AGTAGACGAGCTGCTGAGAACACCAACCTTTGGGCGAGGAGAGATACAGAGG 2021
DB 537 GCGAATAATGATGGCTGAAAATCTATCATATATGGGCAAGAAAGAAATCTGAGTT 596
QY 2022 ATGACTTATGGA 2034
DB 597 GGAATCTAAAGGA 609
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RESULT 5

US-08-480-481-3
Sequence 3, Application US/08480481
Patent No. 5639614
GENERAL INFORMATION:
APPLICANT: Sen, Luyi
APPLICANT: Philipson, Kenneth D.
APPLICANT: Lueis, Aldons J.
TITLE OF INVENTION: GENE MUTATION IN PATIENTS WITH IDIOPATHIC DILATED CARD
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,481
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel B
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: UCLAO12.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX:
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 1050 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Other
LOCATION: 1..1

OTHER INFORMATION: Position 1 corresponds to
OTHER INFORMATION: 7987 of the rabbit cDNA homolog
US-08-480-481-3

Query Match 2.0%; Score 60.2; DB 2; Length 1050;
Best Local Similarity 47.5%; Pred. No. 6.4e-07;
Matches 234; Conservative 0; Mismatches 238; Indels 21; Gaps 1;

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QY 1563 CTTCGCTGCTACCTGTTGATTTACTGATTTACTGCTGCTACATATGTAACAAT 1622
DB 117 CTTTACCCACAACTGTTGATTTACTCTCAATTTTAACTTCTGAGAGTTGAACTT 176
QY 1623 TAGAGATAGCTAGCTGAAATATACAGAAATGCGCTAGTAATAGATGAAAGAG 1682
DB 177 CATTAACAATATGAGAAATCTTCATGACAAATGTCATATGACAAAGTTAGCAATG 236
QY 1683 CTGATGTAAGCGGACGACGAGAAAGATTGCAAGATCCACCCCTGCTGTCCTT 1742
DB 237 ATGATTTATGAGAAATATATTCAGACTCTCCAGATTCACCTTGATGAAACATA 296
QY 1743 CGAGGACTCCCACTGCTGAGAAAGATAGACATACAACTCGCTGTCAGACATCA 1802
DB 297 TAACTATTATTTGAAAGAAAGAAATTTATGCTGCGCAATCAAGAAATCTCTCA 356
QY 1803 GACTATCTGCTGCTGCTGCTACTACAT-----CAGCTTAGATTA 1841
DB 357 AACTATGTTGCTTGGGGTTGGAAGATTGAAAGAACCCAGAAAGACAGATGGCCT 416
QY 1842 GCTTCAGACGACATCCGACAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1901
DB 417 TTATTAACCGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 476
QY 1902 CTACAGGACGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1961
DB 477 TTATGTTCCCGAGCATTTGACATGACATGTTACATCTACAGACCTGCTGCTAT 536
QY 1962 AGTAGACGAGCTGCTGAGAACACCAACCTTTGGGCGAGGAGAGATACAGAGG 2021
DB 537 GCGAATAATGATGGCTGAAAATCTATCATATATGGGCAAGAAAGAAATCTGAGTT 596
QY 2022 ATGACTTATGGA 2034
DB 597 GGAATCTAAAGGA 609
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RESULT 6

US-08-785-420-3
Sequence 3, Application US/08785420
Patent No. 6001976
GENERAL INFORMATION:

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1 APPLICANT: MacLennan, David H.
2 APPLICANT: O'Brien, Peter J.
3 TITLE OF INVENTION: DIAGNOSIS FOR PORCINE MALIGNANT
4 TITLE OF INVENTION: HYPERTHERMIA
5 NUMBER OF SEQUENCES: 3
6 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: Bell, Seltzer, Park & Gibson
8 STREET: P.O. Drawer 34009
9 CITY: Charlotte, North Carolina 28234
10 STATE: No. 6001976th Carolina 28234
11 COUNTRY: U.S.A.
12 ZIP: 28234
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: PatentIn Release #1.0, Version #1.25
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/08/785,420
20 FILING DATE:
21 CLASSIFICATION:
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: 08/249,388
24 FILING DATE:
25 APPLICATION NUMBER: US 08/030,159
26 FILING DATE: 15-MAR-1993
27 ATTORNEY/AGENT INFORMATION:
28 NAME: Layton, Jr., Samuel G.
29 REGISTRATION NUMBER: 22807
30 REFERENCE/DOCKET NUMBER: 3477-73
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: 704-377-1561
33 TELEFAX: 704-334-2014
34 TELEX: 57-5102
35 INFORMATION FOR SEQ ID NO: 3:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 1598 base pairs
38 TYPE: nucleic acid
39 STRANDEDNESS: single
40 TOPOLOGY: linear
41 MOLECULE TYPE: DNA (genomic)
42 HYPOTHEICAL: NO
43 ANTI-SENSE: NO
44 IMMEDIATE SOURCE:
45 CLONE: p1g RYR1 gene
46 POSITION IN GENOME:
47 UNITS: bp
48 US-08-785-420-3
49
50 Query Match 1.9%; Score 58; DB 3; Length 1598;
51 Best Local Similarity 58.8%; Pred. No. 3.5e-06;
52 Matches 100; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
53
54 QY TGGGCGGCACCTTAAGTCAATGAAGTGTCGTATTGCTGTCGCTCGTTAAGGCGTGC 854
55 Db TGACCTTAGCCCTTAGTGCTGAGATGCTCTGTGTTCCCTGTGTGTGCCAAATGCTGTC 988
56
57 QY GATGCGCTCGTCAACAGAACAATCTGTGACTACTTACGCCCCGACGAACCTGTCT 914
58 Db CGTGGCTTCCAACAGATCTCATTAAGTGAAGACTTGTCTCTGCGCGGAGCTTCTCT 1048
59
60 QY GCAAACTGCGCTGTGATCAAGTATCTAGTCCGTCGACGAACATCTTGC 964
61 Db GCAGCAAACTCATCACTAATGTATCAACAGGCTGCGCCCCCAACTTTG 1098
62
63 RESULT 7
64 US-08-480-481-6
65 Sequence 6, Application US/08480481
66 Patent No. 5639614
67 GENERAL INFORMATION:
68 APPLICANT: Sen, Luyt
69 APPLICANT: Philipson, Kenneth D.
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1  APPLICANT: Lustig, Alons J.
2  TITLE OF INVENTION: GENE MUTATION IN PATIENTS WITH IDIOPATHIC DILATED CAR
3  NUMBER OF SEQUENCES: 6
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE: Knobbe, Martens, Olson & Bear
6  STREET: 620 Newport Center Drive 16th Floor
7  CITY: Newport Beach
8  STATE: CA
9  COUNTRY: U.S.A.
10 ZIP: 92660
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: Diskette
13 COMPUTER: IBM Compatible
14 OPERATING SYSTEM: DOS
15 SOFTWARE: FastSeq Version 1.5
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/08/480,481
18 FILING DATE: 07-JUN-1995
19 CLASSIFICATION: 435
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER:
22 FILING DATE:
23 ATTORNEY/AGENT INFORMATION:
24 NAME: Altman, Daniel E
25 REGISTRATION NUMBER: 34,115
26 REFERENCE/DOCKET NUMBER: UCLA012.001A
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: 714-760-0404
29 TELEFAX: 714-760-9502
30 TELEX:
31 INFORMATION FOR SEQ ID NO: 6:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 900 base pairs
34 TYPE: nucleic acid
35 STRANDEDNESS: both
36 TOPOLOGY: linear
37 MOLECULE TYPE: Genomic DNA
38 HYPOTHETICAL: NO
39 ANTI-SENSE: NO
40 FRAGMENT TYPE:
41 ORIGINAL SOURCE:
42 FEATURE:
43 NAME/KEY: Other
44 LOCATION: 1...1
45 OTHER INFORMATION: Position 1 corresponds to
46 OTHER INFORMATION: 8137 of the rabbit cDNA homolog
47 NAME/KEY: Other
48 LOCATION: 230..230
49 OTHER INFORMATION: Position distinguishes idiopathic
50 OTHER INFORMATION: dilated cardiomyopathy
51 NAME/KEY: Other
52 LOCATION: 626...626
53 OTHER INFORMATION: Position distinguishes idiopathic
54 OTHER INFORMATION: dilated cardiomyopathy
55 US-08-480-481-6
56
57 Query Match 1.5%; Score 46.2; DB 2; Length 900;
58 Best Local Similarity 46.4%; Pred. No. 0.0074;
59 Matches 211; Conservative 0; Mismatches 223; Indels 21; Gaps 1;
60
61 QY 1601 TGCCTACATATGTGTGAACCAATTAGAGATAGACTGAGTGAATAATACGAGAAATGTGG 1660
62 |||||
63 Db 5 TTCTGTGAAGTTGGAATATCTTCATTAAACAAATATGACAGAAATCTCTCATGACCAATGGT 64
64 |||||
65
66 QY 1661 CTATGAAATTAAGATCGAAGCAGCGCTGATATGACGCGACACAGAGAGAGCTTGCAACA 1720
67 |||||
68 Db 65 CAATGACCAAGTTAAGCAAAATGATGATTTATGAGAAATATATTCAGACTCTCCACAGA 124
69 |||||
70
71 QY 1721 TCCAGCCCTGCGCTCGGCCCTTGAGCGCACTCCACCTGCTAGAAACGATACGACATAC 1780
72 |||||
73 Db 125 TTGACACCTTGATGAACCAATATACTATATCTGAAAAAGAAAAATTTATCGCT 184
74 |||||
75
76 QY 1781 AACTCGCTGTGACAGACACTCAAGACTATTCCTGCGCTCGGGCTATACAT----- 1829

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Db	185	GGCCATCAAGAATCTCTCAAACTAATGTTGGCTTGGGTTGGAAAGTTGAAGAACC	244
Qy	1330	-----CAGCTTAATTAAGCTCCAGACGCATCCGGAAGCTGCTGCCCAAG	1879
Db	245	CAGAAAGAGACAGCATGGCCCTTTATTAACGAACTCGTGTATTTCTAAGCAAGCCAG	304
Qy	1880	AACCTTTCATGCACTCCAAAGGCTTACAAGCACACTGACCTGAGTCTGTCAACC	1939
Db	305	TTTCTGTATGATGCTGCCCATGATGTTATATCTCCCGACATTGACATGACATGTTCAC	364
Qy	1940	TGACACCCAAAGATGATGAGCTAGTAGACCAAGTGGCTGAAACAACCCACAACCTTTGG	1999
Db	365	TATTCAGAGACTGATGCTTAATGGCAGAAATAGATGGCTGAATATCATTAACATATGG	424
Qy	2000	CCAGGAGAGGATACAGACGGAGATGCACTTAATGA	2034
Db	425	CAAAAGAAAAGAACTGGAGTTGCAAGTCTAAAGAA	459

RESULT 8
US-08-232-463-14/c
Sequence 14, Application US/08232463

1 GENERAL INFORMATION:
2 APPLICANT: DORNER, F.
3 APPLICANT: SCHEIFLINGER, F.
4 APPLICANT: PALMER, F. G.
5 TITLE OF INVENTION: RECOMBINANT FOXLPOX VIRUS
6 NUMBER OF SEQUENCES: 52
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: Foley & Lardner
9 STREET: 1800 Diagonal Road, Suite 500
10 CITY: Alexandria
11 STATE: VA
12 COUNTRY: USA
13 ZIP: 22313-0299
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: IBM PC compatible
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: PatentIn Release #1.0, Version #1.25
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/08/232,463
21 FILING DATE:
22 CLASSIFICATION: 435
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: US/07/935,313
25 FILING DATE:
26 APPLICATION NUMBER: EP 91 114 300.6
27 FILING DATE: 26-AUG-1991
28 ATTORNEY/AGENT INFORMATION:
29 NAME: BENT, Stephen A.
30 REGISTRATION NUMBER: 29,768
31 REFERENCE/DOCKET NUMBER: 30472/114 IMMU
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (703) 836-9300
34 TELEFAX: (703) 683-4109
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Query Match 1.4%; Score 43; DB 2; Length 7218;
Best Local Similarity 4.1%; Pred. No. 0.2;
Matches 16; Conservative 21; Mismatches 166; Indels 0; Gaps 0;

OY		91	GAAACGAAGGAAAGGGATGGGTGAAGTGAAGAAGAACCAATTCTCCACGAGAA	150
D8		1427	RR	1368
OY		151	GGCAAGATGACGATGGCCTCGACTTCGCAGGTCA CAGAGGAAGAATAGACTGCT	210
D8		1367	RRR	1308
OY		211	CGAATTATCGAAGAGTGTTCTTGCGCTGTCACTAAGTTATCAA TGCTCGAAAACTCA	270
D8		1307	RRR	1248
OY		271	C AAGAGAACC GTG TCA CTGCA GTTCTTG CGCTCA GTA ACTGG GCAGATGTG ATC	330
D8		1247	RRR	1188
OY		331	TGCTCGAGATCTCATCAACTTTCGACAAGCCCGTAGAGATATGAA CAAGA AA	390
D8		1187	RRR	1128
OY		391	A AACAAA CAAT TC GG GGC AC TC CC GA ACC GT C AGA CCT GTTCCA AGGA AGG ATA	450
D8		1127	RRR	1068
OY		451	CTGAACCTGATCTCGAAGCTATATGA CAAGATC	483
D8		1067	RATCGAAGCTCCCTCGA C T T G C A C C T G C A C C A G C T C	1035

RESULT 9
US-09-485-529-14
; Sequence 14, Application US/09485529
; Patent No. 6762348

```

1  APPLICANT: Harberd, Nicholas P
2  APPLICANT: Richards, Donald E
3  APPLICANT: Peng, Jinyong
4  TITLE OF INVENTION: Genetic Control of Plant Growth and Development
5  FILE REFERENCE: 620-91
6  CURRENT APPLICATION NUMBER: US/09/485,529
7  CURRENT FILING DATE: 2000-03-01
8  PRIOR APPLICATION NUMBER: PCT/GB98/02383
9  PRIOR FILING DATE: 1998-08-07
10 PRIOR APPLICATION NUMBER: GB 971192.0
11 PRIOR FILING DATE: 1997-08-13
12 NUMBER OF SEQ. ID NOS: 108
13 SOFTWARE: Patentln Ver. 2.0
14 SEQ ID NO 14
15 LENGTH: 2125
16 TYPE: DNA
17 ORGANISM: Trifolium aestivum
18 US-09-485-529-14

```

Query Match 1.3%; Score 38.6; DB 3; Length 2125;

Best Local Similarity 47.6%; Pred. No.:2;
Matches 147; Conservative 0; Mismatches 159; Indels 3; Gaps 1;

QY	609	AAACTGGCCGCAAGTTCCTGCAATCCGCTCACTGGGTGTTCTCGGCTCCGGCTC	668
Db	1194	GAAGCTGGCCAGATTGGGGACACACATCCGGGTGATTCAGATACCGGGCTCTGTGCG	1253
QY	669	GCAGGCTCTCGGGCCAGGGCACCCGGCATATGCTGACGTCGTGCATCTGCTTTATAGATC	728
Db	1254	---GGCACCCTGGCGGACCTGGAGCCGTTTCATGCTGACGCGGAGGGCCAGGAAGACC	1310
QY	729	GCCTGAAGCTTCAATATGATGAAGGACGAACACATAAATGATTAATCTCTCATATTAGA	788
Db	1311	GAACGAGGAGCCACAGATTAATCGCCGTCATCTCAGTTCGAGATGACACCGGCTGCTGCG	1370
QY	789	AAAGCATGGGCGGCAACCTTAAGTACTAGATGTCTATGTTCCGCTGTGCGTCGTTAACGG	848
Db	1371	GCAGCCCGCGGCTCTGGAGAAAGTCTCTGGGACCGTGCAGCCGCTGGGGGCCACAGATCGT	1430

/ Sequence 11838, Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenstein et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ CURRENT FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 11838
/ TYPE: DNA
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11838

Query Match 1.3%; Score 37.8; DB 3; Length 294;
Best Local Similarity 52.2%; Pred. No. 1.2; Mismatches 77; Indels 0; Gaps 0;
Matches 84; Conservative 0;

QY 2016 GCAGGATGACTTATGACTTATGAGACTCGCATGCTCCCGCACTGAT 2075
DB 84 GCAGGATGACTTATGAGACTTATGAGACTCGCATGCTCCCGCACTGAT 143
QY 2076 GCCATACCCGAGGTTGACATGATCAAGAGCCCAAGAGACAGCCTCGAGAC 2135
DB 144 AGGGCGCTGACATCGCCGGGTATCTACAAAGACCACTGTGAGCGCTGTGGAT 203
QY 2136 TGTGAGAGCCCTGTGCTATGAGGATATGCTGAGACCCG 2176
DB 204 GGTCCCGCGCGCTGTGCTACAGAGACTCGCAGGCGAGC 244

RESULT 14
US-09-668-097A-35
/ Sequence 35, Application US/09668097A
/ Patent No. 6673988
/ GENERAL INFORMATION:
/ APPLICANT: Cahoon, Edgar B.
/ APPLICANT: Cahoon, Rebecca E.
/ APPLICANT: Klein, Ted
/ APPLICANT: Shen, Jennie
/ TITLE OF INVENTION: Plant Lipases
/ FILE REFERENCE: B01401 US NA
/ CURRENT APPLICATION NUMBER: US/09/668,097A
/ CURRENT FILING DATE: 2000-09-22
/ PRIOR APPLICATION NUMBER: 60/157309
/ PRIOR FILING DATE: 1999-10-01
/ NUMBER OF SEQ ID NOS: 41
/ SOFTWARE: Microsoft Office 97
/ SEQ ID NO 35
/ LENGTH: 1334
/ TYPE: DNA
/ ORGANISM: Trifolium asclepium
US-09-668-097A-35

Query Match 1.3%; Score 37.6; DB 3; Length 1334;
Best Local Similarity 57.8%; Pred. No. 3; Mismatches 49; Indels 0; Gaps 0;
Matches 67; Conservative 0;

QY 600 CAACGACGAACTGCGCGCACTTCCGAACTGAAACCGCTCAACTGCTGTTCTCGCG 659
DB 728 CAACCGCGCGCACTGACAGCACTGACGCTGCTGAAAGCGTTCAACGCGCTGCTCGCGCG 787
QY 660 CTTGCGCTGCGAGCGCTGCGGAGAGGCAACCGCATGCTGCAAGCTGCTGCACTGCG 715
DB 788 CCACAACTGCTGCTGCTGCAAGAGAGTGAACAGCTGCAAGGCAAGTACCTCTACG 843

RESULT 15
US-09-513-999C-35034/c
/ Sequence 35034, Application US/09513999C
/ Patent No. 6783961
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Duclert, A.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
/ Patent No. 6783961
/ FILE REFERENCE: 59, US2, RSG
/ CURRENT APPLICATION NUMBER: US/09/513,999C
/ CURRENT FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/122,487
/ PRIOR FILING DATE: 1999-02-26
/ NUMBER OF SEQ ID NOS: 36681
/ SOFTWARE: Patent.pm
/ SEQ ID NO 35034
/ LENGTH: 299
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 80
/ OTHER INFORMATION: s=g or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 124
/ OTHER INFORMATION: n=a, g, c or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 126
/ OTHER INFORMATION: r=a or g
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 131
/ OTHER INFORMATION: r=a or g
US-09-513-999C-35034

Query Match 1.2%; Score 37.4; DB 3; Length 299;
Best Local Similarity 60.8%; Pred. No. 1.5; Mismatches 54; Indels 2; Gaps 2;
Matches 90; Conservative 2;

QY 314 TGGCGAGATGATGATGCTCGAGATCATCACTACTTGCACAGCCCGATGAG 372
DB 169 TAGAAGAGTCTCTGACAGCCTTACGACTTGATCGCTTCTTCCAGCCCGAGAGAG 110
QY 373 GATATGAAACGAG 432
DB 109 GAGATGCAATGAG 51
QY 433 TTCCAG 460
DB 50 TTCAAG 23

Search completed: April 14, 2006, 15:14:14
Job time : 505.5 secs

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XX The present invention describes an isolated nucleotide fragment (I) comprising: (a) a nucleic acid sequence encoding a ryanodine receptor having an amino acid sequence identity of at least 80% when compared to a polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8, 128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO. 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant construct comprising (I) operably linked to at least one regulatory sequence; (2) a transformed host cell comprising the recombinant construct; (3) a method to isolate (I) encoding ryanodine receptors and related polypeptides; (4) an isolated polypeptide having ryanodine receptor activity; (5) a method for evaluating at least one compound for its ability to modulate calcium homeostasis; (6) a method for evaluating at least one compound which modulates ryanodine receptor activity; (7) an isolated nucleic acid fragment encoding an insect ion channel comprising at least two fully defined polypeptide sequences selected from SEQ ID NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56, 120-126; (8) a method for identifying a nucleic acid sequence encoding an insect ion channel; (9) a method for expressing an isolated nucleic acid fragment encoding a toxic insect ion channel; and (10) recombinant construct comprising in the 5' to 3' direction a promoter operably linked to an isolated nucleic acid fragment encoding a toxic insect ion channel. The isolated nucleic acid fragment (I) encoding a ryanodine receptor is useful for the isolation of other pest ryanodine receptors and developing of screens to identify insecticidally active compounds. The nucleic acid fragments are useful as pesticides, fragments of protein for antibody production, fragments of protein for determination of the structure of insecticide binding sites and in the identification of insecticides that disrupt the calcium balance in cells through other messengers that interact with the receptor calcium release mechanism. The present sequence is used in the exemplification of the present invention.

Sequence 15387 BP; 4065 A; 3845 C; 4182 G; 3295 T; 0 U; 0 Other;

Query Match 100.0%; Score 3001; DB 12; Length 15387;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCATAGGCGCGCCCATCATCAAAATATGTGACTCACCGTCAATTGTGACATTCCGAG 60
DB 1000 GTCATAGGCGCGCCCATCATCAAAATATGTGACTCACCGTCAATTGTGACATTCCGAG 1059
QY 61 ACTGCGTTGTGCTGTCTTATTAAGCTTTACGAAACGAAAGAAAGAGTGGTAAAGTA 120
DB 1060 ACTGCGTTGTGCTGTCTTATTAAGCTTTACGAAACGAAAGAAAGAGTGGTAAAGTA 1119
QY 121 GAAAGAAAGCAAGGATTTCTCAGAGAAAGCAAGATGACATGGCTTGAATTCTCC 180
DB 1120 GAAAGAAAGCAAGGATTTCTCAGAGAAAGCAAGATGACATGGCTTGAATTCTCC 1179
QY 181 AGGTCAAGAGAGAAATCTAGAGACTGCTGAGTTATCAGAAAGTGTCTTCGCTGTTTC 240
DB 1180 AGGTCAAGAGAGAAATCTAGAGACTGCTGAGTTATCAGAAAGTGTCTTCGCTGTTTC 1239
QY 241 ACTAAGTTTATCAATGTGTCTGAAACTCTACAAAGAAACCGTGTCACTCGATGTTCTTC 300
DB 1240 ACTAAGTTTATCAATGTGTCTGAAACTCTACAAAGAAACCGTGTCACTCGATGTTCTTC 1239
QY 301 GCGTCAAGTGAACCTGGGGGAGATGTGTGCTTCGAGATCTCATCAATCACTTGGCA 360
DB 1300 GCGTCAAGTGAACCTGGGGGAGATGTGTGCTTCGAGATCTCATCAATCACTTGGCA 1359
QY 361 CAGCCCGATGAGATATATGAAACAGAAAGAAACAAATTCGCGGCACTCCGAAAC 420
DB 1360 CAGCCCGATGAGATATATGAAACAGAAAGAAACAAATTCGCGGCACTCCGAAAC 1419
QY 421 CGTCAAGACCTGTTCCAAAGAGAAAGCATATGAACTGATCTCGAAGCTATAGACAG 480
DB 1420 CGTCAAGACCTGTTCCAAAGAGAAAGCATATGAACTGATCTCGAAGCTATAGACAG 1479
QY 481 ATCAAGCTCATCAGTCCAGGGGTTCTCGCTGATTCCTGGCGGAGACGAATCTGGA 540
DB 1480 ATCAAGCTCATCAGTCCAGGGGTTCTCGCTGATTCCTGGCGGAGACGAATCTGGA 1539
QY 541 CAGAGCTGGGAAATGATATATGATATTTGATCACTGCTGCGGCAATATATAGAGGC 600
DB 1540 CAGAGCTGGGAAATGATATATGATATTTGATCACTGCTGCGGCAATATATAGAGGC 1539
QY 601 AACCAACGAACTGCGCGCAGTTGCGCAACTCGAACCGCTCAACTGCTGTTCTCGGC 660
DB 1600 AACCAACGAACTGCGCGCAGTTGCGCAACTCGAACCGCTCAACTGCTGTTCTCGGC 1659
QY 661 CTGGGCTCGAGGCTTGGGCGAGGGGACCGGCACTGTCAGCGTGCACCTGGTGTCT 720
DB 1660 CTGGGCTCGAGGCTTGGGCGAGGGGACCGGCACTGTCAGCGTGCACCTGGTGTCT 1719
QY 721 ATAGACTCGCTGAAGCTCTCAATATATATGAGAGGACGAAACATATATATATCTCT 780
DB 1720 ATAGACTCGCTGAAGCTCTCAATATATATGAGAGGACGAAACATATATATATCTCT 1779
QY 781 CTATTAGAAAAGCATYGGGCGGACCTTAAGTACTAGATGTCTATGTCTGCTGCGTC 840
DB 1780 CTATTAGAAAAGCATYGGGCGGACCTTAAGTACTAGATGTCTATGTCTGCTGCGTC 1839
QY 841 GGTAAAGCGCTGCGGCGGCTGCTGTCACAGAAACAACTGTGACTTACTTACGCCGCGC 900
DB 1840 GGTAAAGCGCTGCGGCGGCTGCTGTCACAGAAACAACTGTGACTTACTTACGCCGCGC 1899
QY 901 AAGAACCTGTTGCTGCAAACTGCGCTGCGGATCACTATATAGTGTCCGTCGAAATC 960
DB 1900 AAGAACCTGTTGCTGCAAACTGCGCTGCGGATCACTATATAGTGTCCGTCGAAATC 1959
QY 961 TTGCTGGGTGAGTGAAGAGGTGCGCAGTGTACCGCAATGTGTACTTGAAGTACTATG 1020
DB 1960 TTGCTGGGTGAGTGAAGAGGTGCGCAGTGTACCGCAATGTGTACTTGAAGTACTATG 2019
QY 1021 GACCACTATAGAAAGACCAACATATGATATCCATCTTACGATAGAGATGGCCAAACT 1080
DB 2020 GACCACTATAGAAAGACCAACATATGATATCCATCTTACGATAGAGATGGCCAAACT 2079
QY 1081 ACTGTTATGTCCATATCCGCGCGGTGCGAGAAATGCGGAGGTAAACGCGTGGAGAT 1140
DB 2080 ACTGTTATGTCCATATCCGCGCGGTGCGAGAAATGCGGAGGTAAACGCGTGGAGAT 2139
QY 1141 GACCTGTATCTGTACGCGGTTGACGCGGCTTACCTGTGTTCCGGGGGAGAGAACTCC 1200
DB 2140 GACCTGTATCTGTACGCGGTTGACGCGGCTTACCTGTGTTCCGGGGGAGAGAACTCC 2199
QY 1201 GTCAATAGACTCATGCTGAAGAGCCTTAATATAGAAAGGTGACGATAGTGTGGCA 1260
DB 2200 GTCAATAGACTCATGCTGAAGAGCCTTAATATAGAAAGGTGACGATAGTGTGGCA 2259
QY 1261 TTGGAACCTGACGGTACCCATATCACTTATGATTTCAACGGAAGTGCGGGTGACGGATCC 1320
DB 2260 TTGGAACCTGACGGTACCCATATCACTTATGATTTCAACGGAAGTGCGGGTGACGGATCC 2319
QY 1321 TTCAACAACTTCAATCTGAAAGGATGTTCTTCCGGTCACTAGCTCTTATGATCTG 1380
DB 2320 TTCAACAACTTCAATCTGAAAGGATGTTCTTCCGGTCACTAGCTCTTATGATCTG 2379
QY 1381 AGTTGCGGTTCTGCTGCGGCGGAGAAACAGGTGCTCTCCGATACGCGGCTCCAGAAAGC 1440
DB 2380 AGTTGCGGTTCTGCTGCGGCGGAGAAACAGGTGCTCTCCGATACGCGGCTCCAGAAAGC 2439
QY 1441 TACTCTCCCTTGGTGAAGTCTCTCTGCGCAGACAGATCTCAGCTGAGAGCGTGTCTC 1500
DB 2440 TACTCTCCCTTGGTGAAGTCTCTCTGCGCAGACAGATCTCAGCTGAGAGCGTGTCTC 2499
QY 1501 TACTCTGGAACCTGTTCGAAGCGGCGCTTGGCTGGAACCTTCGCTAAGTACAGAGATAGC 1560
DB 2500 TACTCTGGAACCTGTTCGAAGCGGCGCTTGGCTGGAACCTTCGCTAAGTACAGAGATAGC 2559
QY 1561 GCGTGTGCTGCTACCTGTGTATCTTTTACATTTTACTGTGCTACTATGTGGAAACA 1620
DB 2560 GCGTGTGCTGCTACCTGTGTATCTTTTACATTTTACTGTGCTACTATGTGGAAACA 2619

QY 1621 ATTGAGATTAAGCTAGCTGAAAAATATACAGAAATGTGGGCTATGAAATTAAGATCGAAGCA 1680
 DB 2620 ATTGAGATTAAGCTAGCTGAAAAATATACAGAAATGTGGGCTATGAAATTAAGATCGAAGCA 2679
 QY 1661 GGCTGATGTACGGCGGACCAAGAGAAAGACTTTCACAGATCCACCCCTGCTCGTCCG 1740
 DB 2660 GGCTGATGTACGGCGGACCAAGAGAAAGACTTTCACAGATCCACCCCTGCTCGTCCG 2739
 QY 1741 TTGAGCGACCTCCACCTGCTGAGAAAGATACATCACTGCTGTGAGACATC 1800
 DB 2740 TTGAGCGACCTCCACCTGCTGAGAAAGATACATCACTGCTGTGAGACATC 2799
 QY 1801 AAGATATCTGGCTCTGGGCTACTACATCAGCTTAAGATTAAGCTTCAGACGCAATCCG 1860
 DB 2800 AAGATATCTGGCTCTGGGCTACTACATCAGCTTAAGATTAAGCTTCAGACGCAATCCG 2859
 QY 1861 AAGCTTCTGCTGCGCAAGAACCTTTCATGTCAGTCGCAAGCTTCAAGCTCAGACGCAATC 1920
 DB 2860 AAGCTTCTGCTGCGCAAGAACCTTTCATGTCAGTCGCAAGCTTCAAGCTCAGACGCAATC 2919
 QY 1921 GACCTGAGTGTGCTGACCCCTGACCCCAAGATGATGAGCTAGTACCAAGCTGCTGAG 1980
 DB 2920 GACCTGAGTGTGCTGACCCCTGACCCCAAGATGATGAGCTAGTACCAAGCTGCTGAG 2979
 QY 1981 AACACCCACAACTTTGGGCGAGGAGAGATACAGAGGATGACTTAATGACTTAAT 2040
 DB 2980 AACACCCACAACTTTGGGCGAGGAGAGATACAGAGGATGACTTAATGACTTAAT 3039
 QY 2041 GAGGACTGGACATGATGCTTCCCGCACTGTGCTCCTACCCGAAAGTTGACGATGCC 2100
 DB 3040 GAGGACTGGACATGATGCTTCCCGCACTGTGCTCCTACCCGAAAGTTGACGATGCC 3099
 QY 2101 ATCAAGAAAGGCCAACAGGAGACACAGCTGTGAGAGACCTGTGCTGCTTACGCG 2160
 DB 3100 ATCAAGAAAGGCCAACAGGAGACACAGCTGTGAGAGACCTGTGCTGCTTACGCG 3159
 QY 2161 TATATGCTGGACCCGCTACTGTGGGAGCAGATGAAGCACTCTTGTGGAACGTCGAA 2220
 DB 3160 TATATGCTGGACCCGCTACTGTGGGAGCAGATGAAGCACTCTTGTGGAACGTCGAA 3219
 QY 2221 CAGAAAGCAGAGACTTCAGAACATACCGCGCTGAGAGAACTATGCGCTGAGCTTGG 2280
 DB 3220 CAGAAAGCAGAGACTTCAGAACATACCGCGCTGAGAGAACTATGCGCTGAGCTTGG 3279
 QY 2281 AAGTGTACTTGAAGTTTGAATCTTAAGCGCTGAGACCTATGAGGGTCCGCTGGCTCAC 2340
 DB 3280 AAGTGTACTTGAAGTTTGAATCTTAAGCGCTGAGACCTATGAGGGTCCGCTGGCTCAC 3339
 QY 2341 GCTGATATGCGACCAAGAAATGATGCTCGGACAGACGAGAACTTTGGCATTTGATG 2400
 DB 3340 GCTGATATGCGACCAAGAAATGATGCTCGGACAGACGAGAACTTTGGCATTTGATG 3399
 QY 2401 TACAAATGAGAAAAAGTGTACAGCGGTAACTGATCTTTTCGCAAGCATGCGCTGTT 2460
 DB 3400 TACAAATGAGAAAAAGTGTACAGCGGTAACTGATCTTTTCGCAAGCATGCGCTGTT 3459
 QY 2461 GGTGACGTAGTGGGGGTGTTCTAGATCTCATTTGATTAAGCATTAAGTTTCTCAT 2520
 DB 3460 GGTGACGTAGTGGGGGTGTTCTAGATCTCATTTGATTAAGCATTAAGTTTCTCAT 3519
 QY 2521 GGTGAGTTGCTTGAATGATGCTCTTGGCGGAGAGACTAGCTTTGCTGAGTGTGAC 2580
 DB 3520 GGTGAGTTGCTTGAATGATGCTCTTGGCGGAGAGACTAGCTTTGCTGAGTGTGAC 3579
 QY 2581 AACTTTGTACAGCTTGCACACTTGTGTGGCCAAAAAGCCAGGTTTAACTATGCGCAA 2640
 DB 3580 AACTTTGTACAGCTTGCACACTTGTGTGGCCAAAAAGCCAGGTTTAACTATGCGCAA 3639
 QY 2641 GATGTGAATATCTCTGAATATCTTACACAATGTGTCTTCAAGAGGAGATATGAACATTT 2700
 DB 3640 GATGTGAATATCTCTGAATATCTTACACAATGTGTCTTCAAGAGGAGATATGAACATTT 3699

QY 2701 TGGCTCAATATGAAAGAGAGAGCTGATCTGATGTAACACCAAGACAGCCGATTTGAG 2760
 DB 3700 TGGCTCAATATGAAAGAGAGAGCTGATCTGATGTAACACCAAGACAGCCGATTTGAG 3759
 QY 2761 AATATGATGAGATGATGAGACCAAGATTAAGTGAACAGGATTAACAGCTGTTCAAT 2820
 DB 3760 AATATGATGAGATGATGAGACCAAGATTAAGTGAACAGGATTAACAGCTGTTCAAT 3819
 QY 2821 ACACCTCAATGCTTCAAGATTTCCCAACAAGCTTTCAGAGAGATGAGAAAAAGCTA 2880
 DB 3820 ACACCTCAATGCTTCAAGATTTCCCAACAAGCTTTCAGAGAGATGAGAAAAAGCTA 3879
 QY 2881 GAGTTCTTAAGCTCTCTACCTGCTGTTATCTGCCATTAACGATTCATTGACGAGCA 2940
 DB 3880 GAGTTCTTAAGCTCTCTACCTGCTGTTATCTGCCATTAACGATTCATTGACGAGCA 3939
 QY 2941 AAAGCAGACGTTGGTGTGAATGAAATGACGAGTCAAGATCCCTAATGAAGAAGCA 3000
 DB 3940 AAAGCAGACGTTGGTGTGAATGAAATGACGAGTCAAGATCCCTAATGAAGAAGCA 3999
 QY 3001 G 3001
 DB 4000 G 4000

RESULT 2
 ADM68901
 ID ADM68901 standard; DNA; 15303 BP.
 XX
 AC ADM68901;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Heliothis virescens ryanodine receptor encoding DNA SEQ ID NO:145.
 XX
 KW ryanodine receptor; insect ion channel; insecticide; pesticide;
 KW calcium balance disruption; receptor calcium release mechanism; gene; ds.
 XX
 OS Heliothis virescens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..15303
 FT /tag=a
 FT /product= "ryanodine receptor"
 XX
 PN MO2004027042-A2.
 XX
 PD 01-APR-2004.
 XX
 PF 23-SEP-2003; 2003MO-US029834.
 XX
 PR 23-SEP-2002; 2002US-0412795P.
 PR 18-NOV-2002; 2002US-0427324P.
 XX
 PA (DUPO) DU PONT DE MEMOURS & CO B I.
 XX
 PI Caspar T, Cordova D, Gutierrez S, Rauch J, Smith RM, Wu L;
 PI Tao Y;
 XX
 DR WPI; 2004-295411/27.
 DR P-PSDB; ADM68902.
 XX
 PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
 PT for isolating other pest ryanodine receptors and in developing screens to
 PT identify insecticidally active compounds.
 XX
 PS Claim 6; SEQ ID NO 145; 687BP; English.
 XX
 CC The present invention describes an isolated nucleotide fragment (i)
 CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
 CC having an amino acid sequence identity of at least 80% when compared to a
 CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
 CC 128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a

CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO. 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant CC construct comprising (1) operably linked to at least one regulatory sequence; (2) a transformed host cell comprising the recombinant construct; (3) a method to isolate (i) encoding ryanodine receptors and related polypeptides; (4) an isolated polypeptide having ryanodine receptor activity; (5) a method for evaluating at least one compound for its ability to modulate calcium homeostasis; (6) a method for evaluating at least one compound which modulates ryanodine receptor activity; (7) an isolated nucleic acid fragment encoding an insect ion channel comprising at least two fully defined polypeptide sequences selected from SEQ ID NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56, 120-126; (8) a method for identifying a nucleic acid sequence encoding an insect ion channel; (9) a method for expressing an isolated nucleic acid fragment encoding a toxic insect ion channel; and (10) recombinant construct comprising in the 5' to 3' direction a promoter operably linked to an isolated nucleic acid fragment encoding a toxic insect ion channel. The isolated nucleic acid fragment (i) encoding a ryanodine receptor is useful for the isolation of other pest ryanodine receptors and developing of screens to identify insecticidally active compounds. The nucleic acid fragments are useful as pesticides, fragments of protein for antibody production, fragments of protein for determination of the structure of insecticide binding sites and in the identification of insecticides that disrupt the calcium balance in cells through other messengers that interact with the receptor calcium release mechanism. The present CC sequence is used in the exemplification of the present invention.

XX SQ Sequence 15303 BP; 4036 A; 3822 C; 4161 G; 3284 T; 0 U; 0 Other;

Query Match 95.2%; Score 2857; DB 12; Length 15303;

Best Local Similarity 97.0%; Pred. No. 0; Matches 2911; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

OY 1 GTCATAGCGCGCCCATCATCAAAATATGATGATCCACCGTATCTGTCAGCATTCGAG 60
DB 1015 GTCAAGCGCGCTCCCATCATCAAAATATGATGATCCACCGTATCTGTCAGCATTCGAG 1074
OY 61 ACTGCGTTGTGCTGCTTTATTAAGTCTTACGAAAGAAAGAAAGAGTGGTAAAGTA 120
DB 1075 ACTGCGTTGTGCTGCTTTATTAAGTCTTACGAAAGAAAGAAAGAGTGGTAAAGTA 1134
OY 121 GAAAGGAAGCAAGCATTTCTCCAGAGAAAGCAAGAGAGCATGAGCTTCTGCTTCC 180
DB 1135 GAAAGGAAGCAAGCATTTCTCCAGAGAAAGCAAGAGAGCATGAGCTTCTGCTTCC 1194
OY 181 AGGTACAGAGAGAAATCTAGAGCTGCTCGAGTTATCAGGAAGTGTCTTCCGTGTTT 240
DB 1195 AGGTACAGAGAGAAATCTAGAGCTGCTCGAGTTATCAGGAAGTGTCTTCCGTGTTT 1254
OY 241 ACTAAGTTTATCAATGCTGTGAAACTCTACAGAGAAAGCGTCTGCTCATGATGTTCTTC 300
DB 1285 ACTAAGTTTATCAATGCTGTGAAACTCTACAGAGAAAGCGTCTGCTCATGATGTTCTTC 1314
OY 301 GCGTCAGTGAACCTGGGCGAGATGATGAGCTCTCGAGAGATCTCATCACTAATTCCGA 360
DB 1315 GCGTCAGTGAACCTGGGCGAGATGATGAGCTCTCGAGAGATCTCATCACTAATTCCGA 1374
OY 361 CAGCCGATGAGATATGAAACAAGAAAGAAACAAATTCGCGGCACTCCGAAC 420
DB 1375 CAGCCGATGAGATATGAAACAAGAAAGAAACAAATTCGCGGCACTCCGAAC 1434
OY 421 CGTCAGAGCTGTTCAGAGAGAGAGCATCTGAACCTGATCTTGAAGCTATAGACAG 480
DB 1435 CGTCAGAGCTGTTCAGAGAGAGAGCATCTGAACCTGATCTTGAAGCTATAGACAG 1494
OY 481 ATCAAGCTATCATCGTCCAGGGGTTCTCGTGGATTCCTGCGGAGACAGATCTGGA 540
DB 1495 ATCAAGCTATCATCGTCCAGGGGTTCTCGTGGATTCCTGCGGAGAGATCTGGA 1554
OY 541 CAGAGCTGGGAAATGATATCTGATATTTGATCATGTTGCGGCGCAATATAAGGGC 600
DB 1555 CAGAGCTGGGAAATGATATCTGATATTTGATCATGTTGCGGCGCAATATAAGGGC 1614

OY 601 AACCAACGAACCTGCGGCGAGCTTCGCAACTCGAACCGCTCAACTGGCTGTTCTCGGC 660
DB 1615 AACCAACGAACCTGCGGCGAGCTTCGCAACTCGAACCGCTCAACTGGCTGTTCTCGGC 1674
OY 661 CTGGGCTCGAGGCGCTCGGGGAGAGGCAACGGGCACTGCTCGACGCTGCGACCTGGGCTTC 720
DB 1675 CTGGGCTCGAGGCGCTCGGGGAGAGGCAACGGGCACTGCTCGACGCTGCGACCTGGGCTTC 1734
OY 721 ATGACTCGCTGAGCTCTCAATATGATGAGGAGCAACATATAAGATATATCTCT 780
DB 1735 ATGACTCGCTGAGGCTCTCAATATGATGAGGAGCAACATATAAGATATATCTCT 1794
OY 781 CTATTTAGAAAAGCATGGGCGGAGACCTTAAAGTACTAATGCTGATGTTGCTGCTGCTC 840
DB 1795 CTATTTAGAAAAGCATGGGCGGAGACCTTAAAGTACTAATGCTGATGTTGCTGCTGCTC 1854
OY 841 GGTACGGCGCTGCGGCGCTGCTGTCACAGAAACATCTGTGACTTATCTGCGCGGC 900
DB 1855 GGTACGGCGCTGCGGCGCTGCTGTCACAGAAACATCTGTGACTTATCTGCGCGGC 1914
OY 901 AAGAACCTGTGCTGCAAACTGCGCTCGTGAATCACTATCTAGTCCGTCCGAACATC 960
DB 1915 AAGAACCTGTGCTGCAAACTGCGCTGTAGATCACTATCTAGTCCGTCCGAACATC 1974
OY 961 TTGCTGGGTGAGTAAAGGCTGCGGAGTGTACCGCAATGCTACTTCTGAGTGAATATG 1020
DB 1975 TTGCTGGGTGAGTAAAGGCTGCGGAGTGTACCGGATGCTACTTCTGAGTGAATATG 2034
OY 1021 GACCAATATGAGAAACACACATATGATGATCCATCTAGGCAATGAGGAGCCAACT 1080
DB 2035 GACCAATATGAGAAACACACATATGATGATCCATCTAGGCAATGAGGAGCCAACT 2094
OY 1081 ACTGTTATGCTCCATACCGGCGGCTGCGAGAAATGAGGAGTAAACCGCTGCGGAGAT 1140
DB 2095 ACTGTTATGCTCCATACCGGCGGCTGCGAGAAATGAGGAGTAAACCGCTGCGGAGAT 2154
OY 1141 GACCTGTACTGTACGCGGCTGACGCGGCTTACTCTGTGCTCGGCGGAGAGAACTGCC 1200
DB 2155 GACCTGTACTGTACGCGGCTGACGCGGCTTACTCTGTGCTCGGCGGAGAGAACTGCC 2214
OY 1201 GTCAATATGAGCTATGCTGAGAGGCTTATTAAGAAAGTATACGTAAGTGTGGCA 1260
DB 2215 GTCAATATGAGCTATGCTGAGAGGCTTATTAAGAAAGTATACGTAAGTGTGGCA 1274
OY 1261 TTGGAACCTGACCGGATCCATATCACTTATGATTCACAGAGTGCAGGCTGACCGGATCC 1320
DB 2275 TTGGAACCTGACCGGATCCATATCACTTATGATTCACAGAGTGCAGGCTGACCGGATCC 2334
OY 1321 TTCAACAACTTCAATCTGAGAGGATGTTCTTCCGGTCAATGAGTGTCTGATGACTG 1380
DB 2335 TTCAACAACTTCAACCTGAGAGGATGTTCTTCCGGTCAATGAGTGTCTGATGAAATG 2394
OY 1381 AGTGTGCTGCTGCTGCGGCGGAGAAACAGGTCGCTCGGTAACGCGGCTCCAGAAAGC 1440
DB 2395 AGTGTGCTGCTGCTGCGGCGGAGAAACAGGTAAGTCCGGAACGCGGCTCCAGAAAGC 2454
OY 1441 TACTCTCCCTTGGTGAAGTCTCTCTGCGCAGACAGATCTCAAGCTGAGCGGTGCTTC 1500
DB 2455 TACTCTCCCTGAGTGAAGTCTCTCTGCGCAGACAGATCTCAAGCTGAGCGGTGCTTC 2514
OY 1501 TACTTGGGCAACTGTTCGAAGCGGCGCTTGGCTGAGACTTCGCTGATGACAGACGATACG 1560
DB 2515 TACTTGGGCAACTGTTCGAAGCGGCGCTTGGCTGAGACTTCGCTGATGACAGACGATACG 2574
OY 1561 GCGTGTGCTGCTCACTGTGTAATCTTATCAATTAATCTGCTGCTCATATGAGAAACAA 1620
DB 2575 GCGTGTGCTGCTCACTGTGTAATCTTATCAATTAATCTGCTGCTCATATGAGAAACAA 2634
OY 1621 ATTAGAGATAGGCTAGCTGAAATATATACAGAAATGAGGCTATGAAATAGATCGAAGCA 1680
DB 2635 ATTAGAGATAGGCTAGCTGAAATATATACAGAAATGAGGCTATGAAATAGATCGAAGCA 2694
OY 1681 GGCTGATGTATCGGCGAACAGAGAAAGACTTGCACAAAGATCAACCCCTGCTGTCGCC 1740

Db	2695	GGCTGGATGTATCGGGGACCAAGAGAAAGACTTTGGACAAGATTCACACCCCTGGCTGTGGCC	2754
Qy	1741	TTCCAGCGACCTCCCACTCTGTGAGAAACGATACGACATACAACTGTGTGACACACTC	1800
Db	2755	TTCCAGCGCTCTCCCGCCTGTGAGAAACGATACGACATACAACTGTGTGTGACACACTC	2814
Qy	1801	AAAGCTATCCGGGCTCTGGGGCTACTACATCAGCTTAAGATTAAGCCCTCCAGCAAGCATCCG	1866
Db	2815	AAAGCTATCCGGGCTCTGGGGCTACTACATCAGCTTAAGATTAAGCCCTCCAGCAAGCATCCG	2874
Qy	1861	AACCTGTGTCGCCCAACGAACTTTCTATGCAATCCACCGGCTACCAAGCCAGCAACACTC	1920
Db	2875	AACCTGTGTCGCCCAACGAACTTTCTATGCAATCCACCGGCTACCAAGCCAGCAACACTC	2934
Qy	1921	GACCTGAGTGTGTCACTCTGACCAACCAAGATGATGACTAGTAGACCAAGCTGGCTGAG	1980
Db	2935	GATCTGAGTGTGTCACTCTGACCAACCAAGATGATGACTAGTAGACCAAGCTGGCTGAG	2994
Qy	1981	AACACCCCAACACTTTTGGGCCAGGAGAGATACAGACAGGATGATCTTAATGACATTAA	2040
Db	2995	AAACAACAACAACCTTTTGGGCCAGGAGAGATACAGACAGGATGATCTTAATGACATTAA	3054
Qy	2041	GAGGACTGGACATGCAATCGTTCCCGGCACTGGGTCCTGATCCGAAGGTTGACGATGCC	2100
Db	3055	GAGGACTGGACATGCAATCGTTCCCGGCACTGGGTCCTGATCCGAAGGTTGACGATGCC	3114
Qy	2101	ATCAAGAAAGCCAAACAGGAGCAACAGCCTCGAGACTGTGAGAGACCTGTGTGTCTACCGG	2160
Db	3115	ATCAAGAAAGCCAAACAGGAGCAACAGCCTCGAGACTGTGAGAGACCTGTGTGTCTACCGG	3174
Qy	2161	TATATGCTGGACCCGCGCTTACTGGGGAGCAGCATGAAAGCATCTTGTGTGAAAGCTCAAA	2220
Db	3175	TATATGCTGGACCCGCGCTTACTGGGGAGCAGCATGAAAGCATCTTGTGTGAAAGCTCAAA	3234
Qy	2221	CAGAAAGCAAGAGCACTTCAGAAACAATACCGCGCTGAGAAACCTATGCGCTGAGCTGGG	2280
Db	3235	CAGAAAGCAAGAGCACTTCAGAAACAATACCGCGCTGAGAAACCTATGCGCTGAGCTGGG	3294
Qy	2281	AAGTGTACTTTCAGATTTGAGATCTTAAACGGCTGGACCTATGAGGGTTCGGCTGGGCTAC	2340
Db	3295	AAGTGTACTTTCAGATTTGAGATCTTAAACGGCTGGACCTATGAGGGTTCGGCTGGGCTAC	3354
Qy	2341	GCTGATATGCAACAAGATATGATGCTCGACCAACGAGAACTCTTGGGCAATTTGATGCT	2400
Db	3355	GCTGATATGCAACAAGATATGATGCTCGACCAACGATGAGAACTCTTGGGCAATTTGATGCT	3414
Qy	2401	TACAAATGAGAAAGATGATACAGCGGTAAACAATGATCTTTCCGCAAGCAATGGGCTGT	2460
Db	3415	TACAAATGAGAAAGATGATACAGCGGTAAACAATGATCTTTCCGCAAGCAATGGGCTGT	3474
Qy	2461	GGTGACGATGAGGGGGTTCCTAGATCTCAATGATTAAGACGATTAAGTTTCTCACTCAAT	2520
Db	3475	GGTGACGATGAGGGGGTTCCTAGATCTCAATGATTAAGACGATTAAGTTTCTCACTCAAC	3534
Qy	2521	GGTGAATTTGATGATGATGCTCTTGGCGAGAGACTACGTTTGTGATGTCCAGGGTAC	2580
Db	3535	GGTGAATTTGATGATGATGCTCTTGGCGAGAGACTACGTTTGTGATGTCCAGGGTAC	3594
Qy	2581	AACCTTTGTACCAAGCTTGTCAACTTGGTGTGGGCAAAAAGCCAGTTAACTATGGCCAA	2640
Db	3595	AACCTTTGTACCTGTGTGACAGCTGTGTGTGGGCAAAAAGCCAGTTAACTAAGGTACG	3654
Qy	2641	GATGTAATATCTGAAATTAATCTTCAACAATGTGGTCTTACAGAGGATATGAACATTT	2700
Db	3655	GACGTGAACAGTTGAATTAATCTTCAACAATGTGGTCTTACAGAGGATATGAACATTT	3714
Qy	2701	TGCGTCAATATGAAGAGAGAGCTGTACTCACTGTGACCAAGAGCAACGACGATCTTCAG	2760
Db	3715	TGTGTCAATATGAAGAGAGAGCTGTACTCACTGTGATTAATAAAGATCAAGCAATCTTCAG	3774
Qy	2761	AATATCAATGAGATATGACCAACCGAATTTGATGTGACCAAGATACCAAGCTGTTCAGAT	2820

Db	3775	AAATCTGATGGAATGATCGAACCCGAAATTGATGCAACAGATATCCAGCTGGTTACAGAT	383
Qy	2821	ACACCTCAGTCCCTCCANAGATTTCCCAACAACGGTTGAGAGATGAGAAAGCTAACTGG	2881
Db	3835	ACACCTTCATCCCTCCANAGATTTCCCAACAACGGTTGAGAGATGAGAAAGCTAACTGG	389
Qy	2881	GAGTTCTTACGCTCTCTCACTCCCTGTATTGTCGCATTAACGAGTTCAATTGACGAGGCAGA	2944
Db	3895	GAGTTCTTACGCTCTCTCACTCCCTGTATTGTCGCATTAACGAGTTCAATTGACGAGGCAGA	395
Qy	2941	AAAGCCAGACGTTGGGTAGAAATCAAGGACCGTCAACGATCTTAATGAAAGGCAAGTT	3000
Db	3955	AAAGCCAGACGTTGGGTAGAAATCAAGGACCGCCCAACAGATTTTAATGAAAGGCAAGTT	401
Qy	3001	G 3001	
Db	4015	G 4015	

RESULT 3
ID ADM68757
ID ADM68757 standard; DNA; 15679 BP.

XX	ADM68757;	
XX	17-JUN-2004	(first entry)
DE	Heliothis virescens ryanodine receptor encoding DNA SEQ ID NO:1.	
XX	ryanodine receptor; insect ion channel; insecticide; pesticide;	
KW	calcium balance disruption; receptor calcium release mechanism; gene; de.	
XX	Heliothis virescens.	
OS		
XX	Key	Location/Qualifiers
FM	CDS	251..15679
FT		/*tag=a
FT		/product="ryanodine receptor"
XX		
PN	WO2004027042-A2.	
XX		
PD	01-APR-2004.	
XX		
PF	23-SEP-2003; 2003WO-US029834.	
XX		
PR	23-SEP-2002; 2002US-0412795P.	
PR	18-NOV-2002; 2002US-0427324P.	
XX		
PA	(DUPLO) DU POINT DE MEMOIRS & CO E I.	
XX		
PI	Caepar T, Cordova D, Gutierrez S, Rauh JJ, Smith RM, Wu LJ,	
PI	Tao Y;	
XX		
DR	WPI; 2004-295411/27.	
XX	P-PSDB; ADM68758.	
PT		
PT	New isolated nucleotide fragment encoding a ryanodine receptor, useful	
PT	for isolating other pest ryanodine receptors and in developing screens to	
PT	identify insecticidally active compounds.	
XX		
PS	Claim 6; SEQ ID NO 1; 687bp; English.	
XX		
XX	The present invention describes an isolated nucleotide fragment (1)	
CC	comprising: (a) a nucleic acid sequence encoding a ryanodine receptor	
CC	having an amino acid sequence identity of at least 80% when compared to a	
CC	polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,	
CC	128, 130, 144, or 146; or (b) the complement of (a). (1) comprises a	
CC	nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.	
CC	1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant	
CC	construct comprising (1) operably linked to at least one regulatory	
CC	sequence; (2) a transformed host cell comprising the recombinant	
CC	construct; (3) a method to isolate (1) encoding ryanodine receptors and	
CC	related polypeptides; (4) an isolated polypeptide having ryanodine	

OY	1801	AAAGATATATCCGAGGCTCTGGGGCTACATCAATCAAGCTTAAGTAAGCCCTCCAGCAAGCATCCG	1860
Db	3065	AAGATATATCTGGGCTCTGGGGCTACTACATCAAGCTTAAGTAAGCCCTCCAGCAAGCATCCG	3124
OY	1861	AACGTTCCGTCTGGCCCAAGCAAACTTTCAATGCAAGTCCAAACGGCTACAAACCGACACCACTC	1920
Db	3125	AACGTTCCGTCTGGCCCAAGCAAACTTTCAATGCAAGTCCAAACGGCTACAAACCGACACCACTC	3184
OY	1921	GACCTGAAGTCTGTCAACCCCTGACACCCAAAGATGATGAGCTAAGTAAAGACCAAGCTGGCTGAG	1980
Db	3185	GACCTGAAGTCTGTCAACCCCTGACACCCAAAGATGATGAGCTAAGTAAAGACCAAGCTGGCTGAG	3244
OY	1981	AAACACCCCAAACTTTGGGCGAAGGAGATACAGCAAGGAGATGGACTTAAGCACTTAAT	2040
Db	3245	AAACACCCCAAACTTTGGGCGAAGGAGATACAGCAAGGAGATGGACTTAAGCACTTAAT	3304
OY	2041	GAGAGCTCGGACATGTCATCGTTCCCGGACCTGGGGCCATACCCGAAGTTGAAGATGCC	2100
Db	3305	GAGAGCTCGGACATGTCATCGTTCCCGGACCTGGGGCCATACCCGAAGTTGAAGATGCC	3364
OY	2101	ATCAAGAAAGGCCAACAGGAGCAACAGCTTCGAGACCTGTGTAGAGACCTGTGCTGCTACACGG	2160
Db	3365	ATCAAGAAAGGCCAACAGGAGCAACAGCTTCGAGACCTGTGTAGAGACCTGTGCTGCTACACGG	3424
OY	2161	TATATGCTGGAACCCCGCTTACTGGGGAGACGACTGAAGCATCTTTGTGTGAACCGTCAAA	2220
Db	3425	TATATGCTGGAACCCCGCTTACTGGGGAGACGACTGAAGCATCTTTGTGTGAACCGTCAAA	3484
OY	2221	CAGAAAGCAAGGACCTTGAGAACATACCGCGCTGAGAAAGACTATAGCGCTGAGCTCTGG	2280
Db	3485	CAGAAAGCAAGGACCTTGAGAACATACCGCGCTGAGAAAGACTATAGCGCTGAGCTCTGG	3544
OY	2281	AAAGTGTACTTCGAGTTTGAGATCTTAAACGGCTGACCTTAATGAGGGTCCGCTGGGCTAC	2340
Db	3545	AAAGTGTACTTCGAGTTTGAGATCTTAAACGGCTGACCTTAATGAGGGTCCGCTGGGCTAC	3604
OY	2341	GCTGATATGACCAAGAAATGATGCTTCGAGCAAGCAAGAACTTTGGGCACTTTGATGCT	2400
Db	3605	GCTGATATGACCAAGAAATGATGCTTCGAGCAAGCAAGAACTTTGGGCACTTTGATGCT	3664
OY	2401	TACAAATGAGAAAGTGTACAGCGGTAACACTGAGCTTTTCGGAACCAATGGGCTGT	2460
Db	3665	TACAAATGAGAAAGTGTACAGCGGTAACACTGAGCTTTTCGGAACCAATGGGCTGT	3724
OY	2461	GGTGACGTAGTGGGGGTGTTCTTAATCTCAATTGATTAAGACGATTAAGTTCTCACTCAAT	2520
Db	3725	GGTGACGTAGTGGGGGTGTTCTTAATCTCAATTGATTAAGACGATTAAGTTCTCACTCAAC	3784
OY	2521	GGTGATGTTGTGATGGAATGCTTTGGCGAGAGACTACGTTTCTGATGTCCAAGGTAC	2580
Db	3785	GGTGATGTTGTGATGGAATGCTTTGGCGAGAGACTACGTTTCTGATGTCCAAGGTAC	3844
OY	2581	AACTTTGTATCCAGCTTGACACTTGGTGGGCCAAAAAGCCAGGTTAAATATGAGCCAA	2640
Db	3845	AACTTTGTATCCAGCTTGACACTTGGTGGGCCAAAAAGCCAGGTTAAATATGAGCCAA	3904
OY	2641	GATGTGAATACCTCTGAATACTTCAACAATGTGATCTTACGGAAGGATATGAACATTT	2700
Db	3905	GATGTGAATACCTCTGAATACTTCAACAATGTGATCTTACGGAAGGATATGAACATTT	3964
OY	2701	TGCGTCAATATTAAGAGAGACGTGACTGACTGGTACACCAAGAGCAACCGCATCTTCCAG	2760
Db	3965	TGCGTCAATATTAAGAGAGACGTGACTGACTGGTACACCAAGAGCAACCGCATCTTCCAG	4024
OY	2761	AATACTGATGAGATGATCGACCAAGAAATTGATGACCAAGATACCAAGCTGTTCAGAT	2820
Db	4025	AATACTGATGAGATGATCGACCAAGAAATTGATGACCAAGATACCAAGCTGTTCAGAT	4084
OY	2821	ACAACCTCAATGCTCAAGATTTTCCCAACAACGTTCCGAGACGATGGAAGAAAGCTTAACG	2880
Db	4085	ACAACCTCAATGCTCAAGATTTTCCCAACAACGTTTGAAGCAATGGAAGAAAGCTTAACG	4144

OY		2881	GAGTTCCTTAACGCTCTCACTCCCTGGTATCTGCATTAACGAGTTCAATTGACGAGCGA	2940
Db		4145	GAGTTCCTTAACGCTCTCTCACTCCTCTGTCACTGCGCATTAACGAGTTCAATTGACGAGCGA	4204
OY		2941	AAAGCCAGCACGTTGGGTAGAATAATCAAGAACCGTCAACAGATCCTTAATGAAGAAGCGAGTT	3000
Db		4205	AAAGCCAGCACGTTGGGTAGAATAATCAAGAACCGTCAACAGATCCTTAATGAAGAAGCGAGTT	4264
OY		3001	G 3001	
Db		4265	G 4265	
 RESULT 4 ADM68885 ID ADM68885 standard; DNA, 15405 BP.				
XX	AC	ADM68885;		
XX	AD	ADM68885;		
Dt	17-JUN-2004	(first entry)		
XX	DE	Heliothis virescens ryanodine receptor encoding DNA SEQ ID NO:129.		
XX	KM	ryanodine receptor; insect ion channel; insecticide; pesticide;		
XX	KW	calcium balance disruption; receptor calcium release mechanism; gene; ds.		
OS		Heliothis virescens.		
XX	Key	Location/Qualifiers		
FH	CDS	1..15405		
FT		/*tag= a		
FT		/product= "ryanodine receptor"		
PN		WO2004027042-A2.		
PD		01-APR-2004.		
XX	PP	23-SEP-2003; 2003WO-US029834.		
XX	PR	23-SEP-2002; 2002US-0412795P.		
PR		18-NOV-2002; 2002US-0427324P.		
PA		(DUBO) DU PONT DE NEMOURS & CO E I.		
PI		Caspar T, Cordova D, Gutierrez S, Rauh JJ, Smith RM, Wu L;		
PT		Tao Y,		
DR		WPI; 2004-295411/27.		
XX	P-PSDB;	ADM68895.		
PT		New isolated nucleotide fragment encoding a ryanodine receptor, useful		
PT		for isolating other pest ryanodine receptors and in developing screens to		
PT		identify insecticidally active compounds.		
PS		Claim 6, SEQ ID NO 129; 687bp; English.		
XX		The present invention describes an isolated nucleotide fragment (1)		
CC		comprising: (a) a nucleic acid sequence encoding a ryanodine receptor		
CC		having an amino acid sequence identity of at least 80% when compared to a		
CC		polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,		
CC		128, 130, 144, or 146; or (b) the complement of (a). (1) comprises a		
CC		nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.		
CC		1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant		
CC		construct comprising (1) operably linked to at least one regulatory		
CC		sequence; (2) a transformed host cell comprising the recombinant		
CC		construct; (3) a method to isolate (1) encoding ryanodine receptors and		
CC		related polypeptides; (4) an isolated polypeptide having ryanodine		
CC		receptor activity; (5) a method for evaluating at least one compound for		
CC		its ability to modulate calcium homeostasis; (6) a method for evaluating		
CC		at least one compound which modulates ryanodine receptor activity; (7) an		
CC		isolated nucleic acid fragment encoding an insect ion channel comprising		
CC		at least two fully defined polypeptide sequences selected from SEQ ID		
CC		NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,		

CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an insect ion channel; (9) a method for expressing an isolated nucleic acid fragment encoding a toxic insect ion channel; and (10) recombinant CC construct comprising in the 5' to 3' direction a promoter operably linked to an isolated nucleic acid fragment encoding a toxic insect ion channel. CC The isolated nucleic acid fragment (I) encoding a ryanodine receptor is CC useful for the isolation of other pest ryanodine receptors and developing CC of screens to identify insecticidally active compounds. The nucleic acid CC fragments are useful as pesticides, fragments of protein for antibody CC production, fragments of protein for determination of the structure of CC insecticide binding sites and in the identification of insecticides that CC disrupt the calcium balance in cells through other messengers that CC interact with the receptor calcium release mechanism. The present CC sequence is used in the exemplification of the present invention.

XX Sequence 15405 BP; 4086 A; 3850 C; 4173 G; 3296 T; 0 U; 0 Other;

Query Match 94.7%; Score 2841; DB 12; Length 15405;

Best Local Similarity 96.7%; Pred. No. 0;

Matches 2901; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 1 GTCATAGGCGGCCCATCATCAAAATATGGTGAATCCACCGTCAATGTGCAGCATTCGAG 60
DB 1000 GTCAATAGGCGGCCCATCATCAAAATATGGTGAATCCACCGTCAATGTGCAGCATTCGAG 1059
QY 61 ACTGGCTTGTGGCTGTCTTATTAAGTCTTAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 120
DB 1060 ACTGGCTTGTGGCTGTCTTATTAAGTCTTAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 1119
QY 121 GAAAGAAAGAAAGAAAGAAATCTCCAGAGAAAGCAAGATGAGACGATGGCTCGACTTC 180
DB 1120 GAAAGAAAGAAAGCAATCTCCAGAGAAAGCAAGATGAGACGATGGCTCGACTTC 1179
QY 181 AGGTCAAGAGAAAGAAATCTAGACCTGCTCGAGTTATCAGGAAGTGTCTTCGCTGTT 240
DB 1180 AGGTCAAGAGAAAGAAATCTAGACCTGCTCGAGTTATCAGGAAGTGTCTTCGCTGTT 1239
QY 241 ACTAAGTTATCATATGTTCTGAGAACTCTCAAGAAACCGTCTCACTCGATGTTCTTC 300
DB 1240 ACTAAGTTATCATATGTTCTGAGAACTCTCAAGAAACCGTCTCACTCGATGTTCTTC 1239
QY 301 GCGTCAGTGAACCTGGGCGAGATGAGTATGCGCTCGAGATCTCATCACTTCGCA 360
DB 1300 GCGTCAGTGAACCTGGGCGAGATGAGTATGCGCTCGAGATCTCATCACTTCGCA 1359
QY 361 CAGCCGATGAGATATGAGAACAGAGAAACAAATTCGCGGCACTCCGAAC 420
DB 1360 CAGCCGATGAGATATGAGAACAGAGAAACAAATTCGCGGCACTCCGAAC 1419
QY 421 CGTCAGAACCTGTTCCAAAGAGAGCAATCTGAATCTGAATCTGAATCTGAATCTGA 480
DB 1420 CGTCAGAACCTGTTCCAAAGAGAGCAATCTGAATCTGAATCTGAATCTGAATCTGA 1479
QY 481 ATCAACGTCATCAAGTCCAGAGGCTTCTCGCTGATCTCGAGCGGAGAGAAATCGGA 540
DB 1480 ATCAACGTCATCAAGTCCAGAGGCTTCTCGCTGATCTCGAGCGGAGAGAAATCGGA 1539
QY 541 CAGAGCTGGGAAATATATCTGATATTTGATCTGATCTGAGCGGCAATATAAGGCG 600
DB 1540 CAGAGCTGGGAAATATATCTGATATTTGATCTGATCTGAGCGGCAATATAAGGCG 1539
QY 601 AACCAACGAACTGGGCGCAAGTTGCGAACTCGAAACGCGCTCAACTGGCTGTTCTCGG 660
DB 1600 AACCAACGAACTGGGCGCAAGTTGCGAACTCGAAACGCGCTCAACTGGCTGTTCTCGG 1659
QY 661 CTGGCTGCGAGGCTCTGGGCGAGAGGCAACGCGCAATGCTCGAATGCTGCGATGCTT 720
DB 1660 CTGGCTGCGAGGCTCTGGGCGAGAGGCAACGCGCAATGCTCGAATGCTGCGATGCTT 1719
QY 721 ATGAGCTGCGCTGAGAGCTCTCAATATGATGAGGAGCAACATATAAGTATATCTCT 780
DB 1720 ATGAGCTGCGCTGAGAGCTCTCAATATGATGAGGAGCAACATATAAGTATATCTCT 1779

QY 781 CTATTAGAAAAGCATGGGCGGAGACCTTAAGTACTAATATGTCATGTTGCTGTCGCTC 840
DB 1780 CTATTAGAAAAGCATGGGCGGAGACCTTAAGTACTAATATGTCATGTTGCTGTCGCTC 1839
QY 841 GGTAAACGCGCTGGGCTGCGCTGCTGCAAGAAACAACTGTGACTACTTACTGCGCGC 900
DB 1840 GGTAAACGCGCTGGGCTGCGCTGCTGCAAGAAACAACTGTGACTACTTACTGCGCGC 1839
QY 901 AAGAACCTGTGTGCTGCAAACTGCGCTGCTGATGATGATGATGATGATGATGATGATG 960
DB 1900 AAGAACCTGTGTGCTGCAAACTGCGCTGCTGATGATGATGATGATGATGATGATGATG 1959
QY 961 TTGCTGGCTGCAAGTGAAGAGGTGCGGAGTGAACCGCAATATGATCTTCTGAGTGA 1020
DB 1960 TTGCTGGCTGCAAGTGAAGAGGTGCGGAGTGAACCGCAATATGATCTTCTGAGTGA 2019
QY 1021 GACCAATAGAGAGACCAACATATGATGATGATGATGATGATGATGATGATGATGATG 1080
DB 2020 GACCAATAGAGAGACCAACATATGATGATGATGATGATGATGATGATGATGATGATG 2079
QY 1081 ACTGTTATATGTCCTCATACCGGCGGCTGCGAGAAATGGGAGGTAAACGCGTGGAGAT 1140
DB 2080 ACTGTTATATGTCCTCATACCGGCGGCTGCGAGAAATGGGAGGTAAACGCGTGGAGAT 2139
QY 1141 GACCTGATCTGATACGGGCTGCAAGCGGCTTACTCTGCTGCGGAGAGAGAACTTCC 1200
DB 2140 GACCTGATCTGATACGGGCTGCAAGCGGCTTACTCTGCTGCGGAGAGAGAACTTCC 2139
QY 1201 GTCAATAGGACCTAGTGTGAAAGAGCTTATATTAAGAAAGGTGAGTATGATGAGCA 1260
DB 2200 GTCAATAGGACCTAGTGTGAAAGAGCTTATATTAAGAAAGGTGAGTATGATGAGCA 2259
QY 1261 TTGACCTGAACGATACCATATATCACTTCAATGTTCAACGAGATGCGGATGACCG 1320
DB 2260 TTGACCTGAACGATACCATATATCACTTCAATGTTCAACGAGATGCGGATGACCG 2319
QY 1321 TTCAACCACTTCAATCTGAGAGAGATGTTCTTCCCGTCAATGATGCTCTATGATGATG 1380
DB 2320 TTCAACCACTTCAATCTGAGAGAGATGTTCTTCCCGTCAATGATGCTCTATGATGATG 2379
QY 1381 AGTTGCGGATTCCTGCTGGGCGAGAACAGGTCCTCGGATGCGGCGCTCCAGAAAGG 1440
DB 2380 AGTTGCGGATTCCTGCTGGGCGAGAACAGGTCCTCGGATGCGGCGCTCCAGAAAGG 2439
QY 1441 TACTCTCCCTTGTGAGATCTCTCTGCGGAGAGATCTCAAGCTGAGACCGTGTCTTC 1500
DB 2440 TACTCTCCCTTGTGAGATCTCTCTGCGGAGAGATCTCAAGCTGAGACCGTGTCTTC 2499
QY 1501 TACTTGGGCAACCTGTCCAAAGCGGCTTGGCTGAGACCTCGCTGATGATGAGATGAG 1560
DB 2500 TACTTGGGCAACCTGTCCAAAGCGGCTTGGCTGAGACCTCGCTGATGATGAGATGAG 2559
QY 1561 GCCTTGGGCAACCTGTGATGATCTTCAAGATGATGATGATGATGATGATGATGATGATG 1620
DB 2560 GCCTTGGGCAACCTGTGATGATCTTCAAGATGATGATGATGATGATGATGATGATGATG 2619
QY 1621 ATTAGATATAGCTAGCTGAAATATATCAAGAAATGCGCTATGATGATGATGATGATG 1680
DB 2620 ATTAGATATAGCTAGCTGAAATATATCAAGAAATGCGCTATGATGATGATGATGATG 2679
QY 1681 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
DB 2680 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2739
QY 1741 TTGAGAGGACCTCCGCTGAGAAACGATGATGATGATGATGATGATGATGATGATGATG 1800
DB 2740 TTGAGAGGACCTCCGCTGAGAAACGATGATGATGATGATGATGATGATGATGATGATG 2739
QY 1801 AAGATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
DB 2800 AAGATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2859
QY 1861 AACGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920

Db	2860	AACTGTCGTCGCGCCCAAGAACTTTATGCAATCACAAGCGCTCAACGCTCAACGACCACTC	2919
Qy	1921	GACCTGAAGTCGTGTCACCTTGACAACCCAAATGATGATGACTAGTAAACCACTGACTGAG	1980
Db	2920	GACCTGAAGTCGTGTCACCTTGACAACCCAAATGATGATGACTAGTAAACCACTGACTGAG	2979
Qy	1981	AAACCCCAACACTTTGGGCGAAGGAGAGATACAGACGAGGATGACTTATGACCTTAAT	2040
Db	2980	AAACCCCAACACTTTGGGCGAAGGAGAGATACAGACGAGGATGACTTATGACCTTAAT	3039
Qy	2041	GAGGACTCGGACATGCACTGTTCCCGGACCTGGGACCTACCCGAAGTTGAGATGACC	2100
Db	3040	GAGGACTCGGACATGCACTGATGCCCGACCTGGGACCTACCCGAAGTTGAGATGACC	3099
Qy	2101	ATCAAGAAAGCCACAGGAGCAACAGCTTCGAGACTGTGAGAGACCTGCTGATCGAG	2160
Db	3100	ATCAAGAAAGCCACAGGAGCAACAGCTTCGAGACTGTGAGAGACCTGCTGATCGAG	3159
Qy	2161	TATATGCTGGAACCCGCTCTACTGGGAGCAGCATGAGCACTCTGTTGGAAGCTCAAA	2220
Db	3160	TATATGCTGGAACCCGCTCTACTGGGAGCAGCATGAGCACTCTGTTGGAAGCTCAAA	3219
Qy	2221	CAGAAAGCAAGCACTTCAAGAACATACCGGCTGAGAAAGCTATGCCGTCAAGCTGGG	2280
Db	3220	CAGAAAGCAAGCACTTCAAGAACATACCGGCTGAGAAAGCTATGCCGTCAAGCTGGG	3279
Qy	2281	AAAGTGTACTTCGAGTTTGAGATCTTAAACGCTGGAACCTATGAGGGTTCGCTGGGCTAC	2340
Db	3280	AAAGTGTACTTCGAGTTTGAGATCTTAAACGCTGGAACCTATGAGGGTTCGCTGGGCTAC	3339
Qy	2341	GCTGATATGCAACCAAGAAATGATGCTCGGACAAGACGAGAACTTTGGGCAATTGATGCT	2400
Db	3340	GCTGATATGCAACCAAGAAATGATGCTCGGACAAGACGAGAACTTTGGGCAATTGATGCT	3399
Qy	2401	TACAAATGAGAAAAAGTTACAGCGCTTAACTGAGCTTTCCGAGACAAATGGGCTGTT	2460
Db	3400	TACAAATGAGAAAAAGTTACAGCGCTTAACTGAGCTTTCCGAGACAAATGGGCTGTT	3459
Qy	2461	GGTGACGATGAGGGGGGTGTTCCTAGATCTCAATGTAAGACGATTAAGTTTCTCACTCAAT	2520
Db	3460	GGTGACGATGAGGGGGGTGTTCCTAGATCTCAATGTAAGACGATTAAGTTTCTCACTCAAC	3519
Qy	2521	GGTGAGTTGTTGATGATGCTCTTGCGCGAGAGACTACGTTTGCTGATGTCCAAGGTGAC	2580
Db	3520	GGTGAGTTGTTGATGATGCTCTTGCGCGAGAGACTACGTTTGCTGATGTCCAAGGTGAC	3579
Qy	2581	AACTTTGTAACAAGCTTGCACACTTGTGTGGCCAAAAGCCAGTTAACTATGGCCAA	2640
Db	3580	AACTTTGTAACAAGCTTGCACACTTGTGTGGCCAAAAGCCAGTTAACTATGGCTCAG	3639
Qy	2641	GATGGAATTAATCTGAAATTAATCTTCAACATGTGTCTTCAGAGGGATTAAGAACATTT	2700
Db	3640	GATGGAATTAATCTGAAATTAATCTTCAACATGTGTCTTCAGAGGGATTAAGAACATTT	3699
Qy	2701	TGCGCTAATATGAGAAGAGACGTGACTCACTGTTCAACAAAGCACAGCCGATCTTGAG	2760
Db	3700	TGCGCTAATATGAGAAGAGACGTGACTCACTGTTCAACAAAGCACAGCCGATCTTGAG	3759
Qy	2761	AATACTGATGAGATGATGCAACCAAGATTAATGTGACCAAGATTAACAGCTGTTCAAT	2820
Db	3760	AATACTGATGAGATGATGCAACCAAGATTAATGTGACCAAGATTAACAGCTGTTCAAT	3819
Qy	2821	AACACTCAATGCTCAAAATTTCCCAACAACGTTCCGAGAGATGAGAAAGCTTAACTGG	2880
Db	3820	AACACTCAATGCTCAAAATTTCCCAACAACGTTTGAAGATGAGAAAGCTTAACTGG	3879
Qy	2881	GAGTTCCTTAACGCTCTCACTGCGCTTTATCTGCACTTAACGATTCATTTGACGAGCAGAA	2940
Db	3880	GAGTTCCTTAACGCTCTCACTGCGCTTTATCTGCACTTAACGATTCATTTGACGAGCAGAA	3939
Qy	2941	AAAGCCAGACGTTGGGTGAAATCAAGACGCTCAACGATCTTAATGAAGGCAATT	3000

D6		3940 AAAGCGGCTGTGGTGAATCATAGAACCGCCAACAGATTCTTAACATAAAGGCAGTT	3939
Gy	3001 G 3001		
D8	4000 G 4000		
ID	ADME68899 standard; DNA; 15429 BP.		
XX AC	ADM68899;		
DT XX	17-JUN-2004 (first entry)		
DE XX	Heliopsis virescens ryanodine receptor encoding DNA SEQ ID NO:143.		
KW XX	ryanodine receptor; insect ion channel; insecticide; pesticide; gene; ds.		
OS XX	calcium balance disruption; receptor calcium release mechanism; gene; ds.		
FH XX	Heliopsis virescens.		
CDS PT	Key Location/Qualifiers 1..15429 /tag=a PT CDS /product= "ryanodine receptor"		
PN XX	WO2004027042-A2.		
PD XX	01-APR-2004.		
PF XX	23-SEP-2003; 2003WO-US029834.		
PR XX	23-SEP-2002; 2002US-0412795P.		
PR XX	18-NOV-2002; 2002US-0427324P.		
PA XX	(DUBO) DU PONT DE NEMOURS & CO E I.		
PI XX	Caspar T, Cordova D, Gutierrez S, Rauch JJ, Smith RM, Wu L,		
PI XX	Tao Y;		
DR XX	MPJ; 2004-295411/27. P-P8DB; ADM68800.		
PT XX	New isolated nucleotide fragment encoding a ryanodine receptor, useful for isolating other pest ryanodine receptors and in developing screens to identify insecticidally active compounds.		
PS PS	Claim 6; SEQ ID NO 143; 687bp; English.		
CC CC	The present invention describes an isolated nucleotide fragment (I) comprising: (a) a nucleic acid sequence encoding a ryanodine receptor having an amino acid sequence identity of at least 80% when compared to a polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8, 12B, 13D, 144, or 146; or (b) the complement of (a). (I) comprises a nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO. 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant construct comprising (I) operably linked to at least one regulatory sequence; (2) a transformed host cell comprising the recombinant construct; (3) a method to isolate (I) encoding ryanodine receptors and related polypeptides; (4) an isolated polypeptide having ryanodine receptor activity; (5) a method for evaluating at least one compound for its ability to modulate calcium homeostasis; (6) a method for evaluating at least one compound which modulates ryanodine receptor activity; (7) an isolated nucleic acid fragment encoding an insect ion channel comprising at least two fully defined polypeptide sequences selected from SEQ ID NOB. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56, 120-126; (8) a method for identifying a nucleic acid sequence encoding an insect ion channel; (9) a method for expressing an isolated nucleic acid fragment encoding a toxic insect ion channel; and (10) recombinant constructs comprising in the 5' to 3' direction a promoter operably linked to an isolated nucleic acid fragment encoding a toxic insect ion channel. The isolated nucleotide fragment (I) encoding a ryanodine receptor is		

CC useful for the isolation of other pest ryanodine receptors and developing
CC of screens to identify insecticidally active compounds. The nucleic acid
CC fragments are useful as pesticides, fragments of protein for antibody
CC production, fragments of protein for determination of the structure of
CC insecticide binding sites and in the identification of insecticides that
CC disrupt the calcium balance in cells through other messengers that
CC interact with the receptor calcium release mechanism. The present
CC sequence is used in the exemplification of the present invention.

XX Sequence 15429 BP; 4084 A; 3856 C; 4190 G; 3299 T; 0 U; 0 Other;

Query Match 94.6%; Score 2839.4; DB 12; Length 15429;

Best Local Similarity 96.6%; Pred. No. 0; Mismatches 101; Indels 0; Gaps 0;

Matches 2900; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 1 GTCATAGGCGCGCCCATCATCAATATGATGACCTCACCGTCATTGTGACAGATTCCGAG 60
DB 1015 GTCATAGGCGCGCCCATCATCAATGATGACCTCACCGTCATTGTGACAGATTCCGAG 1074
QY 61 ACTGCTTGTGCTGTCTTATTAAGTCTTAAGAACGAAAGAGAGAGAGAGTGGTAAAGTA 120
DB 1075 ACTGCTTGTGCTGTCTTATTAAGTCTTAAGAACGAAAGAGAGAGAGAGTGGTAAAGTA 1134
QY 121 GAAGGAAAGCAAGCGATTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 1135 GAAGGAAAGCAAGCGATTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1194
QY 181 AGGTCAAG 240
DB 1195 AGGTCAAG 1254
QY 241 ACTAAGTTATCATATGATGCTTGAGAACTCTAAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 1255 ACTAAGTTATCATATGATGCTTGAGAACTCTAAGAGAGAGAGAGAGAGAGAGAGAGAG 1314
QY 301 GCGTCAAGTGAACCTGCGGAG 360
DB 1315 GCGTCAAGTGAACCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1374
QY 361 CAGCCGAG 420
DB 1375 CAGCCGAG 1434
QY 421 CGTCAG 480
DB 1435 CGTCAG 1494
QY 481 ATCAACGTCATCACTGCTCAG 540
DB 1495 ATCAACGTCATCACTGCTCAG 1554
QY 541 CAGAGCTGGGAG 600
DB 1555 CAGAGCTGGGAG 1614
QY 601 AAACCAAG 660
DB 1615 AAACCAAG 1674
QY 661 CTGCGCTGCGAG 720
DB 1675 CTGCGCTGCGAG 1734
QY 721 ATAGAGCTGCGCTGAG 780
DB 1735 ATAGAGCTGCGCTGAG 1794
QY 781 CTATTAG 840
DB 1795 CTATTAG 1854
QY 841 GGTAAAGGAG 900

DB 1855 GGTAAAGGAG 1914
QY 901 AAGAAGCTGTGTGCAAACTGCGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 960
DB 1915 AAGAAGCTGTGTGCAAACTGCGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1974
QY 961 TTGCTGGGTGAG 1020
DB 1975 TTGCTGGGTGAG 2034
QY 1021 GACCAATAG 1080
DB 2035 GACCAATAG 2094
QY 1081 ACTGTTATATGCTCATACCGCGCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
DB 2095 ACTGTTATATGCTCATACCGCGCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2154
QY 1141 GACCTGTATCTGTACGAG 1200
DB 2155 GACCTGTATCTGTACGAG 2214
QY 1201 GTCAATAG 1260
DB 2215 GTCAATAG 2274
QY 1261 TTGAGAGCTGACGAG 1320
DB 2275 TTGAGAGCTGACGAG 2334
QY 1321 TTACAGAACTTCAATCTGAG 1380
DB 2335 TTACAGAACTTCAATCTGAG 2394
QY 1381 AGTTGGGAGTTCCGCTGCGGAG 1440
DB 2395 AGTTGGGAGTTCCGCTGCGGAG 2454
QY 1441 TACTCTCCCTGTGTGAG 1500
DB 2455 TACTCTCCCTGTGTGAG 2514
QY 1501 TACTCTGAG 1560
DB 2515 TACTCTGAG 2574
QY 1561 GCTTGTGAG 1620
DB 2575 GCTTGTGAG 2634
QY 1621 ATTAGAGATAG 1680
DB 2635 ATTAGAGATAG 2694
QY 1681 GGTGTGATGAG 1740
DB 2695 GGTGTGATGAG 2754
QY 1741 TTGAG 1800
DB 2755 TTGAG 2814
QY 1801 AAGAGATATCTGTGAG 1860
DB 2815 AAGAGATATCTGTGAG 2874
QY 1861 AAGCTTGTGTGAG 1920
DB 2875 AAGCTTGTGTGAG 2934
QY 1921 GACCTGAG 1980
DB 2935 GACCTGAG 2994

301 GCGTCAGTGAACCTGGGCGAGATGGTGAATGTGCTCGAGGATCTCATCAATCTTCCGA 360
1237 CAAAAGTCAACCTCAACGAGATGGTCAATGTGCTTTGAGGACTTGATTAATCACTTTTCG 1296
361 CAGCCCGATGAGGATATGGAACAAGAAACAAATTCCTGGGCACTCCGAAC 420
1297 CAACCCGAAGAGATATGAGACAGAGAGAAACGAATCCGATTCCTGGCCCTGGGCAAC 1356
421 CGTCAGACCTGTTCCAAGAGAAAGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 480
1357 CGACAGGATCTGTTCCAGAGAGAGGCGTGTCAATCTGATCTTGAGGCCATTGACAG 1416
481 ATCAACGTATACGTCCTCCAGGGGTTCTCTGTCGATTCCTGGCGGAGACGAAATCTGGA 540
1417 ATCAACATATACCTCGCAGGGCTTCCTAGCCAGCTTCCTGGCCGCGAGACGCGGC 1476
541 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAAGTTCTGCGCGCAATATTAAGGCG 600
1477 CAGAGCTGGGATCTGATCTCCACCTATTTGTACCAACTTTGGCCGCATCAATCAAGGCG 1536
601 AACCAACGAACTGGCGCGAGTTCCGGAACCTGAACCGGCTCAACTGGCTGTTCTCGGC 660
1537 AACCAACGAACTGGCGCGAGTTCCGGAACGATTAACCACTCACTGGCTATTTCTCCGC 1596
661 CTGGGCTCGCAGGCTCTCGGCGAGGCGCACCGGCAATGCTCGACGTCGCTGCGTCTT 720
1597 CTGGGCTCCAGGCTCTCCAGCGAGGGTTCCGGCATGTTGAGAGTACTTCACTGCGTGTG 1656
721 ATGAGCTGGCTGAGGCTCTCAATATGATGAGGAGCAACATATAAGTATATCTCT 780
1657 ATCGATTTGCGCAAGGCACTAAACATGATGCGGATGAGCAATCAAGGTATCATCTCC 1716
781 CTATTAAGAAAGCATGGGCGCGACCTTAAGTACTAGATGTCATGTTCTGCTGTCGCTC 840
1717 CTGCTGAGAGAGCAGCGGACGAGGACCCGAAGTCTTGAAGTTCTGTTCTGTCGCTG 1776
841 GGTAAACGCGCTGCGGCTGCTGTCATCAAGAACAAATCTGTGACTTACTGCTCCGCG 900
1777 GGTAAATGAGTGGCGGTCGATCTCCAGAACAAATTTGCGACTTTTGTGCTACGCGGC 1836
901 AAGAACCTGTGCTGCGAACTGCGCTCGTGATCAAGTATCTAAGTGTCCGTCCGAACATC 960
1837 AAGAAATCTGTGCTACAGACGCTCTGTGAGCAATGTGGCCAGATCCGACCGAACATC 1896
961 TTCTGGGTCAGTGAAGAGGTGCGCAGGTACCGCAATGGTACTTGAAGGTACTATG 1020
1897 TTCTGGGTCGCGTGGACGTTCTTCCATGTCAGAAAGTGTACTTGAAGGTACATG 1956
1021 GACCAATAGAGAGACCAACATATGATGCGACATCTTACGATAGATGGCCAACT 1080
1957 GATCAATAGAGACCAACATATGATGCGACATCTTACGATAGATGGCCGCTAATCT 2016
1081 ACTGTTATATGTCCTCAATCCCGGCGGTGGCGAAATGGGAGGTAAACGCGTGGAAAT 1140
2017 TCCGGGTATATGTCCTGATTCCTCGAGCGCGCAAGATGGGAGGTAAATGAGTAAAG 2076
1141 GACCTGTAATCGTGAAGGTTGACGCGCGCTTACTCTGATCCGCGGAGAGAAAGATCTCC 1200
2077 GACCTGTAATCTTTGGATTTGATGTGCTTTCTTTGAGCGGAGGTGCGAAACACTA 2136
1201 GTCAATAGAGACTCATGCTGAAGAGCTTATATTAAGAAAGTGAAGTGAATGGTTCGCA 1260
2137 GTGTGAGACGCGCTGCCGAGAGACCTTATCCGTAAGGAGATGTTATGTGCGTTC 2196
1261 TTGAGACTGACGCTACCCATATCAACTTCAATGTTCAACGAGAGTGGGCTGACGAGATCC 1320
2197 ATGACCTTTCTGTGCGCATATCAAGTTACTTTTAAACGAGTAAAGTGTGCGGTGCG 2256
1321 TTCAACAATCTCAATCTGGAAGGCAATGTTCTTCCGCTCATCAGCTGCTTATGAAGCTG 1380
2257 TTTAGGAGACTTAACTTGAACGGAATGTTCTTTCCGATGATGATGTGCTCATCAAACTTA 2316

1381 AGTTGTGGTTCTGCTGGGCGAGAAACAGGTGCTCTCCGATACCGGCTCCGAAGGC 1440
2317 AGCTGTGGCTTCTTTTCCGAGGTGATCATGTGTGTTAAAGTGTGCCCCCATGAGG 2376
1441 TACTCTGCTGGGAGTCTCTGCGCGAGGATCCGACCTGGAGCGGTGCTTC 1500
2377 TTTCTGCTCGTGCAGTGTCTATGTCGAGAGATCTTCAATCTGGAATCTTTGCTTC 2436
1501 TACTTCGCAACCTGTCCAAAGCGGCGCTTGGCTGGAACCTCGCTTATGTAACAGATACG 1560
2437 TACTTTGGTATCTTGCAGAAAGATGTTTGGCGGACATAGGCTTATTTAGAGACGACCT 2496
1561 GCTTCTGCTTACCACTCTGTTGATCTTTACATTACTCTGCTCATATGTGAAACA 1620
2497 GCTTTGTTCCGAAGCCCGTTGATACAGCGGTGTGCAATTGCCAAGTTCGTGTGACAA 2556
1621 ATTAAGATAGCTAGCTGAAGAAATATACAGAAATGAGGCTATGAATTAAGATGAAGCA 1680
2557 ATCAAGAGAAAGCTGGCGGAGAAATATCAAGATGTGGCTTTAAACAAATCGAGGCG 2616
1681 GGTGATGTATCGGCGACCAAGAGAAAGCTTGGCAAGATCCACCCTGCTGTCGCC 1740
2617 GGTGTGTGTGGGCGAGCACCGAGATGACTACACCGGCAATCCATCTTGGCTCACCAT 2676
1741 TTGAGGAGCTCCCACTGCTGAGAAAGATACGATACATCAATCTGCTGTGACACATC 1800
2677 TTTGAGAGAGCTTCCGCGCGGAGAAAGCATACCAATCAATCAATGCTGTGCAACCTG 2736
1801 AAGACTATCCGTGGCTGGGCTACTATCATGATGCTTATGAAGCTCCAGACGAGATCGCG 1860
2737 AAGACATATCTGTGGGATCTTACTATTAATCATGACAGGACCAACGACGCAATTCGC 2796
1861 AACGTTGCTGTGCCCAACGAACTTTATGAGATCCAAAGCTTCAAGCCGACCACTC 1920
2797 CCAGTGGCGCTGCCCAAGAGATCTTATGAGGCGAATGGCTACAGCGGCTCACTT 2856
1921 GACCTGAGTGTGTACCTCTGACACCCGAATGATGATGATGATGATGATGATGATGATG 1980
2857 GACCTTAAGCGCGGTGACATCACCCCAAGTTGAGAGGCTTGTGACACAGCTGGCGAG 2916
1981 AACACCAACACTTTGGGCGAGGAGAGGATACAGCAGGAGATGGACTTATGACTTAAT 2040
2917 AACCTCAATCTGTGGGACCGGAGCGATCCAGAGGTTGAATTTATGTGTGAAC 2976
2041 GAGGACTCGACATGATCTGTTCCCGCACCTGTGCAATACCGGAAGTTGACATGCC 2100
2977 GAGGATGTGAACCAACAGAGATCCACATCTTGTGCAATATGCAAAATGAGAGAGCT 3036
2101 ATCAAGAAAGCCAAACAGGACACAGCTCGGACACTGTGAGAACCTGTGCTTACGCG 2160
3037 ATCAAGAAAGCCAAACAGGACACAGCTCGGACACAGTGGGAAAGCTTCTGTGTTACG 3096
2161 TATATGTGAGCCCGCTACTCTGGGAGCAGCATGAACACTCTTGTGGAAGCTCAAA 2220
3097 TATGTCTTGAATCTTCCGATCTGGAGAGAGAACGAGGCACTTCTGGCGAGGCAACGCG 3156
2221 CAGAGCAAGGACACTTCAAGACATACCGCGCTGAGAAAGATATGCGCTCAGCTTGG 2280
3157 CTCAAGTTCCGCGAATTCGCGACTTACAGGATGAGGCAACTACGCGGTGACATCGGGC 3216
2281 AAGTGTACTTCAAGTTTGAATTTTAAACGCTGAGACTTATGAGGTCGCTGGCTCAC 2340
3217 AAGTGTACTTCAAGTTTGAAGTCTTCACTCTCGGACCAATGCGAGTGGTGTGGACG 3276
2341 GCTGATATGCAACGAGAAATGATGCTGCGCAAGAGAGAACTTTGGGCAATTTGATGAT 2400
3277 GCCATTTGCTATCCGAGAGGATGCTGGGACGAGGACACCAAGTTGGCTTTGATGGA 3356
2401 TACAATGAGGAAAGTGTACAGCGGTATACATGAGCTTTTCGCAAGCAATGCGCTGTT 2460
3337 CACAAATGTGACAAATATGACGCGGATCCATTTGAGCACTTCCGAGTGGGTATGAGGCT 3396
2461 GGTGAGCTAGTGGGGGTGTTCTTGAATCTCATTTGATTAAGACGATTAAGTTTCTCAT 2520


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Db 3397 GGGCAGTGCATGTTGTTTCATCATGTCAGAGCAAAAGATCAGCTTCGTTGAAC 3456
Qy 2511 GGTAGTTGTGATGAGAGCTTTGGCCGAGACTACGTTGCTGATGT-----CGAG 2574
Db 3457 GAGAGAACCTCGATGAGACGCGCTGGCGGAGAGACTTTTGGCGAGTAACCGCCGAG 3516
Qy 2575 GGTGACAACTTTGTACAGCTTGACACTTGTGTGTGGCCAAAGAACCGAGTTAATAT 2634
Db 3517 GGGGTGGGCTTGTGTGCTCCGCTGACCTCGGAGATGGGCGAGAGGCGGCTCATTAAC 3576
Qy 2635 GGGCAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2694
Db 3577 GGGCAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3636
Qy 2655 CCATTTTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2754
Db 3637 CCGTCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3696
Qy 2755 TTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2814
Db 3637 TTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3756
Qy 2815 TCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2874
Db 3757 GCGGACACCCCGCCGACCTTAAGATCTGCAACACCTTGAGAGACATGAGAGAGCC 3816
Qy 2875 AACTGGAGTTCTTACGTTCTGATGCTGCTGTTATGTCGATTAAGATTTACAGAG 2934
Db 3817 AACTGGAGTTCTTACGTTCTGATGCTGCTGTTATGTCGATTAAGATTTACAGAG 3876
Qy 2935 GCAGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2994
Db 3877 CAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3936
Qy 2995 GCAG 2998
Db 3937 GCGG 3940

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RESULT 7
ADM68765
ID ADM68765 standard; DNA; 16363 BP.

AC ADM68765;
XX
DT 17-JUN-2004 (first entry)
XX
DE Drosophila melanogaster ryanodine receptor encoding DNA SEQ ID NO:9.
XX
KW ryanodine receptor; insect ion channel; insecticide; pesticide;
KM calcium balance disruption; receptor calcium release mechanism; gene; ds.
XX
OS Drosophila melanogaster.
XX
FH Key Location/Qualifiers
FT 1..15330
FT CDS /tag= a
FT /product= "ryanodine receptor"
XX
XX MO2004027042-A2.
XX
XX 01-APR-2004.
XX
XX 23-SEP-2003; 2003WO-US029834.
XX
XX 23-SEP-2002; 2002US-0412795P.
XX
XX 18-NOV-2002; 2002US-0427324P.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX Caspar T, Cordova D, Gutierrez S, Rauch J, Smith RM, Wu L,
XX
XX Tao Y,

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XX WPI; 2004-295411/27.
DR P-PSDB; ADM68766.
XX
PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT for isolating other pest ryanodine receptors and in developing screens to
PT identify insecticidally active compounds.
XX
PS Claim 6; SEQ ID NO 9; 687bp; English.
XX
CC The present invention describes an isolated nucleotide fragment (1)
CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (1) comprises a
CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC construct comprising (1) operably linked to at least one regulatory
CC sequence; (2) a transformed host cell comprising the recombinant
CC construct; (3) a method to isolate (1) encoding ryanodine receptors and
CC related polypeptides; (4) an isolated polypeptide having ryanodine
CC receptor activity; (5) a method for evaluating at least one compound for
CC its ability to modulate calcium homeostasis; (6) a method for evaluating
CC at least one compound which modulates ryanodine receptor activity; (7) an
CC isolated nucleic acid fragment encoding an insect ion channel comprising
CC at least two fully defined polypeptide sequences selected from SEQ ID
CC NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC insect ion channel; (9) a method for expressing an isolated nucleic acid
CC fragment encoding a toxic insect ion channel; and (10) recombinant
CC construct comprising in the 5' to 3' direction a promoter operably linked
CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC The isolated nucleotide fragment (1) encoding a ryanodine receptor is
CC useful for the isolation of other pest ryanodine receptors and developing
CC of screens to identify insecticidally active compounds. The nucleic acid
CC fragments are useful as pesticides, fragments of protein for antibody
CC production, fragments of protein for determination of the structure of
CC insecticide binding sites and in the identification of insecticides that
CC disrupt the calcium balance in cells through other messengers that
CC interact with the receptor calcium release mechanism. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 16363 BP; 3940 A; 4448 C; 4559 G; 3414 T; 0 U; 2 Other;

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Query Match 53.9%; Score 1617.2; DB 12; Length 16363;
Best Local Similarity 71.4%; Pred. No. 0; Mismatches 853; Indels 6; Gaps 1;
Matches 2145; Conservative 0;

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Qy 1 GTCATAGGCGGCCCATCATCAAAATATGTAATCTCACCGTCATTTGTGACATTTCCAG 60
Db 997 GTGATGCGCTGCGCATATCAAGTACGAGCACTACCTCATGTCTCAGCATGCGAG 1056
Qy 61 ACTGCTTGTGAGCTGTTCTTATAGCTTTACGAAAGGAAAGAGAGAGTGAAGTA 120
Db 1057 ACTAGCTTGTGAGCTGAGTACGTAAGAGTATGAGAGGAAAGAGAGGAGTGAAGT 1116
Qy 121 GAGAGAGCAAGCATTTCTCCAGAGAGAGCAAGATGAGCATGCTGATCTTCC 180
Db 1117 GAGGAGAGCAAGCATTTCTCCAGAGAGAGCAAGATGAGCATGCTGATCTTCC 1176
Qy 181 AGGTACAGAGAGAGAGATCTAGAGCTGCTGAGATTCAGAGAGTGTCTTCCGCTGTC 240
Db 1177 CGCTCCAGAGAGAGAGATCTAGAGCGGCTGCTGATTCGAGAGAGAGAGCTCTTCC 1236
Qy 241 ACTAAGTTATCAATGCTCTGAGAACTCTACAGAGAGAGCGTCTGATCTGATGTTCTTC 300
Db 1237 ACCAGTTTATTAAGCTCTGAGAACTCTGAGAGAGAGCGGCTGATCTGATGTTCTTC 1296
Qy 301 GCGTACGTGAACCTGAGAGAGAGATGAGTGTGCTGAGAGATCTCATCAATCTTCCCA 360
Db 1297 CAAAAGTCAACCTCAAGAGAGAGATGAGTGTGCTGAGAGATCTCATCAATCTTTCG 1356
Qy 361 CAGCCGATGAGAGATGAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

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Db 1357 CAACCCGAAGCAGATATGAGCAACAGAGAAACGAAACGATTCGGCCCTGCGAAC 1416
Oy 421 CCGTCAGAGCTGTTCCAAAGAGAAAGCACTGAACTGATTCCTGAAAGCTATAGAACAG 480
Db 1417 CGACAGAGATCTGTTCCAGAGAGAGGCGTGCATCTGATCTGAGAGCCATTAGCAAG 1476
Oy 481 ATCAACGTCATCAAGTCCCAAGGAGTTCCTGCTGATTCCTGCGGAGACGAAATCTGGA 540
Db 1477 GTCAACATATACCTCGCAGAGGGCTTCAGCAGACTTCCTGGCCGCGACGAGACCGGC 1536
Oy 541 CAGACTGGGAAATGATATCTGGAATTTGTTATGAGTTGCTGCGGCAATATAAGGCG 600
Db 1537 CAGACTGGGATCTCAATCTCACTATTTGTACCACTTTGGCCGCAATCAATCAAGGCG 1596
Oy 601 AACCAACGAACTGCGCGGAGTTGCGAACTGAAACCGGCTCAACTGAGCTGTTCTCGGC 660
Db 1597 AACCAACGAACTGCGCGGAGTTGCGAAACGAACTGAACTGAGCTGATTTCTCCGC 1656
Oy 661 CTGCGCTGCAAGGCTTCGGGCGAGGGCAACCGGCATGCTGACGTCGACCTGCGCTT 720
Db 1657 CTGCGGTTCCAGGCTTCAGAGAGGGTTCGGGCAATGTTGAGAGTCACTGCGCTG 1716
Oy 721 ATAGACTGCGCTGAAAGCTCTCAATATGATGAGGAGCAACACATATAAGTATATCTCT 780
Db 1717 ATCGATTCGCCAGAGGCACTMAAACATGATGCGGAGTGAACATCAAGGTGCTCATCTCC 1776
Oy 781 CTATTAGAAAGCATGCGGCGGAGCCCTAAAGTACTAGATGTCATGTTGCTGTCGTCGCTC 840
Db 1777 CTGCTGAGAGAGCAGCGCAGGAGCCCGAAAGTCTTAGAGCTTCTGTTCTTGTGCGTG 1836
Oy 841 GGTAAACGGGCTGCGCGGTGCGCTGTCACAGAAACAATCTGATCTACTGCTGCGCGC 900
Db 1837 GGTAAATGAGTGGCGGTGAGTCTCTCCAGAAACAATTTGGGACTTTTGTGCTACCGGCG 1896
Oy 901 AAGAACCTGTTGCTGCAAACTGCGCTGCTGATCACTGATCTAGTGTCCGTCCAAACATC 960
Db 1897 AAGAACTGTGTGCTACAGACGCTCTGTGAGCACTGTGCGCAGATCCGACCGAAACATC 1956
Oy 961 TTGCGGGGTGAGTGAAGGGGTGCGGAGGTATCCGCAATGATGTTGAGGAGTCAATG 1020
Db 1957 TTGCGGGGTGCGGTGAGCGGTTCTTTCATGTAACGAAAGTGTGATTTGAGGTAACATG 2016
Oy 1021 GACCAATAGAGAGACCAACATATGATGCGCACTCTACGATAGATGAGGCGCAACT 1080
Db 2017 GATCAATAGAGACCAACCAACGCAATGATGCGCACTGCGGATTTGGCTGGCTATATCT 2076
Oy 1081 ACTGTTATGTCCTCAATCCCGGCGGTGCGAAGATGAGGAGTAAACGCGTGGAGAT 1140
Db 2077 TCCGGGTATGTAACCGTATCCCGGAGCGCAAGAGTGGGTGCAATGAGTGGCGAT 2136
Oy 1141 GACCTGTACTGTTACGGGTTGAGCGGCGCTAACCTGTGTCGGGGGAGAGAAAGCTCC 1200
Db 2137 GACCTGTACTGTTGATTTGATGATGCTTTCTTTGAGCGGAGGTCGCAAAACATTA 2196
Oy 1201 GTCAATAGAGACTCATGTAAGAGCCTTATATTAGAAAAGTGAAGTATAGTTGCGCA 1260
Db 2197 GTGATGAGCGCGCTGCCGAGAGGCTTTATCCGTAAAGGAGATTTATGGGCTTGC 2256
Oy 1261 TTGACCTGACGATACCAATATCACTTCATGTTCAACGAGTGGGCTGACGGGATCC 1320
Db 2257 ATGACCTTTGTCGCCATCATCACTTTACTTTTAACGAGTAAAGTCCGCGGTAGC 2316
Oy 1321 TTCAACAACTTCAATCTGGAAGGCACTGTTCTCCGCGCATCAGGTGCTTATAGTGTG 1380
Db 2317 TTTAAGGACTTTAACTTGAGCGAAATGTTCTTCCGATGATGTTGCTCATCAAACTTA 2376
Oy 1381 AGTTGCGGTTCTCTGCGCGAGAAACGAGTCTCTCCGTAACGCGGCTCCAGAAAGC 1440
Db 2377 AGCTGTGCTTCTTTTGGAGGTATCATGTGCTTTAAAGTTTGGCCGCCCAATGGA 2436
Oy 1441 TACTGTCCCTGTGAGTCTCTCTGCGCAGAGATCTCAAGCTGGAAGCGGTGCTTC 1500

Db 2437 TTCTTGCCCTCGTGAGTGTCTATGCCGAGAGATCTCAAGTCTGATCTTGTCTTC 2496
Oy 1501 TACTTCGCAACCTGTCCAAAGCGGCTTGGCTGAACTCCGCTAGTATCAGAGAGATACG 1560
Db 2497 TACTTGGTATATCTTGCAGAAATGTTTGTGGCCGACCAATGGCTTATTTAGAGAGACT 2556
Oy 1561 GCCTTGCTTACACTGTTGATCTTTACAGTTACTCTGCTTACATATGTAACAA 1620
Db 2557 GCTTTGTTCCGAAGCCCGTTGATACACAGGTGTGACATTTGCCAAATTCGTGACCAA 2616
Oy 1621 ATTAGATTAAGCTAGCGAAATATACAGAAATGGGGCTATGATTAAGATGGAAGCA 1680
Db 2617 ATCAAGAGAAAGCTGCGAGAAATATCAGAGATGAGGCTTAAACAAATGAAAGCG 2676
Oy 1681 GCGTGAATGTAACGCGACCAAGAGAGACTTGCACAAGATCCACCCTGCTGTGCC 1740
Db 2677 GCGTGTCTGTGGGCGAGACCGAGATGATCAACACCGCATTCATCTTGTGCTACCCAT 2736
Oy 1741 TTGAGCGACTCCCACTGCTGAGAAACGATACGATACAACTGCTGTGACAGACTC 1800
Db 2737 TTGAGAGAGCTTCCGCGCGGAGAAACGATACGACATCAACTAGCTGTGCAAACTG 2796
Oy 1801 AAGACTATCTGCTGCTGCTGCTACTATAGCTTATATTAAGCTCCAGACGATCCGC 1860
Db 2797 AAGACGATTAATCTGCTGAGATTAATCAATGAGAACCAAGCAACGACGATTCGC 2856
Oy 1861 AACGTTGCTGCGCCCAAGAACTTTCATGACATGCAACGAGCTTACAGCAGCACTC 1920
Db 2857 CCAATGGCGCTGCCCAAGAGATCTTCAATGACAGGCAATGGCTTACAGCCGCTCACTT 2916
Oy 1921 GACCTGATGCTGTACCTTGAACACCCAGATGAGTGAAGCTTATGACCAAGCTGCTGAG 1980
Db 2917 GACCTTAAGCCCGTGACATCACCCCAATTTGAGAGAGCTTGTGACACAGCTGGCCGAG 2976
Oy 1981 AACCAACCAACCTTTGGGCGAGAGAGATACAGAGGAGATGAGCTTATATGACTTAAT 2040
Db 2977 AACCTCAAAATTTGTGGGCAACGAGAGCGATCAGAGGAGTTGAGCTTATATGCTGAAC 3036
Oy 2041 GAGGACTCGGACATGATCGTTCCCGCACCTGGTGCATTAACGAAAGTTTGAAGTGC 2100
Db 3037 GAGGATGATGAAACCAACAGAGATCCACACTTGTGTCCATATGCCAAATGAGAGAGCT 3096
Oy 2101 ATCAAGAGGCGAACAGAGACACAGCCTCGGAGACTGTGAGAACCTGCTGTGTACGG 2160
Db 3097 ATCAAGAGGCGAACAGAGACACAGCCTCGGAGACTGTGAGAACCTGCTGTGTACGG 3156
Oy 2161 TATATGCTGAGACCGCTTACTGAGGAGACAGATGAGCACTTGTGTGAGAGCTCAAA 2220
Db 3157 TATGTCTTGAATCTCTCGAGGAGGAGAAACGAGGCACTTCTGCGCGAGGCAACGCG 3216
Oy 2221 CAGAGCAACAGACTTCAGAAACATACCGGCTGAGAAAGAACTATGCGGTCAAGCTTGG 2280
Db 3217 CTCAAGTTCCCGGATTTCCGACTTACAGAGGTGAGGCGCACTACCGCTGACATCGGGC 3276
Oy 2281 AAGTGTACTTGCAGTTTGAATCTTAAACGCTGGAACCTATGAGGCTCGGCTGGCTCAC 2340
Db 3277 AAGTGTACTTGCAGTTTGAATCTTAAACGCTGGAACCTATGAGGCTCGGCTGGCTCAC 3336
Oy 2341 GCTGATATGAGCAACAGAAATGATGCTGAGCAAGAGAGAACTCTTGGGCAATTTGATGT 2400
Db 3337 GCCGATTTGCTATCCGAGAGGATGCTGGGAGGAGGACACAGTTGGGCTTTCAGTGA 3396
Oy 2401 TACAATAGGAAAAAGTATCAGCGGTTAACAGTGAAGCTTTCGGCAAGCAATGGGCTGT 2460
Db 3397 CAATATGAGCAAAATATGACGCGCGATCCATTTAGAGCACTTCCGAGTGGCTTATGAGGCT 3456
Oy 2461 GGTGACGTAATGGGAGTGTCTTCAATCTTCAATTAAGAGATTAAGTTTCTCATCTCAAT 2520
Db 3457 GGGGATGATTAATGGTTGTTTCAATGATGTAAGAGAGAAACGATTCGTGTGAAAC 3516
Oy 2521 GGTGAGTTGTTGATGATGCTTGTGGCGAGAGACTACGTTGTGATGT-----CGAG 2574
Db 3517 GGAGAACTCTGATGAGCGGCTGGGCGGAGAGCACTTTTGCAGCTTAACCGCGGAG 3576

QY 2575 GGTGCAACTTGTACAGCTTGCAACTTGTGTGAGGCAAAAAGCCAGTTAATAT 2634
DB 3577 GGGGTGGGCTTGTGTCGCCCTGCACTCGGAGTGGGCAAGGCGGCTCATCTAC 3636
QY 2635 GGGCAAGATGTAATCTCTGAATATCTTCAACAATGTGTCTTCAAGAGGATATGAA 2694
DB 3637 GGGCCAGAGCTGGAATCACTCAAGTTCTTCACTTGTGCTGCAAGAGGATATCGAG 3696
QY 2655 CCATTTTGGTCAATATGAAAGAGACCTGACTCTGTGTACCAAGAGACAGCCGATC 2754
DB 3697 CGTTCTGTGTAACATGCGCGCGCGGTACCTGTGTACCAAGAGACAGCCGATC 3756
QY 2755 TTGAGAAATCTGATGATGATGATGCAACCAAGATGATGATGATGATGATGATGAT 2814
DB 3757 TTGAGAAACCGAGAGAGATGCGGACCTGCGGACCTGATGATGATGATGATGATGAT 3816
QY 2815 TCAGATACCTCTCATGCTCTCAAGATTTTCCACAAACGTTGAGAGATGAGAAAGCT 2874
DB 3817 GCGGACACCCCGCACTTAAGATCTGCAACAACCTTGAGAGCAATGAGAAAGCC 3876
QY 2875 AACTGGAGTTCTTACGTCTCTCATGCTCTGTTATCTGCAATAGATTCATTGACGAG 2934
DB 3877 AACTGGAGTTCTTGTGCTCTTCCCTGCGCGGACCTGATGAGGATGATGATGATGATG 2936
QY 2935 GCAGAAAAGCCAGAGCTTGGGAGAAATCAAGAACCTGCAACAGATCTTAATGAAAGAG 2994
DB 3937 CAGAGAAAGCCAGAGCTTGGGAGAAATCAAGAACCTGCAACAGATCTTAATGAGGAG 3996
QY 2995 GCAG 2998
DB 3997 GCGG 4000

RESULT 8

ADM68763
ID ADM68763 standard; DNA; 15413 BP.

AC ADM68763;

DT 17-JUN-2004 (first entry)

DE Peregrine maids ryanodine receptor encoding DNA SEQ ID NO:7.

KM ryanodine receptor; insect ion channel; insecticide; pesticide;
calcium balance disruption; receptor calcium release mechanism; gene; ds.

OS unidentified.

PH Key Location/Qualifiers

FT CDS 17..15400
FT /tag a
FT /product "ryanodine receptor"

PN WO2004027042-A2.

PD 01-APR-2004.

PP 23-SEP-2003; 2003WO-US029834.

PR 23-SEP-2002; 2002US-0412795P.

PR 18-NOV-2002; 2002US-0427324P.

PA (DUPO) DU PONT DE NEMOURS & CO E I.

PI Caspar T, Cordova D, Gutierrez S, Rauch JJ, Smith RM, Wu L;

PI Tao Y;

DR MPI, 2004-295411/27.

DR P-PSDB; ADM68764.

PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
for isolating other pest ryanodine receptors and in developing screens to

PT identify insecticidally active compounds.

XX Claim 6; SEQ ID NO 7; 687bp; English.

PS The present invention describes an isolated nucleotide fragment (1)
XX comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (1) comprises a
CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC construct comprising (1) operably linked to at least one regulatory
CC sequence; (2) a transformed host cell comprising the recombinant
CC construct; (3) a method to isolate (1) encoding ryanodine receptors and
CC related polypeptides; (4) an isolated polypeptide having ryanodine
CC receptor activity; (5) a method for evaluating at least one compound for
CC its ability to modulate calcium homeostasis; (6) a method for evaluating
CC at least one compound which modulates ryanodine receptor activity; (7) an
CC isolated nucleic acid fragment encoding an insect ion channel comprising
CC at least two fully defined polypeptide sequences selected from SEQ ID
CC NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC insect ion channel; (9) a method for expressing an isolated nucleic acid
CC fragment encoding a toxic insect ion channel; and (10) recombinant
CC construct comprising in the 5' to 3' direction a promoter operably linked
CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC The isolated nucleotide fragment (1) encoding a ryanodine receptor is
CC useful for the isolation of other pest ryanodine receptors and developing
CC of screens to identify insecticidally active compounds. The nucleic acid
CC fragments are useful as pesticides, fragments of protein for antibody
CC production, fragments of protein for determination of the structure of
CC insecticide binding sites and in the identification of insecticides that
CC disrupt the calcium balance in cells through other messengers that
CC interact with the receptor calcium release mechanism. The present
CC sequence is used in the exemplification of the present invention.
CC XX

Sequence 15413 BP; 4666 A; 2966 C; 3619 G; 4160 T; 0 U; 2 Other;

Query Match 51.4%; Score 1542.2; DB 12; Length 15413;

Best Local Similarity 70.1%; Pred. No. 0; Mismatches 890; Indels 6; Gaps 2;

Matches 2101; Conservative 1; Mismatches 890; Indels 6; Gaps 2;

QY 1 GTCATAGGCGGCCCATCATCAATATGATGCTCCACCGTATGTGACGATTCGAG 60
DB 1013 GTTATAGGTGACCAATATATCAATGATGATGATGATGATGATGATGATGATG 1072
QY 61 ACTGCTGTGTGCTGCTTATATAGTCTTACGAAAGAAAGAGAGAGTGGTAAAGTA 120
DB 1073 ACTGCTGTGTGCTTATATATCAATATCATATGAAACTAAAGAAAGAGTGGAAAGTT 1132
QY 121 GAAAGAAAGCAAGCATTTCTCAAGAGAAAGCAAGAGAGAGAGAGAGAGAGAGAG 180
DB 1133 GAAAGAAAGCAAGCTGCTCATAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 1192
QY 181 AGGTACAG 240
DB 1193 CGCATCAAG 1252
QY 241 ACTAAGTTATCATATGCTGTGAAACTCTACAGAGAAACCGTCTCACTCGATGTTCTTC 300
DB 1253 ACTCAGTTTATAGAGAGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1312
QY 301 GCGTCAAGTGAACCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 1313 GCAACTGTGAATTTGAATGAATGATATGCTCGAAGATTTGATTAATTTTTCG 1372
QY 361 CAGCCGATGAGATATGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 1373 CAGCCAGAGATGATATGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1432
QY 421 CGTCAGACCTGTTCCAAAG 480
DB 1433 CGTCAAGATGCTTTCAAG 1492

QY 481 ATCAACGTCATCATCGTCCAGGGGTTCTCGCTGATTCCTGGCGGAGACGAAATCTGGA 540
DB 1493 ATAAATGATTAACGCTCAAGGATTCCT---TGTAAATTAGCAGGAGATGAATCAGGA 1549
QY 541 CAGACCTGGGAAATGATATCTGGATATTTGTATCATGTTGCTGGCGGCAATATTAAGGCG 600
DB 1550 CAACACTGGGATATATATTTCTGGTTACCTGTATCAACTCTTGGCTGTATATTAATGA 1609
QY 601 AACCAACGAACTGGCGCAGTTCCGCAACTCGAACCGCTCACTGCTGTTCTCGCGC 660
DB 1610 AATCATACAAATTTGGCTCAGTTTGGAAATTCAAATCGTGTAAATGGCTGTTCAGCAGA 1669
QY 661 CTGGCTCGCAGGCTCGGGCGAGGGCAACCGGCATGCTCGAGGTGCTGCATCTGCTGCTT 720
DB 1670 CTGGGCTCAACAGCATCAAGTGAAGGCAACGGGAATGTTGATGTATCATTTGTGTCTC 1729
QY 721 ATAGCTGGCTTGAAGCTCTCAATATGATGAGGACGAAACATATAAGTATATCTCT 780
DB 1730 ATGTATGCTCGTAAGCGTTGAAATGATGAGGATGAGCATAATAAGTTATATATCT 1789
QY 781 CTATTAAGAAAAGCATGGCGCAGACCTTAAGTACTAGATGTCTATGTTGCTGTGCGCTC 840
DB 1790 CTCTTGAGAAACATGGAAGGATCCGAAAGTTTGAATGTTCTCTGTTCACGTGTGTG 1849
QY 841 GGTAAACGCGCTCGCGGTGCGCTCGTCAAGAAACAATCTGTGACTTACTGCTCCGCGC 900
DB 1850 GGTATGAGTGTGCTGTTCTGTATGCTCACAAAAATTAATTTGTGATTTCTCTTACCTGGA 1909
QY 901 AAGAACCTGTGTCTGCAAACTGCGCTCGTGTATCAAGTATCTAGTGTCCGTCCGAACATC 960
DB 1910 AAAAACTCTTCTTCTCAACGCACTAGATGATCAATGTGCTGATGTCCTGCTCAAAATTA 1969
QY 961 TTCTGGGTGCGATGAGAAAGGTGCGCAGTGTACCGCAATGTATCTTCAAGGTGACTATG 1020
DB 1970 TTTGTGGGCGGTGTTGTGGCTCTGCAATTTATCAAAAATGTATTTTGAAGTTACATG 2029
QY 1021 GACCAATAGAGAAAGACCAACATATATATGCCATCTTACGATATGATGAGGCCAACAT 1080
DB 2030 GATCAATTTGAGCAGACCAACACATGACACTTCAAGAAATTTGGCTGGGCGAACACT 2089
QY 1081 ACTGTTATATGCCATATCCCGGCGGTGGCGAATAATGGGAGGTAAACGGGTGGAGAT 1140
DB 2090 AGTGATATATGCTTATCTGAGAGAGTGAATAAGGGGTGGAATAAGAGTTGTGTAT 2149
QY 1141 GACCTGTACTGTACGGGTTGACGCGGCTACCTGTGCTCGGGGGGAGGAAAGCTCCC 1200
DB 2150 GATCTTATTTCTATGAGTTGATGCGCGAATTTATGACAGAGACGTAAACCTTGT 2209
QY 1201 GTCAATAGACTCATGTGAAAGGCTTATATAGAAAAGTGAAGTATAGTTGCGCA 1260
DB 2210 GT---TCAACGCAATGCGACTGAGCCATTTCAAGAAAGCGATGTATTTGAGGTCT 2266
QY 1261 TTGGAACCTGAGAGTACCAATATCAACTTCAATGTTCAACGAGATGCGGGTACCGGATCC 1320
DB 2267 CTAGATTTATAGTGGCAATCATATCAATTTCAATTCATATGTTGCTCATTAATGAGGCGCTGC 2326
QY 1321 TTCAACAACTCAATCTGAAAGGAGTCTTCCCGGTCATCAGGTGCTTATAGATG 1380
DB 2327 TTCAAGATTTCAACTATGATGAAATGTTCTTCTGTATATAGTTGCTCCACAAAGTAT 2386
QY 1381 AGTTGTGCGTCTCTGCTGGGCGAGAAACACGCTGTCTCCGTTACGCGGCTCCAGAAAGC 1440
DB 2387 AGTGGCGAATTTCTTTAAGTGAAGACATAGTGAAGTGAATATGTTCCACAGAAAGAA 2446
QY 1441 TACTCTCCCTTGTGGAAGTCTCTCTGCGCAGCAATCTCAGCTGGAAGCCGTGCTTC 1500
DB 2447 TTTCTCTCACTGTGTGAAGTCTGCTCTCAACAAGTGTGTCCATTTGATCCATGTTTC 2506
QY 1501 TACTTGGCAACCTGTCCAGAGGGGCTTGGCTGGAAGCTCCGCTAGTATAGGAAGATAGC 1560
DB 2507 TACTTGGTAAATTTGAACAAATGTGTATTAACAGGCCCAATGACAGTTGAGAGATATCA 2566

QY 1561 GCCTTGGCTTACACCTGTTGATCTTTACAGTTTACTGTGCTTACATATGTGGAACAA 1620
DB 2567 GCATTTGTTCCAAACCTGTGTATACAAACAAGGTTTCGTCCCAATTTATATGAGAGC 2626
QY 1621 ATTAAGATTAAGCTAGTGAATAATATACAGAAATGAGGCTATGAATTAAGATGGAAGA 1680
DB 2627 ATTAAGATTAAGTTGGCAGAAATATTCATGAATATGAGGCTATGAACAGATATGAAGCT 2686
QY 1681 GGCTGATGTATCGCGCAGCAGAGAGAACTTTGACAAAGATCCACCCCTGCTGTGCC 1740
DB 2687 GGCTGATGTATGGGAGAAAGCGAGATGACATAGTAAAGTATCATATGCTTATTCAG 2746
QY 1741 TTGAGAGCATCCCACTGCTGAGAAACATATGACATATCACTGCTGTGACACATC 1800
DB 2747 TTCCAGCAACTTCCACAGCTGAGAAAGCGCTATGACTCAACAATCGGATTTCAAACTCTC 2806
QY 1801 AAGATATCTGTGCTGGGCTCTATATGACTTGAATTAAGCTTCCAGACAGATCCGC 1860
DB 2807 AAGCAATTTGGGACTGGGCTACTATATACATGATGATGAGCTCTTGGCTATTAATA 2866
QY 1861 AACGTTGCTGTGCCCAACGAACCTTTATGATGATCCAAACGGCTTACAGCAGACCACTC 1920
DB 2867 ACAATTTGCTTCCAAATGAGCTTTTATGATCAATCAATATGCTTACAGCAGACCACTT 2926
QY 1921 GACCTGATGCTGTACCTTGAACCCAGATGAGTATGATGATGATGATGATGATGATG 1980
DB 2927 GATCTCAGGCGCAATATCATTAACACCGAAATGAGGAAATTAAGTATCAACTAGCCGAG 2986
QY 1981 AACCCCAACACCTTTGGGCGCAGGAGAGATACAGAGGAGATGATATATATATATAT 2040
DB 2987 AATACATATATCTATGAGGCGCAAGAAACGAATCAACAAAGGTGAGAGTATGACTCAAT 3046
QY 2041 GAGGACTCGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2100
DB 3047 GAGGACTGATATGTTGAGAAATGAGGAGCTGTGTGCTTATGCAAAATGTTGAGAGCT 3106
QY 2101 ATCAAGAGGCGCAACAGGAGCAAGAGCTCGAGACTGTGAGAGCTGTGTGTCTACG 2160
DB 3107 ATTAATAAAACCTAAACAGGAGTACTGCAAGTGAACCGTCAAGAACTTATTTGTATG 3166
QY 2161 TATATGCTGAGACCCGCTTACTGGGGAGACAGATGAAGCACTTGTGGAAGGCTCAAAA 2220
DB 3167 TACATATTAATCCCCCAACGGGAGAGCAATGAAGCTTTCTTGGAGGCTAGTCT 3226
QY 2221 CAGAGCAACCAACTTCAAGAAATATCCGCTGAGAGAACTATGCTGCTGAGCTGAG 2280
DB 3227 TTAAGACAGACTCACTTCAAGACGTATCCAGCAGAAAGAACTATGCTGCTGAGCA 3286
QY 2281 AAGTGTACTTCAAGTTTGAATCTTAAACGGCTGAGCTATGAGAGGTGCGCTGAGCTCAC 2340
DB 3287 AAGTGTATTTGAATTTGAAATCTTTAATGCTGAGCAATGAGAGATGAGTGGGCA 3346
QY 2341 GCTGATATGAGCAGAGAAATGATGCTCGAGCAAGAGAACTTTGGGATTTGATGT 2400
DB 3347 TCAAGATTTGCTGGCAGAGTCAATTTGGAAGAAATGAGAAATTTGAGGATTTGAGTGC 3406
QY 2401 TACATATGAGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2460
DB 3407 TTCAAGAGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3466
QY 2461 GGTGACGTATGAGGAGTGTCTTGAATCTTGAATGATGATGATGATGATGATGATGAT 2520
DB 3467 GGAATGTGTGAGATATTTCTTGAATGATGATGATGATGATGATGATGATGATGATG 3526
QY 2521 GGTGATGTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2580
DB 3527 GGAAGACTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3586
QY 2581 AACTTGTAACCACTTGCACACTTTGATGAGGCGCAAAAAGCGGTTAATATATGAGCA 2640
DB 3587 AGCTTTGTTCTGCTTTCACCTTGGCGTATGAGGCGCAAAAGCTTAACTGACTTTTGGCA 3646
QY 2641 GATGTGAATATCTTGAATATCTTCAACAATGTGTCTTCAAGAGGATATGAACATTT 2700

Db	3647	GATGTACTGTAATTAAAGTTTTCACACTTCGCGTCTTCAAGAAAGATNTGACCATTT	3700		
Qy	2701	TGCGCAATATGAGAGAGACGTGACTCACTGCTACACCAAGACCGCATCTTTCGAG	2766		
Db	3707	TGTGTCAATATGAGACAGACGGGTACGTAATGTGTACACCAAGACCAACCAATTTTTCAG	3766		
Qy	2761	AATATCTAGTATGATATGACACCAAGATTTATGTGACCAAGATATACAGCTGTTCAGAT	2822		
Db	3767	AATACTGAAAGATTATGATCCGACCTCAAGAAATTTGATTTTCAAGAAATTCACACTGTTCGAGT	3822		
Qy	2821	ACACCTCATGCGCTCAAGATTTCCCAACAACAGCTTCGAGACGATGGAAGAACTAACTGG	2888		
Db	3827	ACTCCACCTTGTGCTCAAAATTAAGTACAACTTAATTCGATCAATGGAAGAAAGCTAACTGG	3888		
Qy	2941	AAAGCCAGACGTTGGGTGAATATCAAGACCGTCAACAGATCTTAATGAAGAGCGAG	2998		
Db	3947	AAATTTGAACGTTGGCAGGAGATTAAGAAATCCGTACAGCATAGACTGTAGTCGAGGCTG	4004		
RESULT 9					
ADMe8761	ADMe8761 standard; DNA; 15315 BP.				
AC	ADMe8761;				
XX	17-JUN-2004	(first entry)			
DT	Periplaneta americana	ryanodine receptor encoding DNA SEQ ID NO:5.			
XX	ryanodine receptor; insect ion channel; insecticide; pesticide;				
XX	calcium balance disruption; receptor calcium release mechanism; gene; ds.				
KM	Periplaneta americana.				
XX	OS				
XX	Key	Location/Qualifiers			
FT	CDS	1..15315			
FT		/*tag= a			
FT		/product= "ryanodine receptor"			
XX	WO2004027042-A2.				
PN	01-APR-2004.				
PD	23-SEP-2003; 2003WO-US029834.				
XX	23-SEP-2002; 2002US-0412795P.				
XX	18-NOV-2002; 2002US-0427324P.				
PR	(DDBP) DU PONT DE NEMOURS & CO E. I.				
PA	Caapar T, Cordova D, Gutteridge S, Rauh J, Smith RM, Wu L;				
XX	Tao Y;				
PI	WPI; 2004-295411/27.				
XX	P-ESDB; ADMe8762.				
DR	New isolated nucleotide fragment encoding a ryanodine receptor, useful				
XX	for isolating other pest ryanodine receptors and in developing screens to				
PT	identify insecticidally active compounds.				
XX	Claim 6; SEQ ID NO 5; 687bp; English.				
PS	The present invention describes an isolated nucleotide fragment (I)				
XX	comprising: (a) a nucleic acid sequence encoding a ryanodine receptor				
CC	having an amino acid sequence identity of at least 80% when compared to a				
CC	polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,				
CC	128, 130, 144, or 146; or (b) the complement of (a). (1) comprises a				
CC	nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.				

Query Match	44.5%	Score 1335.4	DB 12	Length 15315	Matches 1988	Conservative 0	Mismatches 1001	Indels 12	Gaps 4
1	GTCAATAGCGCGCCCATCATCAAAATATGATGATCTCCACCGTCATTTGACAGATTTCGAG	60							
2	GTAAATTTGGAGACCACTAATATTAAGATATGATGTCACAGTCGATTTATTAAGCAACATTCGAT	1055							
3	ACTGCGCTTGCGCGCTGCTTATTAAGCTTTAGCAAGAAAGAAAGAAAGGAGTGGTAAAGTA	120							
4	ACAGGTTATGCTTAAACATACAGCTCTATGAAACAAAAAAAAGGCTCGTAAAGTA	1119							
5	GAAAGAAAGCAAGCGATTTCTCACAAGGAAAGCAAGATGACAGATGCGCTTCACTTCTCC	180							
6	GAAAGAAAGCAAGCGATTTCTCACAAGGAAAGCAAGATGACAGATGCGCTTCACTTCTCC	180							
7	GAAAGAAAGCAAGCGATTTCTCACAAGGAAAGCAAGATGACAGATGCGCTTCACTTCTCC	180							
8	AGGTCAACGAGAGAAATCTTAGACATGCTCGAGTTATCAGAAAGTGTCTTTCGCTGTC	240							
9	AGGAGTCAAGAAAGAGTCTAGAACTGCTAGATGATACCTAAATATGCTTCTCTCAATATTC	1239							
10	ACTAAGTTATCAATGCTGTGGAAGAACTTAAGAAAGAAAGCGTCCGCACTGATGTTCTTC	300							
11	ACACAGTTATTTCCGACCTGGAAGAAATTTAACAAGTAACAGACGTTGCTCATTAATTTGCT	1299							
12	GCGTCAGTGAACCTGGGCGAGATGGTATGCTCCGAGATCTCATCACTACTTCCGA	360							
13	TCATTCGTTAATCTTAATGAATGGTCAATGCTCTAGAAAGTTTAATTAATTTTGGCT	1355							
14	CAGCCCGATGAGATATGGAACAGAGAAAGAAACAAATTCGCGGCACTCCGAAC	420							
15	CACTCGAAGAAATATGGAACAGAGAAAGAAACAAATTCGCGGCACTCCGAAC	420							
16	CACTCGAAGAAATATGGAACAGAGAAAGAAACAAATTCGCGGCACTCCGAAC	420							
17	CCTCAGACCTGTTCCAAAGAGAGGACATCTGAACCTGATCTTCGAAGCTTATAGACAG	480							
18	AGACAGATTTATTTCAAGAAAGAGGCAATTTAATTCGATTTTGAAGAGCTATTGATTA	1479							
19	ATCAACGTCATCAGTCCGAGGGGTCTCGCTGGAATTCCTGGGCGGAGAGCAATCTGGA	540							
20	GTTAATATTTATTAAGTCAAGAGATTTATGCTCAGTT---TAGCTGGGAGAGAGCTTGG	1536							
21	CAGAGCTGGAGAAATGATATCTGGAATTTGATCAAGTTGCTGGCGGCAATATTAAGGCG	600							
22	CAAGGTTGGAGATGATTTCTGTTATTTATTAACAGGTTGCTAGCTGCATATTAAGGGA	1596							
23	AACACAGAAAGTGGCGGCACTGCGGCACTCGAAGCGGCTCAACTGCTGTTCTCGGCG	660							

Db 1597 AATCATACTAATTTGGCTCAATTTGCTAACTTAACCGATTAATGGTTATTTAGTCGA 1656
 Qy 661 CTGGCTCGCAGAGCCCTCGGGCGAGGACACCGCATGCTCGAGCTGCGACTGCTT 720
 Db 1657 TTAGGATCTCAAGCATCCAGTAGAGGAACTGGTATGTTAGATGTACTTCACTGCTTCTC 1716
 Qy 721 ATGACTCGCTGAAGCTCTCAATATGATAGAGGACGAACATTAAGTAATCTCT 780
 Db 1717 ATGATTTCTCCGGAAGCTTTAATATGTAAGAAAGATGAACATATTAAGTAATATCT 1776
 Qy 781 CTAATAGAAAGCAGGGCGGACCTTAAGTACATGATGCTATGTTCCGTGCGCTC 840
 Db 1777 CTTTGGAAAAACATGCTGATGTAAGAAAGTGTAGACGTTTATGTTTCCCTAAGCGTT 1836
 Qy 841 GGTAAACGGCTGCGGGCTGCTGCTCAACAGAAACAATCTGATCACTACGTCGCCGAC 900
 Db 1837 GGTAAACGGTGGCCGTAAGAAAGTTCACAAATTAATATGATGTTCTTATTAACAGGA 1896
 Qy 901 AAGAACTGTTGCTGCAAACTGCGCTCGTGATCAAGTATCTAGTGTCCGTCGAACATC 960
 Db 1897 AAAAATTTAATTCTTACAGCTTACTGTGATCATGTAGCCAGGTGACGTCCCAATAT 1956
 Qy 961 TTCCGGGCTCAGTAGAAGGCTCGCGCATGTAACCGCAATGCTACTTGGAGTGAATG 1020
 Db 1957 TTTGTTGCTCATGTAGTGAATCTGCCGTTATGCAAAATGATATTAAGATAGCAATA 2016
 Qy 1021 GACCATATAGAGAAACCAACATATGATGCAATCTACGATAGATGGGCCAACT 1080
 Db 2017 GATCATGTAAGAACAACTACATTTAATTCACACATTCGAATTTGGATGGGCAAAATCT 2076
 Qy 1081 ACTGTTATGTCCTACACCCGGGCGGTGGCGAATAAGGAGTAAACGGCTGGAGAT 1140
 Db 2077 GCAGGTTATGTTCCGTATCTGCTGCGGAGAAATAGGGGTGAAATGGCGTTGGGAT 2136
 Qy 1141 GACCTGTACTGTACGGGTTGCAACGGCCGCTACCTCTGCTCCGGGGGAGAGAACTCC 1200
 Db 2137 GATTTATATTTCTTCGGATTTGATGGGTATATTTATGACACGAGGACGTAATCAGAA 2196
 Qy 1201 GTCAATAGGACTCATGCTGAAGAGCCTTATATTTAAGAAAGTGAAGTATAGTTGCGCA 1260
 Db 2197 GT---GATGCTGCTTCAAGAAATTTCTTAACATTTAAAAAGGTGATGTATGCTTGTGCA 2253
 Qy 1261 TTGACCTGACGGTACCCATATCAATCTCATGTTCACACGAGTGGGTGACGGGATCC 1320
 Db 2254 TTAGATTTAATCAATTCATTAATTAATCTTTTACATTTGAACGGTCAATGCTCCAGAGACC 2313
 Qy 1321 TTCAACAATTCATCTGGAAGGCAATTTCTCCCGGTCATCAGCTGCTTAATGCTG 1380
 Db 2314 TTCAGAGACTTCAATTTGATGGAGATGTTTTCAGATTAATGTTTCACTCAAAAGTTC 2373
 Qy 1381 AGTTGTGGGTTCTGCTGGGCGAGAAACAGGTCGCTCCGGTACGCGGCTCAGAAAGGC 1440
 Db 2374 GGGTCTGCTTTTATATGGGCGAGATCATGTGATGAAGTTTACTCTCCAGAGCA 2433
 Qy 1441 TACTCTCCCTTGGTGAAGTCTCTCTCGCGACAGATCTCAGCCTGGAACCGTCTTC 1500
 Db 2434 TTTTCTCCTATTTGAAGTTTATTAATCTCAACAAATTTTGAACATGATCGGCGTTC 2493
 Qy 1501 TACTTCGGCAACTGTCCAGGGGCTTGGCTGACCTCCGCTATGACAGAGATGCG 1560
 Db 2494 TATTTTGAAGAACTTTAGTAATGCTACTCAGGGACGTTGTATGTTGAAGATGATACA 2553
 Qy 1561 GCGTTGCTGCTCAACACTGTTGATPACTTTACAGATTACTTCCGCTACATATGGAACAA 1620
 Db 2554 GCATTTGTTCCAAATTCAGATTGATACATATGCTCACTTTAATCTTACATTAAGAAAT 2613
 Qy 1621 ATTAGAGTAAGTAGCTGAATAATATACAGAAATGTGGCTATGAATAGATCGAAGCA 1680
 Db 2614 ATTAAGATTAATATGACAGAGATATTCATGAATGTGGGCAATGAATTAATGAAGCT 2673
 Qy 1681 GGGTGAATGTACGGGACCAAGAGAGACTTTCACAAAGATCCACCCCTGCTGCTGCC 1740

Db 2674 GGTGGCAATATGCTGATTAAGAAATGATATCAGAAATATCATTCATGTTAATATACG 2733
 Qy 1741 TTCAGGCACTCCCACTGCTGAGAAACGATATACATCACTCGCTGTGACACATC 1800
 Db 2734 TTTGACAAAGTTGCTCCAGCGAGAGAGCGTTATGATTTCTGAATTAAGCTGTGCAACGCTT 2793
 Qy 1801 AAGCATATCTGGCTCTGGGCTACTACATCAGCTTAATGAAGCTTCCAGACGCAATCCGC 1860
 Db 2794 AAAACGGTTATGTGGTGGATATCATATTCATCATATATCCACGCTCCCGCATTTAAA 2853
 Qy 1861 AAGCTGTGCTGCCAAGAACCTTTGATGAGTCAACGCGTACCAAGCCAGCAACCTC 1920
 Db 2854 ACGGTACGTTGCTCCAGAGAACATTTATGATTCATGATGTTTACAAACAGCACACTA 2913
 Qy 1921 GACCTGAGTGTGCTCACTGACACCCCAAGTGAATGAGTATGATGACAGCTGCTGAG 1980
 Db 2914 GATTTATCTGAATTAATTTGTGAGGAAATGGAABATTAATTTAGACGATTAGCTGAG 2973
 Qy 1981 AACCCCAACAATTTGGGCGAGGAGAGATACAGAGGATGACTTATGACCTTAAT 2040
 Db 2974 AATACATTAATTTATGGGCAAAAGAAAGATACAAAGGATGAGCGTATGTTTAAAT 3033
 Qy 2041 GAGGACTGAGCATGATCGTTCCCGCACCTGGTGCATACCCGAAGTTGACGATGCC 2100
 Db 3034 GAAAGATTTACAAATGTTATCGCATCTCATTTTGTATCCGTACAGAAATGATGACGCT 3093
 Qy 2101 ATCAAGAAAGCCCAACAGGACACAGCCTCGAGACCTGTGAGGACCTGCTGCTTACGGG 2160
 Db 3094 ATTAAGAAAGCTATATAGATACAGCAAGTGAACATCCGCACTTTATTAATGATAGCT 3153
 Qy 2161 TATATGCTGACCCGCTTACTGGGAGCAGCATGAG--CACTCTTGTGGAAGCTCA 2217
 Db 3154 TACAACTTAAGCCCAACGACCTGAGAGAAACAAAGAGCGACACTCTTAACAGACGAAAC 3213
 Qy 2218 AAAACAGAGAGAGAGACTTCAAGAACATCCGCGTGAAGAACTATGCGTCAAGCTCT 2277
 Db 3214 ACTAATGATATCTTGAAGCTTCAAGAACATATGCTGTAAGAAACATATGCTGTGCAAGT 3273
 Qy 2278 GGGAAAGTGTACTTTCAGTTTGAATCTTAAACGGCTGGAACCTATGAGGGTCTGCGTGGCT 2337
 Db 3274 GGAATAATGATATTTCAAGTTTGAAGATTTGACAAACGGGCCCATGCGAATTTGATGGGCT 3333
 Qy 2338 CACGCTGATATGCAACAGGAATGATGCTCGAACAAAGCAGAACTCTTGGGCAATTTGAT 2397
 Db 3334 AGGTTTACATGTTCTCGGGGTATCAAAATCGGATGAGACAAAAATCTTGGGCAATTTGAT 3393
 Qy 2398 GGTTCAAATGAGAAAAAGTATACAGCGGTAAACATGAGCTTTCGGCAGCAATGGGCT 2457
 Db 3394 GGTATATACGAAGAAAAATTTATATGGGACAGCCGAATCATTTGGAGGCGAGTGGCAA 3453
 Qy 2458 GTTGTGACGTATGAGGGGTGTTCTTATGATCTCATTTGATTAAGACGATTAAGTTTCTCACTC 2517
 Db 3454 GTTGGAGATGTCGTGGAGAGTGTTTTATAGACTTAATGATCATTAATATTTTTCGTTG 3513
 Qy 2518 AATGTGAGTTGTTGATGATGATGCTCTTGGCGAGAGACTACGTTTGTGATGTCAGGGT 2577
 Db 3514 AATGAGAAATTTACTTAATGATATCATTTGGGAGGAGAACTACGTTTCTGAAGTTCAAGGA 3573
 Qy 2578 GACAACTTTGTACACGTTGCAACATTTGTGTGGGCCAAABAACGAGTTTAATATATGCG 2637
 Db 3574 GAAAGATTTGTACCTGATTTACTGTGGGACTGAGCAAAABAACAAATTAATCTTTTGT 3633
 Qy 2638 CAAGATGTAATCTCTGAAATATCTTCAACAACATGCTCTTCAAGGAGGATATGAACCA 2697
 Db 3634 CAAGAGCTAACTCATTTGAATATCTTCAAGCATTTGTGTCTTCAAGAGATATGAACCA 3693
 Qy 2698 TTTTGGCTCAATATGAAGAGAGCTGACTCACTGTTACCAAGAACACGCGGATCTTC 2757
 Db 3694 TTTTGGCTAAACATGAAGAGACAGTAAACATATTTGGTATCTTAAGGATCAACAAATTTT 3753
 Qy 2758 GAGAAATTCATGATGATGATGACACAGGATTTGATGACAGATATCCAGCTGCTTCA 2817
 Db 3754 GAAAAATACGATGA---CTTTGCTGTGATTAATGATGTTAACAAGATTTCCAGCTGTGTTCA 3810

QY 2818 GATACACCTCCATGCTCAAGATTTCCCAACAGCTTCAGACGATGAGAAAGCTAAC 2877
 DB 3811 GATACACACCTGCTCTAAATAAAGTCAATAATGATGAAACATGAAAGACCTAAAT 3870
 QY 2878 TGGAGATCTTAACTGCTCTCACTGCTGTTATCTCCATTAACGAGTTCAATGACAGCA 2937
 DB 3871 TGGGAATTTTTCAGGCTATCTTGGCTGTCATATGCTTACCAAAATTTATGATGACAA 3930
 QY 2938 GAAAAAGCAGACGTTGGGTAAATCAAGACCGTCAACAGATCTTAATGAAAGCA 2997
 DB 3931 GAAAAACAAAGAGATGCGAAGAAATCAAGATTTAGCGACAGGATTATGTCACAACTT 3990
 QY 2998 G 2998
 DB 3991 G 3991
 RESULT 10
 ADM68759
 ID ADM68759 standard, DNA, 15845 BP.
 AC ADM68759;
 DT 17-JUN-2004 (first entry)
 XX
 DE Myzus persicae ryanodine receptor encoding DNA SEQ ID NO:3.
 XX
 KW ryanodine receptor, insect ion channel, insecticide, pesticide, calcium balance disruption, receptor calcium release mechanism, gene, ds.
 KM
 OS Myzus persicae.
 XX
 FH Key Location/Qualifiers
 FT CDS 277..15582
 FT /tag= a
 FT product= "ryanodine receptor"
 XX
 PN WO2004027042-A2.
 XX
 PD 01-APR-2004.
 XX
 PF 23-SEP-2003, 2003WO-US029834.
 XX
 PR 23-SEP-2002, 2002US-041295P.
 PR 18-NOV-2002, 2002US-0427324P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Caspar T, Cordova D, Guteridge S, Rauch JJ, Smith RM, Wu L;
 PI Tao Y;
 DR WPI, 2004-295411/27.
 DR P-P8DB, ADM68760.
 XX
 PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
 PT for isolating other pest ryanodine receptors and in developing screens to
 PT identify insecticidally active compounds.
 XX
 PS Claim 6, SEQ ID NO 3, 687bp, English.
 CC
 CC The present invention describes an isolated nucleotide fragment (1)
 CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
 CC having an amino acid sequence identity of at least 80% when compared to a
 CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
 CC 128, 130, 144, or 146; or (b) the complement of (a). (1) comprises a
 CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
 CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
 CC construct comprising (1) operably linked to at least one regulatory
 CC sequence; (2) a transformed host cell comprising the recombinant
 CC construct; (3) a method to isolate (1) encoding ryanodine receptors and
 CC related polypeptides; (4) an isolated polypeptide having ryanodine
 CC receptor activity; (5) a method for evaluating at least one compound for

CC its ability to modulate calcium homeostasis; (6) a method for evaluating
 CC at least one compound which modulates ryanodine receptor activity; (7) an
 CC isolated nucleic acid fragment encoding an insect ion channel comprising
 CC at least two fully defined polypeptide sequences selected from SEQ ID
 CC NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
 CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
 CC insect ion channel; (9) a method for expressing an isolated nucleic acid
 CC fragment encoding a toxic insect ion channel; and (10) recombinant
 CC construct comprising in the 5' to 3' direction a promoter operably linked
 CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
 CC The isolated nucleotide fragment (1) encoding a ryanodine receptor is
 CC useful for the isolation of other pest ryanodine receptors and developing
 CC of screens to identify insecticidally active compounds. The nucleic acid
 CC fragments are useful as pesticides, fragments of protein for antibody
 CC production, fragments of protein for determination of the structure of
 CC insecticide binding sites and in the identification of insecticides that
 CC disrupt the calcium balance in cells through other messengers that
 CC interact with the receptor calcium release mechanism. The present
 CC sequence is used in the exemplification of the present invention.
 XX
 SO Sequence 15845 BP; 5273 A; 2716 C; 3325 G; 4528 T; 0 U; 3 Other;

Query Match 44.0%; Score 1319; DB 12; Length 15845;
 Best Local Similarity 66.0%; Pred. No. 0;
 Matches 1974; Conservative 0; Mismatches 1005; Indels 12; Gaps 4;

QY 1 GTCATAGGCGGCCCATCATCAAAATATGTAAGTCAACGCTCATTTGTCAGACTTCGAG 60
 DB 1276 GTAATGTGTGACCTTAATTAATTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1335
 QY 61 ACTGCTTGTGCTGCTCTTATTAAGTCTTACGAAACGAAAGAAAGGAGTGGTAAAGTA 120
 DB 1336 ACAGGTTATGTATTAACATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1395
 QY 121 GAAGAGAAAGCAAGCAATTCCTCAAGAGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 180
 DB 1396 GAAGAAAAACAAGCAAGTATTAACAGAAAGAAAGTAAAGCAAGTATGAGCTTAAAGT 1455
 QY 181 AGGTACAGAGAGAAAGTATTAAGCAAGTCTGAGATTAACAGAAAGTCTTCCGTGCTC 240
 DB 1456 AGAGGTCAAGAAAGAAAGTCAAGAAAGTCTGAGATTAACAGAAAGTCTTCAATTAATTC 1515
 QY 241 ACTAAGTTATCAATGATCTGAGAACTCTCAAGAGAAAGTCTGATGATGCTTC 300
 DB 1516 AACAGTTATTTCTGATTTGAGAACTTAACAGAAAGTCAAGAGTCTGATTAATTTGT 1575
 QY 301 GCGTCAGTGAACCTGGGCGAATGATGATGCTCTGAGATCTCATTAATTAATTAATTAAT 360
 DB 1576 TCATTGCTTAATCTAAATGAATGATGATGCTAGAAAGTAAATTAATTAATTAATTAAT 1635
 QY 361 CAGCCGAGTGAAGATTAAGCAAGAAAGAAAGAAAGAAAGTCTGAGTCAAGTCAAGTCAAG 420
 DB 1636 CAACCTGAAGAGATTAAGCAAGAAAGAAAGAAAGAAAGTCAAGTCAAGTCAAGTCAAG 1695
 QY 421 CGTCAGAGCTGTTCCAAAGAGAAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 480
 DB 1696 AGACAAAGTTATTTCAAGAAAGAAAGAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1755
 QY 481 ATCAAGCTATCAAGTCTCCAGAGGCTCTGCTGATTCCTGGGCGAGCAAGTCTGA 540
 DB 1756 GTTAACATTAACATCTCAGAGGATTCAGTCAAGT---TAGCCGAGTGAAGAGTCTGA 1812
 QY 541 CAGAGCTGGAAAGATTAATCTGATTAATTTGATCAAGTCTGGGCGCAATTAAGAGGC 600
 DB 1813 CAAGGTGGAGATGATTTCTGTTATTTAATCAAGTGTGATGCTGCAATTAATTAAGGA 1872
 QY 601 AACCAAGAACTGCGCGCAAGTTCGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 660
 DB 1873 AATCAATCAACTGCTGCTCAATTTGCTAATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1932
 QY 661 CTGCGCTGCAAGGCTCGGCGAGAGGACCGGCAAGTCTGCAAGTCTGCAAGTCTGCAAGTCTG 720
 DB 1933 TTAGGATCTCAAGATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCTC 1992

[illegible]

QY	1801	AAGACTATCTGGCTCTGGGCTACTCATCACTTAAGTAAGCTTCCAGACGCACTCCG	1860
DB	3070	AAACCGTTATTTGGCGTTAAGTTATCAATATCTATTGATTAATCCACCGTCCCGCAATTAAA	3129
QY	1861	AAAGTTGGTCTGGCCCAACGAACTTTTATGAGTCAACCGCTCAAGCCAGCAACACTC	1920
DB	3130	ACAGTCGGCGGCCCAACGAAACAATTTATGCAATTCGAATGATATTAACCAACGACCACTA	3189
QY	1921	GACCTGAAGTGTCTCAACCTTGACACCCAGATGAGTATGAGTACGACGCTGGCTGAG	1980
DB	3190	GATTTATTCGTCTATCTTTTGTCAAGAAAATGGAABATCTAATTGATTCAGTTAGCCGGG	3249
QY	1991	AACACCCACAACTTTGGGCCAGGAGAGATACAGACGGATGACTTATGCACTTAAT	2040
DB	3250	AATACACATATCTATGGGCAAAAGAAATACAGACAGATGGAATATGATTAAT	3309
QY	2041	GAGGACTCGGACATGCAATCTTTCCCGGCACTGGTGGCAATCCGAGAGTTTACGATGGCC	2100
DB	3310	GAAAGATTTACAAATGTTTGGCGAGTCTCTATTTAATATCCGTAACAGAAAGTAAAGAGCGCT	3369
QY	2101	ATCAAGAAAGCCAAACAGGACACAGCCTCGGAGCTGTAGAGACCTCGTGGTCTACGGG	2160
DB	3370	ATTAAAAAGCTAATAGATATACGATACAGGAAACAGTCCGCACTATTATGATATAGT	3429
QY	2161	TATATGCTGACCCCGCTTACCTGGGAGCAGCATGAG---CACTCTTGTGGAAGCGTCA	2217
DB	3430	TACATATTTAGATCCCCCAACTGGAGAAACAAACGAAACGACACTCTAACAGATGACAC	3489
QY	2218	AAACGAAAGCAGACAGACTTCAAACTATCCGCGCTGAGAAAGATATGCCCTCAAGCTCT	2277
DB	3490	TCATATGATATTTTGAAGTTCAAGAACTATCTGGGAGAAAAGATATGCCGTTTCTAGT	3549
QY	2278	GGGAAAGTGGTACTTCGAGTTTGAAGATCTTAAACGGCTGACCTATGAGGGGTCCGCTGGGCT	2337
DB	3550	GGAAAAATGATCTTTCGATTTTGAATACGACAGTGGACTTATGCGGGTTTGAATGGGCC	3609
QY	2338	CACGCTGATATGGCAACGAAATGATCTCGGACAAACGAGAACTTTGGGCAATTTGAT	2397
DB	3610	AGGTTTCAATGTTCCTCCGGGTTATCAATATGGCAGTATGAAAATTTCTTGGGCAATTGAT	3669
QY	2338	GGTTTCAATGAGAAAAAGTGTACAGGGGTATACCTGATCTTTTGGCCAAAGCAATGGGCT	2457
DB	3670	GGTTATATACGAAAGAAAAATTTATACATGGGGAACGCCAATCATTTTGGTATACAGTGGCA	3729
QY	2458	GTGGGTGACGATGGGGGGTGTCTTCTGATCTCTAATTGATTAAGATCAATGAATTTCTACCTC	2517
DB	3730	GTTGGAATGTCTGGGAGTGTTTTATGATTTAATGACCACTACATTAAGCTTTTCATG	3789
QY	2518	AATGGTGAATTTGATGATGATCTTTGGCGAGAGACTACGTTTGTCTGATGTTCAGAGT	2577
DB	3790	AACGAGAAATTAATTAATGATACGTTAGAGGGGAAACAATCTCTGAAGTCCAAAGA	3849
QY	2578	GACAACTTTGTACAGCTTGCACTTGGTGTGGGCCAAAAAGCAGTTTATCATATGGC	2637
DB	3850	GAAAGATTTGTACCTGGTGTACCTCTGGGACTGAGCAAAAAGCAAAATTTGACATTTGGT	3909
QY	2638	CAAGATGGAATATCTGAAATTAATTTCAACAATGTGTCTTACAGAGGGATTAAGACCA	2697
DB	3910	CAAGACTTTATCTATTTGAATATCTTACACTTGTGACCTTACAGAGATTAAGACCA	3969
QY	2698	TTTTGCGTCAATATGAGAGAGAGCTGACTTACCTGTATACCAAGACACGCCGATCTTC	2757
DB	3970	TTCTGTGTAATATGAGAGAGGCCGTGTGCTTATTTGGTATCTAAGATTAACAACAATTTT	4029
QY	2758	GAGAAATATCTGATGATGATCGACACAGATTTGATGTGACAGAGATACAGCTGGTTCA	2817
DB	4030	GAGAAATCTGACGA---TTTTTGGTCTGTATTGATGTTCAGAAATACCAAGCTGGTTCA	4086
QY	2818	GATACACTTCACATGCCCTCAAGATTTTCCCAACAACGTTGAGAGAGATGAGAAAGCTAAC	2877
DB	4087	GATACACCACTTGTCTAAAGATTAAGTCAATTAATCAATTTAAACAATGAGAAAAAGCCAAAT	4146
QY	2878	TGGAGATTTTACGCTCTCTCACTGCCGTGTATCTGCATTAACAGATTCATTTGACGAGGCA	2937

Db	19969	CTGTACTCTCTTGGATTGATGGTGCCCTTCTTTGGACGGAGGTCGCAAACTACTAGT	19910
Qy	1203	CAATAGACATCATGCTGTAAGAGCCCTTAATATGAAAAAGTGACGTGATAGTTCGCGATT	1262
Db	19909	GGTGGACGCGTGCGCCGAGGAGCCCTTTATCCGTAAAGGGAATGTTATGGCGTTGCCAT	19850
Qy	1263	GGACTGACGGTACCCTAATATCAACTTCATGTTCAACGGAATGCGGGGTGACGGGATCTTT	1322
Db	19849	TGACCTTCTCTGCGCCATCATCAGGTTTAACTTTTAAAGGAGTAAAGTGCGCGGTAGCTT	19790
Qy	1323	CACCAACTTCAATCGMAAGGCAAGTCTTCCGGTCATCAGCGCTCTAGTAAGCTGAG	1382
Db	19789	TAGGGACTTTAACTTGAACGGAAATGTTCTTTCCGTGATAGTGTCTCATCAAACTAAG	19730
Qy	1383	TTGTCCGTTCTCTGCTGGGCGGAGAACACGGTCTGTCCTGGTACGCGGCTCCAAAGCTTA	1442
Db	19729	CTGTGCTCTCTTTTCCGAGGTGATCATGTCGTTTAAATGTTTGGCCCCCAGTGGGATT	19670
Qy	1443	CTTCTCCCTGGTGAAGTCTCTCTGCGCAGACAGATCTCAGCCTTGAGCCGTCTCTTA	1502
Db	19669	CTTGCCTCCTGTCAGATGTCCTCATGCGCAGACAGATCTCAGCTGGATCTTTGCTCTTA	19610
Qy	1503	CTTGGGCAACCTGTCCAAAGCGCGCTTGGCTGGAACCTCCGCTAGTACAGAGACGATCGGC	1562
Db	19609	CTTTGGTATCTTGCCAAGAAATGTTTGGCCGAGCAATGCTTATTTGAGAGACGACCTGC	19550
Qy	1563	CTTGGTGCCTTACACTGTGTATCTTTACAGATTATCTGCTCATATGTGGAAACAAT	1622
Db	19549	TTTGTGTTCCAAAGCCCTGTATACACGGGTGTGACATTCGCAAGTTCGTGACCAAT	19490
Qy	1623	TAGAGATAGCTAGCTGAAATAATACAGAAATGTGGCGTATGAAATAGATCGAAGCAG	1682
Db	19489	CAAGGAGAGCTGCGGAGAAATTCACGAGATGTGGGCTCTTAAACAATCGAGCGGG	19430
Qy	1683	CTGGATGTAACGGCCACACAGAGAAAGCTTGCAACAATTCACCCCTGCTGTGCTTT	1742
Db	19429	CTGGTCTGGGGCGCAGACCGAGATGTACTACACCGCATCCATCCCTTGCTCACCCATT	19370
Qy	1743	CGACGCACTCCCACTGCTGAGAAAGATACGACATACAACTGCTGTGACAGCACTGAA	1802
Db	19369	CGAAGACTTTCGCGCGCGGAAAGCAGATACGACATTCATGCTGTGCAAACGCTGAA	19310
Qy	1803	-----GACTA	1807
Db	19309	GTAAGTTGGCTACTCTTAAGAAATTAATATACAGCACTTCTTACTCTATAGAGCGA	19250
Qy	1808	TCTGGGCTCTGGGCTACTACATCAGCTTATAGTAAAGCTTCACGACGCAATCGCAAGTTC	1867
Db	19249	TTATCTGCTGGGATTACTATCAATTAACATGACAAAGCACAGCACGCAATCCGCCACGTGC	19190
Qy	1868	GTCGAGCCAAAGCAACCTTTCATGAGAGTCAAGGGCTTAACAAGCACGACCACTCGACCTGA	1927
Db	19189	GCTTGCCCAACAGATTTTATGTGAGGGCAATGGCTTAACAAGCGGCTCCACTTGACCTTA	19130
Qy	1928	GTGCTGTCAACCTTGACACCCAAAGATGGATGATAGACACGACTGCTGAGAACACC	1987
Db	19129	GCGCGGTGACACTACCCCAAGTTGGAAGGATTTGTGACACAGCTGCGCGGAAACATCTC	19070
Qy	1988	ACAACTTTGGGCGAGGAGAGATTAACAGAGGATGACCTTAATGACCTTAATGAGACT	2047
Db	19069	ACAATCTGTGGGCGACGGAGACGATCCAGCAGGGTTTGACTTAATGCTGAAACGAGATA	19010
Qy	2048	CGGACATGATCGTTCCTCCCGCACTGTGTGCAATACCCGAAAGTTGACATGTCATCAAGA	2107
Db	19009	GTGAAAAACAAGAGTTCACACTTGTTGTGCATATGCAAAAGTGAACGAGGCTATCAAGA	18950
Qy	2108	AGGCAACAAGGAGACACAGCTCGGAGACTGTGAGAACCTGCTGCTGCTACGGGTATATGC	2167
Db	18949	AGGCAACAAGGAGACACAGCTCGGAGACATGCGAAACGCTCTGGTTTACGAAATGTCT	18890
Qy	2168	TGACCCGCTTACTGGGAGACAGATGAAGCACTTGTGTGAGAGCTCAAAACGAAGC	2227

Accession	Gene	Species	Chromosome	Position (kb)	Orientation	Length (bp)	GC Content (%)	Repeat Masking	Annotation
Db	18889	TGATCTCCGACTGGCGAAGGACGAGGACCTTGGCCGAGGACAAAGCTTCAACT	18830						
Qy	2228	AAGCAGACTTCAGAAACATACCCGCTGAGAAAGATATATCCGCTCAAGCTCTGGAAATGGT	2287						
Db	18829	TCGCGGATATCCGAGCTTACAGAGGTGAGACGGAACTAGAGCCCGTGAATCGGGCAATGGGT	18770						
Qy	2288	ACTTCGAGTTTGAGATCTTAAAGGCTGACCTATGAGGGTGGCTGAGGCTCAAGCTGATTA	2347						
Db	18769	ACTTCGAAATTCGAGGCTCTCAAGCTCCGAGACAAATGCAATGGGTTGGGCAAGGCGGCTT	18710						
Qy	2348	TGGACACGAGAAATGATGCTCCGACAGACGAGAACTTGGGCAATTTGATGGTTAAATG	2407						
Db	18709	GCTATCCGGAGGAGATGCTGGGACAGGAGACACCAATTTGGGCTTGGATGACACAAATG	18650						
Qy	2408	AG 2409							
Db	18649	TG 18648							
RESULT 12									
ID	AAQ25975	standard; DNA; 15377 BP.							
XX	AAQ25975;								
AC	AAQ25975;								
XX									
DT	25-MAR-2003	(revised)							
DT	08-JAN-1993	(first entry)							
XX									
DE	MH mutant porcine ryanodine receptor cDNA.								
XX									
KW	MH; RYR1; calcium release channel; sarcoplasmic reticulum; transverse tubule; Pietrain; Yorkshire; polymorphism; beta strand; ss.								
XX									
OS	Synthetic.								
XX									
FT	Key	Location/Qualifiers							
FT	CDS	130..15237							
FT		/*tag= a							
FT	variation	207							
FT		/*tag= b							
FT	variation	405							
FT		/*tag= c							
FT	variation	438							
FT		/*tag= d							
FT	variation	876							
FT		/*tag= e							
FT	variation	1329							
FT		/*tag= f							
FT	variation	1972							
FT		/*tag= g							
FT	variation	2007							
FT		/*tag= h							
FT	variation	4071							
FT		/*tag= i							
FT	variation	4383							
FT		/*tag= j							
FT	variation	4462							
FT		/*tag= k							
FT	variation	4494							
FT		/*tag= l							
FT	variation	6867							
FT		/*tag= m							

FT	variation	/label= Polymorphic_site 7692
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FT	variation	/label= Polymorphic_site 11250
FT	variation	/tag= t 12300
FT	variation	/label= Polymorphic_site 14007
FT	variation	/tag= v 15355
FT	variation	/label= Polymorphic_site 15360
FT	variation	/tag= x
XX	polya_signal	
PN	W09211387-A1.	
PD	09-JUL-1992.	
XX	20-DEC-1991;	91WO-CA000457.
XX	21-DEC-1990;	90GB-00027869.
XX	20-MAY-1991;	91GB-00010865.
XX	09-SEP-1991;	91GB-00019250.
PA	(UTOR) UNIV TORONTO INNOVATIONS FOUND.	
PA	(UTGU -) UNIV GUELPH.	
XX	MacLennan DH, O'Brien PJ;	
XX	WPI, 1992-250106/30.	
XX	P-PSDB; AAR25450.	
PT	Purified DNA mol. for diagnosis of porcine malignant hyperthermia -	
PT	comprises DNA sequence encoding normal or mutant ryanodine receptor with	
PT	specified endonuclease restriction map.	
XX	Disclosure; Fig 2; 96pp; English.	
XX	The sequence given is the mutant pig ryanodine receptor (RYR1) gene from	
CC	swine CDNA. The polymorphic sites were observed in comparisons of	
CC	Pietrain and Yorkshire breeds. There are 17 polymorphisms between the two	
CC	breeds. The polymorphism at position 1972 causes a mutation from Arg to	
CC	Cys and this is thought to be the molecular basis of porcine malignant	
CC	hyperthermia (MH). This mutation lies within the region of RYR1 that is	
CC	concerned with the binding of regulators of Ca2+ release channel gating.	
CC	Analysis of surrounding sequences suggests that this mutation lies within	
CC	a beta strand domain comprising roughly of amino acids 520 to 830. RYR1	
CC	is the calcium release channel of the sarcoplasmic reticulum and is a	
CC	large protein which spans the gap between the transverse tubule and the	
CC	sarcoplasmic reticulum. The channel is activated by ATP, calcium, caffeine,	
CC	and micro-molar ryanodine. It is inhibited by ruthenium red, tetracaine,	
CC	calmodulin, high Mg2+ and ryanodine. (Updated on 25-MAR-2003 to correct	
CC	PN field.)	

XX	Sequence	15377 BF; 3197 A; 4630 C; 4755 G; 2773 T; 0 U; 22 Other;
SQ		
	Query Match	22.4%; Score 673.4; DB 2; Length 15377;
	'Best Local Similarity	55.6%; Pred. No. 1.5e-168;
	Matches 1546; Conservative	2; Mismatches 1173; Indels 60; Gaps 11;
QY	1 GTCATAGGCGGCCCATCATCAAAATATATGTATATCTCCACCCGATCTTGTGCAGCAATCCGAG	60
DB	1126 GGCAATGGGCCCCCTTGAGATCAATATATGGGAGTCACTGTGCTTCTGTGCAGCAATGTGGCC	1185
QY	61 ACTGGCTGTAGGCTGTCTTATATAGTCTTATACGAACGAAAGGAAGGAGTGGTAAAGTA	120
DB	1186 TGGGCTGTGTGGCTTACCTATGTCTGCCCCCAAGCCCAAGGCCCTGTGGCTGGC---GTG	1242
QY	121 GAAAGAAAGCAAGCGATTTCTCCACAGAGAAAGCAAGATGACATGTGGCTTCGACTTCTC	180
DB	1243 CTCAAGAAAGAGGCCATTCTGCAACAGGAAGGCCACATGACATGTCACTGAC	1302
QY	181 AGTTCACAGAGAAAGAAATCTTGAATCTGTCTGAATTTACAGAAAGTGTCTTCTGCTGTTC	240
DB	1303 CGCTGTCAAGCAGAGAGATCCACAGCCGCCGCAATGTATATACCACTGTCTGGCTCTTAC	1362
QY	241 ACTAAGTTATCAATATGATCTGGAATACCTTCAAGAAAGCAACCGTGTCTCATCGATGTTC--	297
DB	1353 AACCACTTCATCAATAGGCGCTTGAACAGCTTACAGCGAAAGCCACCGGGCTCTGGGGCCCG	1422
QY	298 ---TTCCGCTGATGAACTCTGGGCGAGATGTGTATGTGCTTCGAGATCTTCATCACTAC	354
DB	1423 GCTGGCAACAGGCTTACCCCTCGAAGGGCGTATCTCGAGCTGTGAGCACTATCGGGCTAC	1482
QY	355 TTCGACACGCCGATGAGATATGAAACAGAGAAACAAACAAATTCGGGCACTC	414
DB	1483 TTTGAGCGCCCTCGGAAGAGCTCAGACAGAGAGAAAGCAGAACAGCTGCGAGCTGT	1542
QY	415 CGAAACCGTCAGAACCTGTTCCAAAGGGAAGGCACTGAAACCTGATCTCTCGAAGCTATA	474
DB	1543 CGCAACCGCAGAGCTCTTCCAGAGAGAGGGAATGCTCTCCCTGTGCTTGAATTGCAAT	1602
QY	475 GACAAGATCAACGTTCATCATCGTCCAGGGGTCTCTCGTGATTCCTGTGCGGAGACGAA	534
DB	1603 GACCGCCCTAAATGTCTACACACCTGTGCGCACTTTGTGTAGT---TTGACAGAGAGAG	1659
QY	535 TCTGACAGAGCTGGGAATATATCTGGAATTTGTATCACTTGTCTGGCGGCATATATA	594
DB	1660 GAAGCGAGGTCTGGAAGAGATTTGTGAACCTGTGTATGTAGATCTGTGCTCTCTGTATC	1719
QY	555 AAGGGCAACCAAGAACTGTGCGGCACTTCCGAACTCGAACCGCTCAACTGGCTGTTC	654
DB	1720 CGTGGCAATCTGTGCAACTGTGTCCCTTTTCTCCAA-----CAACTTGAATTTGG	1767
QY	655 TCGCGCTCTGGCTCGCAGGCTCTCGGGCGAAGGGCAACCGGATGCTCGAGCTGTCTCACTGC	714
DB	1768 CTGTGTACAGAACTGTGATCGACTGAGGCTCTCTCAAGGATCTCTGTGAGGTCTGTACTGT	1827
QY	715 GTGCTTATATAGCTGGCTTGAAGCTCTCAATATGTATGAGGAGCAACATATAAGTGTATA	774
DB	1828 GTCTGATTTGAGAGTCTGAGGTCTGTGAATCATCTCCAGAGAAACCATCAATAGTCCATTC	1887
QY	775 ATCTCTCTATTAAGAAAGCAATGGGCGGCAACCTTAAAGTACATAGATGTGTCTATTTGGTGTG	834
DB	1888 ATCTCCCTTCTGTGACAAAGCATGGAAGAAACCAAGAGTCTGTAGATGTCTGTGTCCCTG	1947
QY	835 TGGCTCGGTAAACGAGCTGTGCGGTGGCTCTCAACAGAAACAATCTGTGACTATCTTACTG	894
DB	1948 TGTGTGTCAATGTGTGTGGCGGTGTGTCTCAACCAAGATCTCTATTACTGAGAACTTGTGTS	2007
QY	895 CCGCGCAAGAACTGTGTCTGCAAACTGCGCTGTGTGATCACTATATGTGTCCGTCCG	954
DB	2008 CTTGGCCGCGAGCTTCTGTCTGCAAGAAACCTCATCAATATGTACACAGGATCCGGCCC	2067
QY	955 AACATCTTCTGTGGTCTGATGAAAGGCTGGCACTGTATCCGCAATGTGTACTTGAAGTGT	1014

Db 2068 AACATCTTTGGGCGGAGCAAGGGCACACACAGTACGCAAAATGCTTAAAGTC 2127
 Qy 1015 ACTATGACACATAGAGAGAC---ACACATATGATGCAACATCTACGATAGATGG 1071
 Db 2128 ATGTGTGAGAGATGGTTCATTTCCGACAGCTCAGGGCACCCACTGTGGGTGGGCTGG 2187
 Qy 1072 GCCAACATCTATGTATGTCCCATACCCGGGCGGTGGGAGAAATGGGAGGTAAAGGC 1131
 Db 2188 GGCCTCACCGAAGGCTACAGCCCTACCTGGGGGGGGAGAGGGCTGGGCGGCAACGGG 2247
 Qy 1132 GTGGAGATGACCTGTACTGTACGGGTTCGACGGGGCTTACTCTGAGTCCGGGGAGG 1191
 Db 2248 GTGGGAGATGACCTGTACTGTACGGGTTCGACGGGGCTTACTCTGAGTCCGGGGAGG 1191
 Qy 1192 AAGATCCCGTCATAAGACCTCATGTGAAAGCTTATATTAAGAAAGGTGACGTGATA 1251
 Db 2302 CAGGTGCAACGCGCTGGTGACTTCCCAAGGGCAGACCTTCTGGCCCCGAGAGACGTGTG 2361
 Qy 1252 GGTTCGCAATTTGACCTGACGGTACCATATCAACTTCAATTTCAAGGAGTGGGGTG 1311
 Db 2362 AGCTCTGCTGTGACCTCAGCGCTGCTCCTCTTCCGATCAACGGCTGCCCGTG 2421
 Qy 1312 AGGGATCTCTACCAACTTCAATCTGAAAGGATGTTCTTCCGGTATCAAGCTGCT 1371
 Db 2422 CAGGGGCTTTGAGGCTTCAACTCAACGGGCTTCTTCTTCCGTCGATCCTTCTG 2481
 Qy 1372 AGTAACTGATGTGTCTGCTGCTGGCGAGAAACAGGTGCTCTCCGGTACGGCT 1431
 Db 2482 GCGGATGTCAGGTGCGGTCTCTCTTGGGGGCGCCGAGGAAATCAAGTTCCTCCT 2541
 Qy 1432 CAGAAAGCTACTCTCTCTGTTGAGTCTCTCTGCGCAGAGATCTCAGCTGAG 1491
 Db 2542 CCGCTGTGTCAGCCCTTTCACAGAGGTGTGTCCACAGAGCGACTCCGTCGTGAA 2601
 Qy 1492 CCGTCTCTACTTGGGCAACTGTCAAGGGG-----CGTTGGCTGAGCTCCGCTA 1545
 Db 2602 CCATCAAGAGATATCGCGAGAAAGGGCCCGGGGACCCCACTGTGGGGCCCAAGCGC 2661
 Qy 1546 GTACAGACGATACGGCTTCTGTGCTTCACTGTGTGATCTTTTACAGATTACTGTCT 1605
 Db 2662 TGCCCTCAACACAGACTTTGTGCTCCGCGGTGACACTGTCAATTTGTCTGTCT 2721
 Qy 1606 ACATATGTGAAACAATTAGATAGCTAGTAAATATACAGAAATGTGGCTATG 1665
 Db 2722 CCCCATCGAGCTATCCGGGAGAGCTGGCAGAGAAATCAATCAAGAACTTGGGCGCTG 2781
 Qy 1666 AATAAGATCGAAGCGGCTGATGTACGGCGACAGAGAAAGATTGCACAAGTCCAC 1725
 Db 2782 ACGCGCATCGAGAGGGCTTGAAGCTATGAGCCCGGTTCCGAGATGACATTAAGCGGCTGAC 2841
 Qy 1726 CCTGCTCTGTGCTCTTGAAGGACTCCCACTGTCTGAGAAACGATACATCAACTC 1785
 Db 2842 CCGTGTCTGTGTGACTTCCAGGCTTCCCGAGGCCGAGAGAAATTAACAATCTGAGATG 2901
 Qy 1786 GCTGTGCAACAATCAAGATATCTGTGCTGTGGCTTACTATCAATCAAGCTT---AGATAAG 1842
 Db 2902 TCGGGGAGAGCGCTCAAGACTGTGCTGGCTGGCTCCAGTGGGATGAGCGAGCAG 2961
 Qy 1843 CCTCCAGACCGATCCGACAGTGTGTGCTGCCCAAGAACTTTTATGACATCCACGGC 1902
 Db 2962 AAGGCAAGAGACMACCTTAGAGAGAGAGAACTCCCAAGAGATATGATAGCAATGGG 3021
 Qy 1903 TACAAGCAGACCACTGACCTGAGTGTGTGACCTGACACCCCAAGATGATGAGGTA 1962
 Db 3022 TACAAGCAGGCGCACTGAGCTTAGAGCATGTGAGACTGAGCTTGGCAGACCAAGCTG 3081
 Qy 1963 GTAGACAGCTGTGAGAAACCCCAACCTTTGGGCGCAGGAGAGAGATACAGCAGGGA 2022
 Db 3082 GTGAGCCGGCTGGCGAGAAAGGGGCAACGATGTGGGCGGAGACCGAGTGGCCCAAGGGC 3141
 Qy 2023 TGAATTAATGAACTTAATGAGAGCTCGACATGATGTTCCCGGCACTGTGTGATAC 2082
 Db 3142 TGAAGCTACAGTGTGTGAGAGACATCCCAAGCGCGCCCAACCTTGGCTGTGCTTAC 3201

Qy 2083 CGAAGGTTGACATGCCATCAAGAGGCCAACAGGACACAGGCTCGAGACTGTGAGG 2142
 Db 3202 CGCCTGTAGACGAGGCCACCAAGCGAGCAACCGGAGCAGGCTTTGCGAGGCTGTGGC 3261
 Qy 2143 ACCCTGTGTCTACGGGTATATGCTGAGCCCGCTTACTGGGAGAGCATGAAGCACTC 2202
 Db 3262 ACCCTGTGTGTACGGGTACMACATGAGCGGCCCAACAGAGGCCAGTCAAGTGGAG 3321
 Qy 2203 TTGTTGAAGCGTCAAAACAGAAACAGACAGACTTCAGAACATACCGGCTGAGAAAC 2262
 Db 3322 AGCCAGTCTGCTGGAGACCGTGTG-----GCACTTCCGGGCTGAGAAATGCC 3389
 Qy 2263 TATCCGCTCAGCTCTGGAAAGTGTACTTCAAGTTTGAATCTTAAAGCTGACCTATG 2322
 Db 3370 TATCGGTGACAGACGGCCGCTGGTATCTTGAAGTTCAAGGCCGTCACACAGGGGAGATG 3429
 Qy 2323 AGGCTGGCTGGGCTCACGCTGATATGACACAGAAATGATGCTCGGACAAAGACAGAAC 2382
 Db 3430 CAGGTGGGCTGGGCGCGGCTGAGCTCGGCTGATGTGAGAGCTGGAGCCGATGAGCTG 3489
 Qy 2383 TCTTGGGCAATTGATGTTCAATGAGAGAAAGGTATACAGCGGTAACTGAGTCTTTC 2442
 Db 3490 GCCTATGCTTCAATGAGGACACCGGGATCAGGCTGGCACTTGGG---CAGGAACTGTTT 3546
 Qy 2443 GGCAGACATGGGCTGTGTGTGACGTAGTGGGGGTGTTCTTATGATCTATTTGATAGACG 2502
 Db 3547 GGGGCTCCCTGGAGAGTGGGGAGTGTGTGGGCTGATGATCAACTCACAGAGAACACC 3606
 Qy 2503 ATTAAGTTTCACTCAATGAGTGTGTTGATGATGCTCTTGGCGGAGACCTAGCTTT 2562
 Db 3607 ATTAATCTTCAACGCTCAACGGGAGGTCTCATGTCCCACTCGGGCTCTGAAACCGCTTC 3666
 Qy 2563 GCTGATGTCAG---GGTGAACAATTGTGACAGCTTGCACACTGTGGTGGGCAAAA 2619
 Db 3667 CGGATATTCAGGTGGGAGATGGCTTCTGCGCTGTGACGCTTGGACCTGGCAGGCTG 3726
 Qy 2620 GCCAGGTTAAATATGACCAAGATGTGAATACTGTGAATACTTCAACAATGTGTCTT 2679
 Db 3727 GGCACCTGAACCTGGGCGAGATGTAGGCTCCCTGGGTTCTTTGCAATGTGGGCTC 3786
 Qy 2680 CAGAGGAGATGAAACATTTTGGCTCAATATGAAAGAGACGTGATCACTGCTGACAC 2739
 Db 3787 CAGGAGGTTTGGACCATTCGCAATCAATGACAGCGTCCGCTCACTGCTGTTGACG 3846
 Qy 2740 AAGGACGAGCGAATCTTTCGAG 2760
 Db 3847 AAAAGCTTCCCAAGTTTGAAG 3867

RESULT 13
 ACAS6556
 ID ACAS6556 standard; cDNA; 4078 BP.
 XX ACAS6556;
 AC
 XX
 AC
 XX
 DT 06-JUN-2003 (first entry)
 XX
 DE Human signalling pathway polynucleotide probe SEQ ID NO 1154.
 XX
 KW Human; probe; ss; array element; Parkinson's disease;
 KW signalling pathway population; cancer; adenocarcinoma; leukaemia;
 KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
 OS Homo sapiens.
 XX
 XX US6500938-B1.
 XX
 XX
 PD 31-DEC-2002.
 XX
 XX 30-JAN-1998; 98US-00016434.
 XX
 XX 30-JAN-1998; 98US-00016434.
 PR

XX	(INCY-) INCYTE GENOMICS INC.
PA	Au-Young J, Sellhammer JJ;
P1	WPI, 2003-352189/33.
XX	
DR	
XX	Combination of polynucleotide probes, useful as array elements in a
PT	microarray for monitoring the expression of a number of target
PT	polynucleotides.
XX	
PS	Claim 1; SEQ ID NO 1154; 65bp; English.
CC	
XX	The invention relates to a combination which, comprises a number of
CC	polynucleotide probes comprising a sequence selected from one of the 1490
CC	sequences mentioned in the specification. The combination is useful as an
CC	array element in a microarray for monitoring the expression of a number
CC	of target polynucleotides. The microarray is particularly useful in the
CC	diagnosis and treatment of cancer and immunopathology and neuropathology.
CC	The microarray is useful in diagnostics and treatment regimens, drug
CC	discovery and development, toxicological and carcinogenicity studies,
CC	forensics and pharmacogenomics. The microarray is also useful for
CC	monitoring progression of diseases and for developing sophisticated
CC	profiles for the effects of currently available therapeutic drugs. The
CC	combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC	and genomic fragments and in research and diagnostic applications. The
CC	array can detect changes in expression in a large number of genes coding
CC	for different signaling pathway populations which can be used to diagnose
CC	various diseases including cancer e.g. adenocarcinoma and leukemia,
CC	immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC	and Parkinson's disease. The present sequence represents a polynucleotide
CC	probe of the invention. Note: The sequence data for this patent did not
CC	form part of the printed specification but was obtained in electronic
CC	format directly from USPRO at
CC	seqdata.uspro.gov/sequence.html?DocID=06500938B1
XX	
SQ	Sequence 4078 BP, 1093 A, 940 C, 1068 G, 977 T, 0 U, 0 Other;
	Query Match 22.3%; Score 668; DB 10; Length 4078;
	Best Local Similarity 55.4%; Pred. No. 2.9e-187;
	Matches 1590; Conservative 0; Mismatches 1225; Indels 57; Gaps 13;
OY	1 GTCATAGCGCGGCCCATCATCAATATAGTGACTTCACCGTCATTGCGACGATTTCCGAG 60
DB	1163 GGCAATGGAAACATCTGAATAATAAAACGCTGCATCAGTAGCTAATATCAACATGTAAAC 1222
OY	61 ACTGCTTGCTGCTCTCTTAATAGCTTAAAGCTTACGAAACGAAGAAGAGCGGCTGTAAACTA 120
DB	1223 ACAGGCCCTATGCTTACTTACCACAGCTCTGTGACGTGAAATCCGTAGATGGAGATCTATA 1282
OY	121 GAAGAAGAACAAGCATTTCTCCACGAGAAAGGACAGATGAGACGATGCGCTCGACTTCC 180
DB	1283 CAAGCTAAG---GCTATTATGATCATGTAAGCCACATGATGATGGCAATAAGTTTGTCG 1339
OY	181 AGGTCAAGAGGAAGAAATCTAGAGCTGCTGAGATTATCAGGAAGTGTCTTCGCTGTTTC 240
DB	1340 AGATCCACGACATGAAGAATCAACGACGACGCCGAGATTATCCGAGACAGACTTCCCTTTC 1399
OY	241 ACTAAGTTTATCAATAGCTCTGGAACCTTAACAAGAACCGTCTCACTCGAATGTTCTTC 300
DB	1400 AATATGATTTTATDAGGGGCGCTGTGATCTCTCAGCAAGAAAGCGAAGGCTTCCACAGTCAT 1459
OY	301 GCGTCAGTGAACCTTGCGGCGAGATGCTGATGTCCTCGAGGATCTCATCAACTATCTTCGCA 360
DB	1460 TTGCTTATAGAGTCCG-----TAAGCTTAAGTCTCGAGATCTCATTTGGCTATCTTCCAC 1513
OY	361 CAGCCGATGAGGATATGGAACACGAGAAAAACAAACAAATTCCGGGACCTCCGAAC 420
DB	1514 CCCCCAGATGACATTTAGAGCATGAACAAACAGAACAGACTACGACCCTGAAGAAT 1573
OY	421 CGTCAGAGACTGTTCTCAAAGAGGAAGCATCTGGAACCTGATCTCTGAAGCTATATAGCAAG 480
DB	1574 CGGCAAAATCTCTTCACGAAAGAGGAATGATCAACTCTGCTTGATGATGATAGACCGT 1633

QY	481	ATCAACGTCATCAGCTCCAGGGGTTCTCGTCGTGATTCCTCGGGGGAGACGAAATCTGGA	540
Db	1634	TTGACGCTCTACACAGTCAGACACACTTGGTCG---ATGTTGCTGGGCGAAGACAGGA	1690
QY	541	CAGAGCTGGGAAATGATATCTGAAATATTGTAATCAGTTGCTGGCGGCAATATATAAGGAC	600
Db	1651	GAGTCCTTGAAATTCATTTCTGAAATTTCTGTGTAATGTTCCGGGGGCTCTAATTAAGAGA	1750
QY	601	AACCAACGAACCTGCGCGCAGTTGCGGAACTCGAACCGCTCAACCTGGCTGTTCTGCGGC	660
Db	1751	AATGTGAAAACTGAGCTCATTTTCTGAGCTC-----CCTCACTGGATTGAT-----C	1798
QY	661	CTCGGCTCGCAGGCTCTGGGGGAGGAGCACCGGACATGCTCAACATGCTGCACTGCGTCTT	720
Db	1799	AGCAGATTGGAAAGACTGGAAGCTTCTTTCAGGCAATTCGGAAGTTTAACTGTTGTTTAA	1858
QY	721	ATAGACTGCGCTGAAGCTCTCAATATGATGAGGAGCGAACACATATAAGTAAATCTCT	780
Db	1859	GTAGAAAGTCGAAAGCTTAATAATTTTAAAGAAAGACATATTAATCTATTAATCTCA	1918
QY	781	CTATTAGAAAAGCATGAGCGCGAACCTTAAGTACTAATGTGCTATGTTGCTGTCGCTC	840
Db	1919	CTTTTAGCAAACTAGGAAGAAATCAAGAGTTTGTGAATGTTCTGTCTCACTGTGTTT	1978
QY	841	GGTAAACGCGCTGCGGGTCGCTCGTCAAGAAACAATCTGTGTAATTAAGTCCCGGC	900
Db	1979	TGCCACGGGGTGTGAGTCCGTTCTTAACAGCATCTCATGTGTGCAATCTCTTACAGGA	2038
QY	901	AAGAACTGTTGCTGCAAACTGCGCTGTGTGATCAAGATATCTAATGTCCGCGGAACATC	960
Db	2039	AGAGCTTGTATTGCAAGACAGTCTTGTGAACATGTCAAGACATAGAGCCCAATATT	2098
QY	961	TTCCGGGTCAGATAGAAAGGTCGCGACGTGACCGCAAAATGTAATCTTCAAGTACATATG	1020
Db	2099	TTTCTGGGCGCTCAGTGAAGGTTCTGTCTCAAGTAAAGAAATGTACTAATTAATTAATG	2158
QY	1021	GACCACATAGAG---AAGACCAACATATGATGTCACATCTACGATAGATGGGCCAAC	1077
Db	2159	GACCAACAGAGCCCTTGTGACAGCTGAAGCACTCACTCGCAGATGGGCTGGCTTCC	2218
QY	1078	ACTACTGTTATATGCCCATACCCGGGGCGGTGGCGAAGAAATGGGAGGTAACGGGTTGGGA	1137
Db	2219	ACTGAAGATATTTCTCCCTACCTGAGAGGGGCGAAGGTGGGATGAAATGATGTTGGA	2278
QY	1138	GATGACCTGTACTGTGACGGGTTGACAGCGGCTCACTACCTGTGATCCGGGGGAGGAAGACT	1197
Db	2279	GATGATCTTCTCTCTATGATTAATTAATGATGACCTTCACTCTGTGTCAAGTTGATTTGCTC	2338
QY	1198	CCCGTCATATAGACTCATGCTGAAGAGCTTATATTGAAGAGGTGAACGTATAGGTTGC	1257
Db	2339	ACTGTAAAGCTCACAAACC-----AACATCTGTTAAAGAACTGATGATCATCAGTTGC	2392
QY	1258	GCATTGGAAGCTGACGGTACCCATATCACTTCAATGTTCAACGGAATGCGGGTGAACGGGA	1317
Db	2393	TGTTTAGATCTGAAGTCCCAAGCATCTGTTCCGAATTATATGACAACCTGTTCAAGGA	2452
QY	1318	TCTTCAACCACTTCATCTGGAAGAGGATGTTTCTCCGCGCATCAGGTGCTCTAGTAAG	1377
Db	2453	ATGTTTGAATTTTCATCATGAAAGGCTCTTCTTTCAGTCTGTTAATGTTTCTTCTGACGA	2512
QY	1378	CTGAGTTTTCGGTTCCTGCTGGGGGAGAAACACGGTGTCTCCCGGTACCGCGGCTACGAA	1437
Db	2513	ATTAAGATACCTTTCTGCTTGGAGGGGACATGGAATTCAAATTTCTTCTCCACCT	2572
QY	1438	GAGTATCTCTCCTTGTGGAAGTCTCTCTGTGCGACAGATCTTCAAGCTTGAAGCCGTGC	1497
Db	2573	GAGTATGCTCTTGTATTAAGAGCTGTTCTCGCAAAAGAAAGTTGAATGGAACACAGC	2632
QY	1498	-----TTCTACTTCCGCAACCTGTCCAAAGGGGCTTGGCTGGAACCTCCGCTATGACG	1551
Db	2633	CGAAGTACAGCAAGAAAGACTTATCACTGCACTGCTGAGGCCCCACATTTTCCCTG	2692

QY 1552 GACGATAGGCGCTTGCTGCTACCTGTTGATTAAGATTACTCTGCTACATAT 1611
 DB 2693 ACGGAGCTGCTCTTCAACCCATCCCTGGATACAGCAGATGCTGCTCTCAT 2752
 QY 1612 GTGGAACAAATTAGATAGTACGTGAAAATATACAGAAATGGGCTATGAATAG 1671
 DB 2753 CTAGAAAGATATAGAAATATGAGAGAAATATCAGAAATCTGGGATATGAATAA 2812
 QY 1672 ATCGAAGAGGCTGATGATACGGCAGACAGAGAGAAAGATTGACAAAGATCCACCTG 1731
 DB 2813 ATTAGAGCTGGCTGAGATGATGTCGGGTTAGATGACAAAGAACACACCATG 2872
 QY 1732 CTCGCGCCCTTGAGGAGCTCCCACTGCTGAGAAACGATAGACATCACTGCTGTG 1791
 DB 2873 CTGGTGAAGTTCTCCAGCTGCTGAAACAGGCGCAATTAACATTAATGTCGCTT 2932
 QY 1792 CAGACACTCAAGACTATCGGCTGAGGCTACTACAT---CAGCTTAGATTAAGCTCCA 1848
 DB 2933 GAGACCTGAAAGACTTTGTCATTAAGATGTCATGTCGGTATATCAGATGAACATGCT 2992
 QY 1849 GCACGCAATCCGCAACGTTGCTGTCGCAACGAACTTTCAATGACAGTCCAAAGCTACAG 1908
 DB 2993 GAAAGCAAGTGAAAAAATGAAAGTACCCAAAGAAATTAACAGCTGACAAAGTGATACAG 3052
 QY 1909 CCAAGCACTGACCTGAGTCTGTCACTGACACCCAGATGAGTACTAGTAC 1968
 DB 3053 CCGTCCCTTAGACCTGATGCTTATCAAACTCACCCCATCGCAAGAAAGCATGTGAC 3112
 QY 1969 CAGCTGCGTGAAGAACCCCAACCTTTGGGCGAGGAGAGATACACAGGATGAGACT 2028
 DB 3113 AAGTTGGCAAAATATGCAATATATGTCGGGCGGAAATCGAATCCGCAAGGCTGAGACT 3172
 QY 2029 TATGACTTAAATGAGACTCGGACATGATCGTTCCCGCACTGTCCTACATCCCGAAG 2088
 DB 3173 TATGGCATTCACAGAGATGAAGAAAGAAATCCGCTGTTCCCTACATCTCT 3232
 QY 2089 GTTGACGATGCCATTAAGAGGCGCAACGAGCACAGCTGAGAGACTGTGAGACCTG 2148
 DB 3233 CTGATGACCGAACCMAAAATCCAAACAGGACACTCCGCGAGGCTGTGCGCACGCTG 3292
 QY 2149 CTGGCTACGGGTATATGCTGAGACCGGCTACTGGGAGAGAGATGAAGCACTCTGTG 2208
 DB 3293 CTGGGCTACGGCTACACTTGAAGAC---AGATCAAGATCAATGACCCAGAGCC 3346
 QY 2209 GAAAGCTCAAAACAGAAACAGACAGACTTCAGAACTACCGGCTGAGAAAGATATGCC 2268
 DB 3347 GAAAGTGCAGGCGGACCGGGGAAAGGTTCCGAATCTTCGCGGAGAAAGCCATATCA 3406
 QY 2269 GTGAGCTTGGGAGTGTACTTGAATTTGATGATCTTAACGGCTGACCTATAGGGTTC 2328
 DB 3407 GTGAAGCGCGACCGTGTATTTGAAATTTGACGCTGCTGAGACATGAGGGTT 3466
 QY 2329 GAGCTGGCTCACGTATATGAGCACAGAAATGATGCTCGGACAAAGAGAGAACTTTGG 2388
 DB 3467 GGTGGAATCGTCTGCTGTTGCAACCGGATCAGAGCTTGGCTCAGATGAACGTGCTTT 3526
 QY 2389 GCATTGATGTTTCAATGAGAAAAAGTATACAGCGGTAAACATGATCTTTGCGCAAG 2448
 DB 3527 GCCTTGAATGCTTCAAGGCCAGCGGATGAGTCAAGG---CAATGAACATATAGGGGCG 3583
 QY 2449 CAATGGGCTGTTGATGATGAGTGGGGTGTCTTAATATCAATTTGATTAAGCAATAGT 2508
 DB 3584 TCTTGGCAAGCAGGAGATGCTGTGGGATGATGTTGATGATGAACGAAACACCATATG 3643
 QY 2509 TTCTCACTCAATGATGATGTTGATGATGCTGTCGGGAGAGACATACGTTTGTGAT 2568
 DB 3644 TTCACTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3703
 QY 2569 GTCCAGGCTGACAA---CTTTGATCAAGCTTGCACATTTGGTGTGGGCAAAAAAGCCAG 2625
 DB 3704 TTTGATGTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3763
 QY 2626 TTAACATATGCGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2685

DB 3764 ATGAACTTTGGAAAGATGTCAGACCTTGAAATATTTACCACTGTCGGCTTCAAGAG 3823
 QY 2686 GGATATGAAACATTTGGTCAATATGAAAGAGACGATGCTGATACCAAGAGAC 2745
 DB 3824 GGTATGAACATTTGGTCAATATGAAAGAGATGATGATGATGATGATGATGATGATGAT 3883
 QY 2746 CAGCCGATCTTGGAAATACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2805
 DB 3884 CTTCTCAGTT---TCTTCAAGTTCCATCAAAACCATGAACATATATGAGGTGACCAAGATA 3940
 QY 2806 CCAGCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2857
 DB 3941 GACGCAACATATGACAGTTCCCATGTTTAAAGGTCACTGAAAGTCTTTGG 3992
 RESULT 14
 AD156352
 ID AD156352 standard; DNA; 4078 BP.
 XX
 AC AD156352;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Human polynucleotide probe #1154.
 XX
 KW Human; probe; ss; receptor-like polypeptide; transducing polypeptide; effector-like polypeptide; cancer; immunopathology; neuropathology; drug development; toxicology; carcinogenicity; signaling pathway polypeptide; adrenal gland; bladder; bone; bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS; diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology; dementia; amnesia; epilepsy; Alzheimer's disease; depression.
 KW
 OS Homo sapiens.
 XX
 FN US2004010136-A1.
 XX
 PD 15-JAN-2004.
 XX
 PF 26-NOV-2002; 2002US-00305720.
 XX
 PR 30-JAN-1998; 98US-00016434.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Au-Young J, Seilhammer JJ;
 XX
 DR WPI; 2004-090520/09.
 XX
 PT New composition comprising polynucleotide probes, useful as array elements in a microarray for monitoring the expression of target polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic fragments.
 PT
 XX
 PS Claim 6; SEQ ID NO 1154; 73bp; English.
 XX
 CC The invention relates to a composition of polynucleotide probes comprising first polynucleotide probes comprising at least a portion of a gene encoding a receptor-like polypeptide, second polynucleotide probes comprising at least a portion of a gene encoding a transducing polypeptide and third polynucleotide probes comprising at least a portion of a gene encoding an effector-like polypeptide. The probes of the composition are useful as array elements in a microarray for monitoring the expression of target polynucleotides. The microarray is useful in the diagnosis and treatment of cancer, an immunopathology or a neuropathology. It can also be used for drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. Microarrays can also be used for monitoring the progression of diseases that may be associated with the altered expression of signaling pathway polypeptides. The composition can also be used to purify a subpopulation of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile is also useful for the diagnosis and treatment of cancer, e.g. cancers of

CC the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,
 CC an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or
 CC ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,
 CC epilepsy, Alzheimer's disease or depression. This sequence represents a
 CC human polynucleotide probe of the invention. Note: The sequence data for
 CC this patent did not form part of the printed specification but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html.

SO Sequence 4078 BP, 1093 A, 940 C, 1068 G, 977 T, 0 U, 0 Other;

Query Match 22.3%, Score 668, DB 12, Length 4078;
 Best Local Similarity 55.4%, Pred. No. 2, 9e-187;

Matches 1590, Conservative 0, Mismatches 1225, Indels 57, Gaps 13;

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QY 1 GTCATAGGCGCCGATCATCAATATGAGTATCCACCGTCATTGTGAGCATTCGCGAG 60
DB 1163 GGCATGAGAAACATCTGAATAAATACGGTACTGATGCTATATACACATGTAGAC 1222
QY 61 ACTGCTGTGCTGCTTATTAAGTCTTACGAACGAGAGAGAGAGAGAGAGAGAGAG 120
DB 1223 AAGGCTTATGCTTATTAAGTCTTACGAACGAGAGAGAGAGAGAGAGAGAGAG 1282
QY 121 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 1283 CAACGTAAAG--GCTATATGATCATGAGAGCCATGATGATGATGATGATGATG 1339
QY 181 AGGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 1340 AGATCCACAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1399
QY 241 ACTAAGTTATCATATGATGATGATGATGATGATGATGATGATGATGATGATG 300
DB 1400 AATAGTTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1459
QY 301 GCGTCAGTGAACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 1460 TTGCTATAGAGTCCG-----TAAGCTTAAGCTCAGAGATCATATGATGATG 1513
QY 361 CAGCCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 1514 CCCCCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1573
QY 421 CGTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 1574 CGGCAAAATCTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1633
QY 481 ATCAACGTATCATCTGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 1634 TTGCAAGTCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1690
QY 541 CAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 1691 GAGTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1750
QY 601 AACCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 1751 AATCGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1798
QY 661 CTGCGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 1799 AAGAGATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1858
QY 721 ATGAGCTCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 1859 GTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1918
QY 781 CTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 1919 CTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1978
QY 841 GGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900

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DB 1979 TGCCACGGGGGTGACAGTCCGTTCTAACAGCATCTCATCTGATGACATCTCTACAGAG 2038
QY 901 AAGAACTGTTGCTGCAAACTGCTGCTGATGATGATGATGATGATGATGATGATGATG 960
DB 2039 AAGAGCTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2098
QY 961 TTGCTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 2099 TTTCTGAGGCGTCAAGTGAAGAGTCTGCTCAGTATGAAGAGAGAGAGAGAGAGAGAG 2158
QY 1021 GACCACTATGAG--AAGACCACTATGATGATGATGATGATGATGATGATGATGATG 1077
DB 2159 GACCACTATGAG--AAGACCACTATGATGATGATGATGATGATGATGATGATGATG 2218
QY 1078 ACTAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1137
DB 2219 ACTGAGAGAGATTTCTCTTACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2278
QY 1138 GATGACCTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1197
DB 2279 GATGATCTCTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2338
QY 1198 CCGGTCAATGAGATCTATGATGATGATGATGATGATGATGATGATGATGATGATG 1257
DB 2339 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2392
QY 1258 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1317
DB 2393 TGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2452
QY 1318 TCCCTTACCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1377
DB 2453 ATGTTGAGAGATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 2512
QY 1378 CTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1437
DB 2513 ATAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2572
QY 1438 GGTACTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1497
DB 2573 GGGTATGCTCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2632
QY 1498 -----TTCTACTGCGCAACCTGTCAGAGCGGGCTTGGCTGAGACTTCCGCTAGTACAG 1551
DB 2633 CGAGAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2692
QY 1552 GACGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1611
DB 2693 ACGCAAGCTGCTTCAACCTCCTGATGATGATGATGATGATGATGATGATGATGATG 2752
QY 1612 CTGGAACAAATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1671
DB 2753 CTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2812
QY 1672 ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1731
DB 2813 ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2872
QY 1732 CTGCTGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1791
DB 2873 CTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2932
QY 1792 CAGAGATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1848
DB 2933 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2992
QY 1849 GACAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1908
DB 2993 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3052
QY 1909 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1968
DB 3053 CCGCCCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3112

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QY 1969 CAGCTGGCTGAGACACCCCAACCTTTGGGCGCAGGAGAGATACAGACGGATGACT 2028
DB 3113 AAGTTGGCAGAAAATGACATAATGTGTGGCGCGGGAATCGAATCCGGCAGGGCTGACT 3172
QY 2029 TATGACCTTAATGAGACCTCGGACATGCACTCTTCCCGGACCTGTGCTCATACCCGAAG 2088
DB 3173 TATGGCATTCCAACAGACGTAAAGAACAGAAATAATCTCTGCTTGTTCCTCAACTCTCT 3232
QY 2089 GTTACGATGCGCATCAAGAAAGGCGCAACAGGCGCAGCCTCGGAGACTGTGAGACCTGTG 2148
DB 3233 CTGATGACCGAACCAAGAAATCCAAAGAGACGCTCCGAGAGGCTGTGTGGCAGCGTG 3292
QY 2149 CTGCTCTACGGGTATATGCTGGACCCGCTACTGCGGAGACAGATGAAGCACTTGTGTTG 2208
DB 3293 CTGGGGTACGGCTACAACTTGGAGACACC-----AGATCAAGATCATGACGACGAGCC 3346
QY 2209 GAAAGCTCAAAAACAGAACAGACAGCTTCAGAACATACCGGGCTGAGAAAGACTATGCC 2268
DB 3347 GAAAGTGCACAGCGGACCGGGGAAAGGTCCGAATCTTCGGTCCGAGAAAGACTATGCA 3406
QY 2269 GTACAGCTCTGGGAGATGCTACTTTCGATTTGATGATCTTAAACGGCTGACCTATGAGGGTTC 2328
DB 3407 GTGAGGCGCGGACGGTGTGATTTTGAATTTGAGACGCTCACTGCTGGAGACATGAGGTTT 3466
QY 2339 GGGCTGGGCTCAAGCTGATATGACACAGAAATGATGCTCGGACAGAGAACTCTTGG 2388
DB 3467 GGTGAGATCGTCTGCTGTGTGTCACCGGATCAGAGGCTTGGCTGAGATGAAGTCCCTT 3526
QY 2389 GCATTGATGCTTACATGAGAGAAAGATGACAGCGGTAACTGATCTTTGGGCAAG 2448
DB 3527 GCGTTGATGCTTCAAGGCGGCGGCTGCGCATCAGGG---CAATGAACACTATGAGGGCGC 3583
QY 2449 CAATGGGCTGTGTGAGAGTGTGGGGGTCTTCTAGATGCTCATGATGAAGCATAGT 2508
DB 3584 TCTTGGCAAGCAGGCGATGTGTGGGGGTGTGTGTGACATGAAGCAACACCATGATG 3643
QY 2509 TTCTCACTCAATGCTGAGCTTGTGATGATGCTCTTGGCGGAGAGACTACGTTTGTGAT 2568
DB 3644 TTCACTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3703
QY 2569 GTCCAGGGTGAACA---CTTTGACACAGCTTGCACACTTGTGTGTGGGCAAAAAGCCAGG 2625
DB 3704 TTGTATGTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3763
QY 2626 TTAACATATGAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2685
DB 3764 ATGACCTTTGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3823
QY 2686 GGATATGAAACATTTTGGCTCAATATGAAAGAGAGAGCTGACTGCTGTAACCAAGGAC 2745
DB 3824 GGGTATGAAACATTTTGGCTCAATATGAAAGAGAGATGATGATGATGATGATGATGATGATG 3883
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QY 2806 CCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2857
DB 3941 GAGCGCACCATGACATGCTCCCATGTTTAAAGTCTACTCAGAGTCTTTTG 3992

RESULT 15
ABA08776
ID ABA08776 standard; cDNA, 14302 BP.
XX ABA08776;
AC ABA08776;
XX 11-JAN-2002 (first entry)
DT Human ryanodine receptor homologue-encoding cDNA, SEQ ID NO:552.
XX Human; cytokine; cell proliferation; cell differentiation; growth factor;

KM haematopoiesis regulation; tissue growth; immunomodulator; activin;
KM inhibin; chemotaxis; chemokines; thrombolytic; oncogenesis;
KM proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KM myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KM chronic inflammatory condition; proliferative retinopathy;
KM atherosclerosis; coronary heart disease; arterial ischaemia;
KM bone disorder; osteoporosis; vascular growth disorder;
KM tissue regeneration; wound healing; infection; immune disorder;
KM cell culture; drug screening; gene therapy; antiinflammatory;
KM antiaesthetic; antiaesthetic; haemostatic; antiatherosclerotic;
KM cytosolic; osteopathic; vasodilator; cardiant; virucide; antibacterial;
KM antifungal; vulnery; antitumor; 88.
XX
OS Homo sapiens.
XX
XX WO200157188-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US003800.
XX
XX 03-FEB-2000; 2000US-00496914.
XX 27-APR-2000; 2000US-00560875.
XX
XX (HXSE-) HXSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX WPI: 2001-457740/49.
XX P-PSDB: ABB11532.
XX
XX Human proteins and DNA encoding sequences useful for preventing, treating
XX or ameliorating a medical condition in a mammalian subject e.g. arthritis
XX and cancer.
XX
XX
XX Claim 1; Page 571-574; 1963pp; English.
XX
XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
XX sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
XX invention also relates to vectors and recombinant host cells comprising a
XX nucleotide of the invention, methods of producing the novel polypeptides,
XX antibodies against the polypeptides, methods of detecting the nucleotides,
XX or polypeptides in a sample, and methods of identifying compounds which
XX bind to polypeptides of the invention. Although novel, many of the
XX polypeptides of the invention have homology to known proteins, thereby
XX giving an insight into their probable biological activities, and hence
XX potential therapeutic applications. The polypeptides of the invention may
XX have various activities, including cytokine, cell proliferation or cell
XX differentiation activities; stem cell growth factor activity;
XX haematopoiesis regulatory activity; tissue growth activity;
XX immunomodulatory activity; activin- or inhibin-related activities;
XX chemotactic or chemokinetic activities; haemostatic, thrombotic or
XX thrombolytic activities; receptor or ligand activities; or may be
XX involved in oncogenesis, cancer cell proliferation or metastasis.
XX Depending on their biological activities, polypeptides and nucleotides of
XX the invention are useful for preventing, treating or ameliorating medical
XX conditions, e.g., by protein or gene therapy. Such conditions include
XX cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
XX disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
XX proliferative retinopathy, atherosclerosis, coronary heart disease,
XX arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
XX vascular growth. Polypeptides involved with tissue regeneration and
XX repair (or nucleic acids encoding them) may be used to promote wound
XX healing (e.g., of burns, incisions and ulcers), while those with
XX immunomodulatory activities may be used in the treatment of viral,
XX bacterial and fungal infections in addition to immune disorders.
XX Polypeptides with growth factor activity may be used in cell cultures to
XX promote cell growth. For example, such polypeptides may be used to
XX manipulate stem cells in culture to give rise to neuroepithelial cells
XX that can be used to augment or replace cells damaged by illness,
XX autoimmune disease or accidental damage. The polypeptides and nucleotides
XX may also be used in the diagnosis of the above conditions, and in drug
XX screening techniques. The present sequence represents a cDNA encoding a

CC novel human polypeptide of the invention
 XX Sequence 14302 BP; 4077 A; 3115 C; 3591 G; 3519 T; 0 U; 0 Other;

Query Match 22.3%; Score 668; DB 4; Length 14302;
 Best Local Similarity 55.4%; Pred. No. 66-187;
 Matches 1590; Conservative 0; Mismatches 1225; Indels 57; Gaps 13;

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 DB ACAGGCTATGCTTACTTACACAGTCTGTGAGAGTGAATCCGTGAGATGGAATCTATA 1282
 QY 1223 GAAAG 180
 DB 1283 CAACGTAAAG--GCTATATGATCATGAGAGCCACATGATGATGAGCATTAAGTTGTG 1339
 QY 181 AGGTCAAG 240
 DB 1340 AATCCACAGATGAG 1399
 QY 241 ACTAAGTTATCATATGCTGTGAGAACTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 DB 1400 AATAGATTTATAG 1459
 QY 301 GCGTCAGTGAACCTGGGCGAGATGCTGATGCTGAGAGATCTCATCACTTCCGCA 360
 DB 1460 TTGCTATAGAGTCCG-----TAAGCTTAAGTCTGAGAGATCTCATTTGGCTTCCAC 1513
 QY 361 CAGCCCGATGAGAGATGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 DB 1514 CCCCAG 1573
 QY 421 CGTCAAG 480
 DB 1574 CCGCAAAATCTCTTCAAG 1633
 QY 481 ATCAACGTATCATGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 DB 1634 TTGCACTCTCAAG 1690
 QY 541 CAGAGCTGGAGAGATATCTGATATTTGTAATGATGCTGAGAGAGAGAGAGAGAGAG 600
 DB 1691 GAGCTTGGAAATCCATCTGAATCTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1750
 QY 601 AACCAACGAG 660
 DB 1751 AATCGTAAATCTGAGTCTAATTTTCTGAGCTC-----CTGAGCTGTTGAT-----C 1798
 QY 661 CTGCGCTCGCAGAGCTCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 DB 1799 AGCAGATGGAG 1858
 QY 721 ATAGAGCTCGCTGAG 780
 DB 1859 GTAG 1918
 QY 781 CTAATAG 840
 DB 1919 CTTTATAG 1978
 QY 841 GGTAAAG 900
 DB 1979 TGCACAG 2038
 QY 901 AAG 960
 DB 2039 AAG 2098
 QY 961 TTGAG 1020

DB 2099 TTTCTGGCGCTGAGTGAAGGTTCTGCTCAGATATAGAAATGTAATATGATGATG 2158
 QY 1021 GACCAATAGAG--AGACCAACATATGATGCAATCTACGATATGATGAGAGAGAGAGAG 1077
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 DB 2933 GAG 2992
 QY 1849 GAG 1908
 DB 2993 GAG 3052
 QY 1909 CAG 1968
 DB 3053 CAG 3112
 QY 1969 CAG 2028
 DB 3113 AAGTTGAG 3172
 QY 2029 TATGAGATTAAG 2088

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Qy 2089 GTTACGATGATCCATCAAGAAAGCCAA CAGGAGACACAGCCTCGAGACTGTGAGAACCTGTG 2148
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Qy 2329 GGCCTGGGCTCAGCGCTGATATGGCACCAAGAAATGATGCTCGGACAAAGACGAATCTTGG 2388
Db 3467 GGTGGAAGTCGTCCTGGTGTGCAACGGATCAGAGACTGGCTCAGATGAAGTGCCTTT 3526
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Db 3527 GCCTTTGATGCTTAAAGGCCACGCGGTGCAATCAAGG---CAATGAACATATAGGGCGC 3583
Qy 2449 CAATGGGCTGTGTGTGACGTAGTGGGGGTGTCTTAGATCTGATGATTAAGACGATTAAGT 2508
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Qy 2806 CCAAGCTGGTTCAATATACCTTCATGCTCAAGATTTCCCAACACACGTTG 2857
Db 3941 GACGGCACCATGACAGTTCCCATGTTTAAAGGTCACTCAGAAAGTCTTTTG 3992
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Job time : 1691.5 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using bw model

Run on: April 14, 2006, 14:57:45 ; Search time 1272.5 Seconds
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Searched: 9281099 seqs, 2013915447 residues

Total number of hits satisfying chosen parameters: 18562198

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	616.8	20.6	15564	US-11-000-688-1500	Sequence 1500, Ap
2	539.8	18.0	14620	US-11-044-111-17	Sequence 17, Appl
3	521.2	17.4	3168	US-11-044-111-8	Sequence 8, Appl
4	155.8	5.2	717	US-11-044-111-18	Sequence 18, Appl
5	138.6	4.6	636	US-11-044-111-19	Sequence 19, Appl
6	96.6	3.2	524	US-11-044-111-20	Sequence 20, Appl
7	81.6	2.7	479	US-10-301-480-3997	Sequence 3997, Ap
8	81.6	2.7	479	US-10-301-480-617406	Sequence 617406,
9	70	2.3	595	US-10-301-480-261241	Sequence 261241,
10	70	2.3	595	US-10-301-480-261242	Sequence 261242,
11	70	2.3	595	US-10-301-480-874650	Sequence 874650,
12	70	2.3	595	US-10-301-480-874651	Sequence 874651,
13	70	2.3	608	US-09-925-065A-169264	Sequence 169264,
14	70	2.3	608	US-09-925-065A-169265	Sequence 169265,
15	67.8	2.3	1761	US-10-750-185-28284	Sequence 28284, A
16	67.8	2.3	1761	US-10-750-623-28284	Sequence 28284, A
17	67	2.2	10129	US-11-044-111-21	Sequence 21, Appl
18	60.8	2.0	1353	US-10-750-185-28296	Sequence 28296, A

19	60.8	2.0	1353	US-10-750-623-28296	Sequence 28296, A
20	54.6	1.8	640	US-09-925-065A-356190	Sequence 356190,
21	54.6	1.8	646	US-10-301-480-427650	Sequence 427650,
22	54.6	1.8	646	US-10-301-480-1041059	Sequence 1041059,
23	44.6	1.5	864	US-10-750-185-41204	Sequence 41204, A
24	44.6	1.5	864	US-10-750-623-41204	Sequence 41204, A
25	44.2	1.5	1522	US-10-750-185-28297	Sequence 28297, A
26	44.2	1.5	1522	US-10-750-623-28297	Sequence 28297, A
27	40.4	1.3	1391	US-10-750-185-41219	Sequence 41219, A
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29	39.6	1.3	600	US-10-750-185-4365	Sequence 4365, Ap
30	39.6	1.3	600	US-10-750-623-4365	Sequence 4365, Ap
31	39.6	1.3	838	US-11-096-568A-24888	Sequence 24888, A
32	39.6	1.3	2104	US-10-750-185-28287	Sequence 28287, A
33	39.6	1.3	2104	US-10-750-623-28287	Sequence 28287, A
34	38	1.3	2196	US-11-052-554A-539	Sequence 539, App
35	37.6	1.3	3252	US-10-750-185-40371	Sequence 40371, A
36	37.6	1.3	3252	US-10-750-623-40371	Sequence 40371, A
37	37.2	1.2	1759	US-11-096-568A-20409	Sequence 20409, A
38	37	1.2	638	US-10-301-480-599001	Sequence 599001,
39	37	1.2	638	US-10-301-480-1212410	Sequence 1212410,
40	37	1.2	1467	US-11-096-568A-20587	Sequence 20587, A
41	36.8	1.2	1424	US-10-750-185-47786	Sequence 47786, A
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43	36.6	1.2	2064	US-11-079-463-4800	Sequence 4800, Ap
44	36.6	1.2	4376	US-11-121-438-15	Sequence 15, Appl
45	36.2	1.2	1590	US-11-159-919-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-11-000-688-1500
Sequence 1500, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOUIGATTE, Remi
; APPLICANT: BIRNBAUM, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-R-03
; CURRENT APPLICATION NUMBER: US/11/000, 688
; PRIOR FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525, 987
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1500
; LENGTH: 15564
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences: primer
; NAME/KEY: misc feature
; LOCATION: (1)..(15564)
; OTHER INFORMATION: ryanodine receptor 3 (RYR3) gene.
US-10-688-1500
Query Match 20.6%; Score 616.8; DB 14; Length 15564;
Best Local Similarity 54.3%; Pred. No. 6.9e-184; Indels 75; Gaps 13;
Matches 1567; Conservative 0; Mismatches 1242;
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Qy 1732 CTGTCGCTTTCAGAGGACCTCCACCTGCTGAGAAACGATAGACATACAACTCGCTGC 1791
Db 2783 CTGTGAGATTTTCAAGCTCCAGAACTGAGAGAACTATTAACCTGCAATGTCACT 2842
Qy 1792 CAGACACTCAAGACTATCTGAGCTCTGGGCTACTACATCAGCTTAAGTAAAGC---CTCCA 1848
Db 2843 GAAACCTTAAGAAACCTCTTGGCTGGGCTGCGAGTGTCTATGTTAACAGAGTGCCT 2902
Qy 1849 GCAAGCACTCCGAACGTTGCTGCTGCCAACGAACTTTATGCAATGCTCAAGGCTACAG 1908
Db 2903 GAGAGGATCTCAAGAAAGTCAAACTGCCCAAAACATATATGATGTCCAAGGCTATAG 2962
Qy 1909 CCAAGCACTGACCGTGAAGTGTGCAACCTGACACCCAAATGATGAGCTATAGAC 1968
Db 2963 CAGCCCTTGTGATTTGTCTGATGAGTGTACCTTCTCAAGAAATTTTATGTGAT 3022
Qy 1969 CAGCTGGCTGAGAACCCCAACCTTTGGGCGAGGAGAGATACAGAGGATGACT 2028
Db 3023 AAGCTTGCAGAAATGACACATATTTGGGCAAAAGACAGATTAACAGAGATGAGAC 3082
Qy 2029 TATGACTTAATAGAGACTGCAATGATGATGTTCCCGCACTGTGTCATACCGGAG 2088
Db 3083 TATGCACTCAACAGATTTGAAGAACAAAGAAATCCCGTGTGGGTCATATGACTTA 3142
Qy 2089 GTTGAAGATGCCATCAAGAAAGCCACAGGAGACAGCTCCGAGACTGTGAGAGACCTG 2148
Db 3143 CTGATGAGGCTCAAGAAAGTCAACAGGAGACGCTCGGGAAGCTGTGCGCATCTTT 3202
Qy 2149 CTGGTCTACGGGTATATGCTGACCCGCTACTGCGGAGAGAGATGAAGCACTTGTG 2208
Db 3203 GTTGTGTTACGGGTATTAATTAAGCCATC-----AGACCAAGAACTTACGTGACTCG 3253
Qy 2209 GAAAGCTCAAAACAGAGACAGCACTTCAAGAACATACCGCGCTGAAGAAATATGCTC 2268
Db 3254 GCTGTGAGAGAGGTTCAGCATAGCAAGATCCGATTTTTCGGGTAGAGCATCTATAGCA 3313
Qy 2269 GTCACTCTGGGAAGTGTACTTCCAGTTTGAATCTTAACGCTGACCTATGAAGGCTC 2328
Db 3314 GTGAGATCTGGAAGAGTGTATTTTGAAGTGTGACTGAGAGACATGCGAGTCTC 3373

OY	1201	GTCAATPAGACATCATGCTGAAGAGCCCTTAATTTAGAAAAAGGAGCTGATAGTGTGGCGCA	1266
Db	2173	AGAGCTGTGGCAATCTGTCAATCAACATTTGCTGTCACTGAATGATGTAGTTCGTCTGC	2232
OY	1261	TTGACCTGACCGTACCCCTAATATCACTTCATGTTCAACGAGTGCGGGTGACGGATTC	1320
Db	2233	TTGGATTATAGGTGTGCCAGCATTTTCATTTCCGCACTTAATGTCAAGCTGTATCAAGGATG	2292
OY	1321	TTACCAACCTTCATATCTGGAAAGGCAATGTTCTTCCGGTCAATCACTGCTCTTAATAGCTG	1380
Db	2293	TTTGAACAATTCTGTATCTGAACAAAGGGTTTTTCTTCCCTGTGTATAGCTTACAGAGTGTGA	2352
OY	1391	AGTTGTGGTTCTCTGCTGGGGGAGAAACACGGTGCCTCCGGTACGGGGCTCCGAAGGC	1440
Db	2353	AAAGCTCGTTTCTTAATGCGGTGGAGCTCATGTGAAGTTTAATTTCTCTCTCTGCTGGC	2412
OY	1441	TACTCTCCCTTGGTGAAGCTCTCTCTGCGCAGAGATCTCAGCTGGAAGCCGTCCTTC	1500
Db	2413	TATGTCTCCTGTATAGAGCCCTGTCTTCCAAAGAAAGATGAAATGGAACTGGAAACAGTGA	2472
OY	1501	TACTTCGGCAACTGTCCAA-----GGGGCTTTGGCTGGACTTCGGCTATACAGAGC	1554
Db	2473	GAATATTAAGAGAGATTCTGATGAGTGAAGAGATTTGCTGGGTACGACAAATTCCTCTCC	2532
OY	1555	GATAGGGCTTCGTGCTCCACACTGTGTATCTTTACGATTTACTCTGCTCAATATGTG	1614
Db	2533	CAAGTTATATTTATACCTTGTCTTATTAACACAGCTCAAGATTGTCTTCTCTTTCATCTT	2592
OY	1615	GAACAAATTAGATTAAGTACCTAGCTGAATATATACGAATATGTGGGCTATGATTAAGTTC	1674
Db	2593	GAAGAAATCAGGGATTAACCTAGCAGAAATATCCATGATCTGTGGGAATGAATTAATTA	2652
OY	1675	GAAGCAGGCTGATGTATGCGGCAACGAGAGAGAACTTGCAAGATTCACCCCTGCTC	1734
Db	2653	GAGCTGGGCTGGACATATGGCAAGATACGGGATGATTAATTAAGGCATCATCTTGTCTT	2712
OY	1735	GTGCCCTTCAGAGCACTCCCACTGTCTGAAGAAAGATACGACATTAACACTGCTGTGAG	1794
Db	2713	GTGAATTTCTCAAAAGTTACCTTGAGACAAAGAAATTTATCTTACAAATGTCAACAGAA	2772
OY	1795	AACATCAAGACTATCTGGCTCTGGGCTACTACATCAAGCTTAGATTAAGATCTCCAGC---A	1851
Db	2773	ACCTCBAABAGCTTTTGGCCCTTGGATGTCAATTTGTCATGTCTAATCCAGCAGCTGAG	2832
OY	1852	CGCATCCGCAACGTTCTGTCTGCCCCAAGAACCTTTCATGACGTCCAAAGGCTACAGAGCA	1911
Db	2833	GAAGATCTTAAAAAAGTCAAGCTTCTAAAAATATATCATGTCAAAATGGTTATTAACCT	2892
OY	1912	GCACCACTCGACCTGATGTCGTGTACCCCTGACACCCAGATGATGACTGTATGACAG	1971
Db	2893	GCCCTCTGTGATCTTCTGAAAGTGAATTTGTACTCTTCAAGAAATTTCTGTGTGAACAA	2952
OY	1972	CTGGCTGGAACACCCCAACCTTTGGGCGAGGAGAGATACAGCAGGAGTGAACCTTAT	2031
Db	2953	CTAGCAGAAAATGCACTAATGTCTGGGCAAAAAGCAGATTAAGCAGAGATGACCTTAT	3012
OY	2032	GGACTTAATGAGCACTCGGACATGCAATGTTCCCGCACTGTGTGCCATACCCAGAGTT	2091
Db	3013	GGCAATTCAGCAGGATCTTAAAGACAAAGTAAATCCTGGCTATGTGCCATATGCAATTACTA	3072
OY	2092	GACGATGCCATCAGAGAGGCCAACAAGGACACAGCTTCGAGACTGTAGGAGCCCTGCTG	2151
Db	3073	GATGAACCTAATAAAAAATCAAAACAGAAATAGCTCCGTGAAAGCTGTATGGAACATTTGCA	3132
OY	2152	GTCTAACGGTATATGCTGGACCCGCTTACTGTGGGAGAGCACTGAAAGCACTTTGTGGAA	2211
Db	3133	GGCTATGTGTATTAATATGTAGCCACTGACCAAGAAATAGCTGACAAACATTTGAAAAA	3192
OY	2212	GCCTCAAAACAGAAAGCAGACACTTCAGACATACCGCGCTGAAGAAATATAGCCGCT	2271
Db	3193	GTCAAGCATGTGACAAAGATACGTTTTTTCAGA-----GTAAACAGCTCTTATGTGACGTG	3243
OY	2272	AGCTTCGGAAGTGTGACTTGAGATTGAGATCTTAAACGGCTGAGCCTATGAGGGTGGC	2331

Db	3244	AACTGTGAAAGTGGTATTTTGAATTTTGAAGCTGTAAACGGTGGAGATATGCTGTTGGC	3307
Qy	2332	TGGGCTCAOCGTGATATGGAACCAAGAAATGATGCTCCGACAAAGACGAACCTTTGGGCA	2393
Db	3304	TGGGCGAAGCCAGGCGCTGTGCACCTGACATTTGAATCGGGAGCTGATGACCAAGCATTTGTT	3363
Qy	2392	TTTGAATGTTTACATATGAGAAAAAAGTATACACGCGGTAACTAGATCTTTCCGCAAGCA	2455
Db	3364	TTTGAAGAAAGCAAAAGGCGACGCTTGGCATCAAGG---CAGTGGGTTTTTGGACGAAGT	3420
Qy	2452	TGGCGCTTTGGTGAAGTATGAGGAGGAGTGGGAGTGTTCCTAGATCTCATTTGATTAAGCATTAAGTTTC	2513
Db	3421	TGGCAACCGGAGATGTGTTGGATGATGATGATTAACCTTGAATGAACAAATTAATCTTT	3488
Qy	2512	TCACTCAATATGATGATGATTTGTAATGATGATCTCTTGGCGAGAGACTACGTTTGGCTGATGTC	2573
Db	3481	ACTGTGAATGAGAGATTTGCTTAATAACAGTAAGAGTTCAAGACTTGTGCTGACTTT	3548
Qy	2572	CAGGGTCACA---ACTTGTATCCAGCTTGCACACTTGTGTGGGCCAAAAGCCAGTTA	2628
Db	3541	GGAAATAGAAAGTGGTTTGTTCCAATTTGCTCACTGGGTCTAGCTCAATTTGACGTATG	3600
Qy	2629	ACATATGGCCAAAGATGTGAATATCTGTAATATCTTCAACAATGATGTCTTCAAGAGGCA	2688
Db	3601	AACCTTGAATATGATGATGCCAGTATCACTTCAAGTATTAATACATATGTGTCTTCCAAAGAGT	3666
Qy	2689	TATGAACCAATTTTGGCTCAATATGTAAGAGAACGCTGACTCATCTGGTACACCAAGGACGAG	2748
Db	3661	TTTGAACCTTTTGCAGTGAACATGAACCGAATGTGCTATGTGTTTAGTAAGCTTTA	3720
Qy	2749	CCGATCTTTCGAGAAAT 2763	
Db	3721	CCAACTTTGTAAAT 3735	

RESULT 3

US-11-044-111-8

/ Sequence 8, Application US/11044111

/ Publication No. US20050272362A1

/ GENERAL INFORMATION:

/ APPLICANT: Chiang, Wen

/ APPLICANT: Strasburg, Gale

/ APPLICANT: Linz, John

/ TITLE OF INVENTION: Genetic Test for PSE-Susceptible turkeys

/ FILE REFERENCE: MSU-09308

/ CURRENT APPLICATION NUMBER: US/11/044,111

/ CURRENT FILING DATE: 2005-01-27

/ NUMBER OF SEQ ID NOS: 27

/ SOFTWARE: PatentIn version 3.3

/ SEQ ID NO 8

/ LENGTH: 3168

/ TYPE: DNA

/ ORGANISM: Meleagris gallopavo

US-11-044-111-8

Query Match 17.4%; Score 521.2; DB 14; Length 3168;

Best Local Similarity 55.4%; Pred. No. 6,5e-154;

Matches 1213; Conservative 0; Mismatches 938; Indels 39; Gaps 9;

Qy	4	ATAAGCGCGCCCATCATCAAAATATGTGACTCCACCGTCATTTGTGCAGATTTCCGAGACT	63
Db	997	ATGGGACCCCGAGATCAAAATATGGGAGTGCCTGTGCTTCGTGACAGCAGCGGCTCG	1056
Qy	64	GGCTTTGTGCTGTCTTAATAGTCTTAAGAAACGAAGAAAGGAGATGGCTTCACTTCTCAGG	123
Db	1057	GGGCTGTGCTCACCTTACGCTGCTGTGACACCAACGCGTGCCTGGGGCTGATGAAA	1116
Qy	124	GAGAAGCAAGGATTTCTCCACGAGAAAGGCAAGATGACATGTGCTCAGACTTCTCAGG	183
Db	1117	CGAGAGC---CAATCTGTGACCAAGAGGCGCACTGACGACGCGCTGTGCTCAGCGCG	1173
Qy	184	TCACAGGAGGAAGATCTAAGACTGTCTAGATTATCAGAAAGATGTTCTTGCCTGTCACT	243

Db 1174 TGCAGAGGCGAGAGTCGAGGCGGCGGATGATTAACAGACCGCGGGCTTACAGGG 1233
Qy 244 AAGTTTATCAATGCTCTGAAACTCT---ACAAGAAACCGTCTCACTCGATGTTCTTC 300
Db 1234 AACTTATCTCGAGGCTTGAGCGCTGAGCTCTCGTGGCGGCGGCGGCGGAGAAC 1293
Qy 301 GCGTAGTGAACCTGCGGCGAGATGATGATGCTCTGAGGATCTCATCACTACTTCCGA 360
Db 1294 GGGGCTCTCCATCGCGCGCTCACTCTCACTCGGAGATCTGATCTCTTATTTCCGC 1353
Qy 361 CAGCCGATGAGATATGGAACGAGAGAAACAAACAAATTCGGGCACTCCGAAC 420
Db 1354 GCGCGGCAACCGAGCTGAGAGAGAGAGCGGCAAGAACCGGCTGGCTCCCTCGGGCGC 1413
Qy 421 GGTGAGAGCTTGTCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 1414 GCGCAGAGACTTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1473
Qy 481 ATCAACGTATCACTGCTCCAGAGAGGTTCTGCTGATGATTCCTGCGGAGAGAGATCTGA 540
Db 1474 CTGAGAGTGTACAGACCGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1530
Qy 541 CAGAGCTGAGAAATGATATCTGATATTTGATCAAGTTGCTGCGGCAATTAATAAAGGC 600
Db 1531 GCGGCTGAGAGAGATGCTCAACTCTCTATGAGCTGCTGCGCTGCTGCTGCTGCGGG 1590
Qy 601 AACCAACAGAACTGCGCGGAGATTCGAGAACTGAAACCGCTCAACTGCTGTTCTCGGC 660
Db 1591 AACCAACAGAACTGCGCGCTGTT---CTCACCAACTGAGCTGCTGCTGCTGCTGCTG 1644
Qy 661 CTGCGCTGCGAGGCTCTGCGGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 1645 CTGAGACGGC-----TGAGAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1698
Qy 721 ATAGA CTGCGCTGAGAGCTCTCAATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db 1699 ATGAGAGGCTCGAGGTTCTGAACATCATCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1758
Qy 781 CATTTAGAAAAGATGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Db 1759 CTGCTGAGAGAAACAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1818
Qy 841 GGTAAAGGCGGCTGCGGAG 900
Db 1819 TGCAATGCTGAGCGGTTGTTCCAAACAAATCTCATCAAGAGAGAGAGAGAGAGAGAG 1878
Qy 901 AAGAACTGCTTGTCTGAG 960
Db 1879 GCGAGACTCTGCTGAG 1938
Qy 961 TTGCTGAGGCTGAG 1020
Db 1939 CTCTGAGGAG 1998
Qy 1021 GAGCACTAG 1077
Db 1999 GATCACTGAG 2058
Qy 1078 ACTACTGCTTATGCTCATACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1137
Db 2059 GCGAGAGGTTACAGGCTTACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2118
Qy 1138 GATGACCTGATCTGATCGAGGTTCAAGCGGCTTCTGCTGCTGCGGAGAGAGAGAGAG 1197
Db 2119 GACGAGCTTATCTTCCCTTGTATGAGCTGACCTCTGAGCGGCGGAGGTTCCCGCG 2178
Qy 1198 CCGGCAATAG 1257
Db 2179 GCGGCGGCTTCCCGGAGC-----AGCAGATCTGAGCGGCGGAGAGAGAGAGAGAG 2232
Qy 1258 GCATTGAGAGCTGAG 1317

Db 2233 TGCCTGAGACTCTCTGTTCCACATCTCTCCGCTCAACAGGAGCGGCGGCTGAGG 2292
Qy 1318 TCCCTACCAACTTCAATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1377
Db 2233 ATGTTGAGAGAGTTAATCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2352
Qy 1378 CTGAGTTGCTGCTCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1437
Db 2353 GTGCGGCTGCGCTCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2412
Qy 1438 GGTACTCTCTCTCTGAG 1497
Db 2413 GGTACTCTCTCTCTGAG 2472
Qy 1498 TTCTACTT-----CGGCAACTGTCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1551
Db 2473 AAGCTTATAG 2532
Qy 1552 GAGCACTAG 1611
Db 2533 CCGCAG 2592
Qy 1612 GTGAG 1671
Db 2593 CTGAG 2652
Qy 1672 ATGAG 1731
Db 2653 ATGAG 2712
Qy 1732 CTGCTGCTTCTGAG 1791
Db 2713 CTGCTGAGATTTCTACAGAGCTCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2772
Qy 1792 CAGACACTCAAG 1848
Db 2773 GAG 2832
Qy 1849 GAG 1908
Db 2833 GAG 2892
Qy 1909 CCAG 1968
Db 2893 CCGGCGGCTGAG 2952
Qy 1969 CAGCTGCTGAG 2028
Db 2953 CCGCTGAG 3012
Qy 2029 TATGAGCTTATGAG 2088
Db 3013 TACAG 3072
Qy 2089 GTTACAG 2148
Db 3073 CTGAG 3132
Qy 2149 CTGCTTACAG 2178
Db 3133 ATCGGCTACGGCTACAG 3162

RESULT 4
US-11-044-111-18
; Sequence 18, Application US/11044111
; Publication No. US2005027362A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Wen
; APPLICANT: Strasburg, Gale
; APPLICANT: Linz, John
; TITLE OF INVENTION: Genetic Test for PRF-Susceptible Turkeys
; FILE REFERENCE: MSU-09308

```
; CURRENT APPLICATION NUMBER: US/11/044,111
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Meleagris gallopavo
US-11-044-111-18
```

```
Query Match      5.2%; Score 155.8; DB 14; Length 717;
Best Local Similarity 54.9%; Pred. No. 3.3e-38;
Matches 401; Conservative 0; Mismatches 312; Indels 18; Gaps 4;
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```
OY 136 ATTCCACAGAGAGGAGCAAGATGACATGAGCCTCGACTTCTCAGAGCTCAGAGAGAA 195
    |||||
DB 1 ATTCGACACAGAGAGGACCAATGACAGAGCGCTGTGTGCTCAGCGCTCCGACAGGCGAG 60
    |||||
OY 196 GAATCTAGACTGCTCGAGTTATCAGAAAGTGTCTTCTGCTGTTCACTAAGTTTATCAAT 255
    |||||
DB 61 GAGTCGACAGCGCGCGCGAGATGATTTAAGACAGCGCGGGGCTCTACGGAGCTTATCCGG 120
    |||||
OY 256 GGTCTGGAACCTCTACAGA---GAACGCTGTCTCATGAGTTTCTTGCGCTCACTGAAC 312
    |||||
DB 121 AGCTTGACGCGCTGAGCTCTCGGGGCGCGCGCGGCTGCGGAGAACGCGCTCTGCGC 180
    |||||
OY 313 CTGGGCGAGATGATGATGCTGCTCGAGGATCTCATCACTAATTCTGACAGCGCGATGAG 372
    |||||
DB 181 ATGCGCGCGCTCATCTCAGCTCTGGGGATCTGATCGCTTATTTCCGCGCCCGACACC 240
    |||||
OY 373 GATATGGAACAGAAAGAAACAAATTCGCGGCACTCCGAAACCGTCAAGACCTG 432
    |||||
DB 241 GAGCTGACAGACAGACAGCGCGAGAACCGCGCTGCGCTCTGCGCGCGCGACAGACCTC 300
    |||||
OY 433 TTCCAGAGAGAGGAGATACCTGAATCTCGAAGCTATAGACAAATCAAGTCAATC 492
    |||||
DB 301 TTCCAGAGAGAGGAGATATCTCTGCTGCTGAATCTGATGACCGGCTGAACCTGTAC 360
    |||||
OY 493 AGCTCCAGAGGTTCTCTGCTGAGATTCTGCGCGGAGAGAGATCTGACAGAGCTGGAA 552
    |||||
DB 361 AGCAGCGCGCGCACTTCCGCGAGTTC---GCCGGGAGAGAGCGCGCGCGCTGGAA 417
    |||||
OY 553 ATGATATCTGATATTTTATTCATGTTGCTGCGGCAATTAATTAAGGCAACCAACGAA 612
    |||||
DB 418 GAGATCTGCAACCTCTCTATGAGCTGCTGGGCTGCTGATCCGGGGAGAACCAACCAAC 477
    |||||
OY 613 TGGCGGAGTTCTGCGAATCTGCAACCGCTCAACTGGGCTGTTCTGCGCGCTGCGCTCGAG 672
    |||||
DB 478 TGCGCCCTGTT-----CTCCACCAACTGGACTGGCTGTGACGAACTGACCGGC-- 529
    |||||
OY 673 GCTTCGCGGAGAGGCAACGCGCATGCTGACGCTGCACTGCGTCTTATAGACTCGCT 732
    |||||
DB 530 ----TGAGGCGTGTCTAGGGATCTTGAAGGTCTTAACTGCTCTGATGAGAGCC 585
    |||||
OY 733 GAAGCTTCAATATGATGAGGAGCAACCAATTAAGTATCTCTTATTAAGAAAG 792
    |||||
DB 586 GAGGTTTGAACATCATCAAGAGAACCAATCAAGTCAATCTCTCTGAGCAAA 645
    |||||
OY 793 CATGGGCGGAGCCCTTAAGTACTGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 852
    |||||
DB 646 CACGCGCGCAACCAATTAAGTCTGAGCGTGTCTGCTGTGTGTGTGCAATGCTGTG 705
    |||||
OY 853 GCGGTGCGCTC 863
    |||||
DB 706 GCCGTTCCGTT 716
    |||||
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RESULT 5
US-11-044-111-19
; Sequence 19, Application US/11044111
; Publication No. US2005027262A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Wen
```

```
; APPLICANT: Strasburg, Gale
; APPLICANT: Linz, John
; TITLE OF INVENTION: Genetic Test for PSR-Susceptible Turkeys
; FILE REFERENCE: MSU-09308
; CURRENT APPLICATION NUMBER: US/11/044,111
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Meleagris gallopavo
US-11-044-111-19
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Query Match      4.6%; Score 138.6; DB 14; Length 636;
Best Local Similarity 56.5%; Pred. No. 9.1e-33;
Matches 324; Conservative 0; Mismatches 224; Indels 15; Gaps 3;
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OY 291 GATGTTCTTGCCTCACTGAACCTGGGCGAGATGATGCTGCTCAGAGATCTCATCAA 350
    |||||
DB 78 GATGATTTAAGACAGCGCGGGGCTCTACGGGAGCTTCATCCGCTGCGGATCTGATGCG 137
    |||||
OY 351 CTACTTTCGACAGCGCCGATGAGATATAGAAACAGAAAGAAACAAATTCGCGGC 410
    |||||
DB 138 TTATTTCCGCGCCCGACACCGAGCTGACAGACAGACAGCGCGCAACCGCTGCGCTC 197
    |||||
OY 411 ACTCCGAACCGTACAGACCTGTTCCAAAGAGAGATATGAACTGATCTCTGAAAC 470
    |||||
DB 198 CTGCGCGCGCGCGACAGACCTCTTCCAGCAGAGAGGATATCTCTGTGCTGAACTG 257
    |||||
OY 471 TATAGACAAATCAACGTATCACTGCTCCAGAGGTTCTGCTGATTTCTGCGGAGAA 530
    |||||
DB 258 CATGACCGGCTGAACGTATACAGACAGCGCGCGCACTTGGCGGAGTTTC---GCCGGGGA 314
    |||||
OY 531 CGATCTGACAGAGCTGGGGAATGATATCTGATATTTGATAGTTGCTGGCGGGAAT 590
    |||||
DB 315 GAGAGCGCGCGCGCTGGAAGAGATCTGAACCTCTCTATGAGCTGTGGGCTGCT 374
    |||||
OY 591 AATTAAGGGAACCAACAGACTGCGCGGAGTTCTGCAACTCGAACCGCTCACTGAGCT 650
    |||||
DB 375 GATCCGGGGGAACCAACCACTGCGCCCTGTT-----CTCCACCAACTGAGCTGGCT 428
    |||||
OY 651 GTTCTCGCGCTGCGCTGCGAGGCTCTGCGCGAGAGGCAACGCGCATGCTGAGCTGCA 710
    |||||
DB 429 GGTACGAACTGGAACCGGC-----TGAGGCGTCTGCTGAGGATCTGAGGCTTTA 482
    |||||
OY 711 CTGCGCTCTATGACTCGCTGAAGCTCTCAATATGATGAGGAGCAACATAAAGT 770
    |||||
DB 483 CTGCGCTCTATGAGAGCCCCGAGGTTCTGAACATCATCAAGAGAACCAATCAAGTCTC 542
    |||||
OY 771 GATATCTCTCTATTGAAGAGCATGCGCGGAGCCCTTAAGTACTAGATGCTATGTTTC 830
    |||||
DB 543 CATATATCTCTGCTGAGCAAAACAGCGCGCAACCAATTAAGTCTGAGACGCTCTGCTC 602
    |||||
OY 831 GCTGTGCTGCTGACGCGCTGCGGCTGCGGCTC 863
    |||||
DB 603 TCTGTGTCTGCAATCTGTGCGCTTCCGTT 635
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RESULT 6
US-11-044-111-20
; Sequence 20, Application US/11044111
; Publication No. US20050272362A1
; GENERAL INFORMATION:
; APPLICANT: Strasburg, Gale
; APPLICANT: Linz, John
; TITLE OF INVENTION: Genetic Test for PSR-Susceptible Turkeys
; FILE REFERENCE: MSU-09308
; CURRENT APPLICATION NUMBER: US/11/044,111
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
```


;; PRIOR APPLICATION NUMBER: US 10/215,598
;; PRIOR FILING DATE: 2002-08-09
;; PRIOR APPLICATION NUMBER: US 60/311,695
;; PRIOR FILING DATE: 2001-08-10
;; NUMBER OF SEQ ID NOS: 1226818
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 261241
;; LENGTH: 595
;; TYPE: DNA
;; ORGANISM: Homo sapien
US-10-301-480-261242

Query Match 2.3%; Score 70; DB 10; Length 595;
Best Local Similarity 62.6%; Pred. No. 5.4e-11;
Matches 109; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 2236 TTCAACATACCGCGCTGAGAGAACTATGCCCTCAGCTCGGAACTGACTTGCAG 2295
DB 27 TTCCGAATCTTCGCGCCGAGAGAACTATGCACTGAGAGCCGAGCGGTGATTTGAA 86
QY 2296 TTTCGATCTTAAACGGCTGACCTATGAGGGTGGCTGAGCTCACTGATATGGACCA 2355
DB 87 TTTCGAGCGGTCACTGCTGAGACATGAGGGTGGTGGAGTCCCTGCTGTTGCAACCG 146
QY 2356 GGAATGATGCTCGGACAAGACGAGAACTCTTGGGCACTTTGATGTTAATGAG 2409
DB 147 GATCAGAGGCTTGGCTCAGATGAACGTGCTTTGCTTGAATGAGCTTCAAGGTG 200

RESULT 10

US-10-301-480-261242
; Sequence 261242, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: In the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 261242
; LENGTH: 595
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-261242

Query Match 2.3%; Score 70; DB 10; Length 595;
Best Local Similarity 62.6%; Pred. No. 5.4e-11;
Matches 109; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 2236 TTCAACATACCGCGCTGAGAGAACTATGCCCTCAGCTCGGAACTGACTTGCAG 2295
DB 27 TTCCGAATCTTCGCGCCGAGAGAACTATGCACTGAGAGCCGAGCGGTGATTTGAA 86
QY 2296 TTTCGATCTTAAACGGCTGACCTATGAGGGTGGCTGAGCTCACTGATATGGACCA 2355
DB 87 TTTCGAGCGGTCACTGCTGAGACATGAGGGTGGTGGAGTCCCTGCTGTTGCAACCG 146
QY 2356 GGAATGATGCTCGGACAAGACGAGAACTCTTGGGCACTTTGATGTTAATGAG 2409
DB 147 GATCAGAGGCTTGGCTCAGATGAACGTGCTTTGCTTGAATGAGCTTCAAGGTG 200

RESULT 11

US-10-301-480-874650
; Sequence 874650, Application US/10301480
; Publication No. US20060057564A1

;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
;; TITLE OF INVENTION: In the Human Genome
;; FILE REFERENCE: 108827.137
;; CURRENT APPLICATION NUMBER: US/10/301,480
;; CURRENT FILING DATE: 2002-11-21
;; PRIOR APPLICATION NUMBER: US 10/215,598
;; PRIOR FILING DATE: 2002-08-09
;; PRIOR APPLICATION NUMBER: US 60/311,695
;; PRIOR FILING DATE: 2001-08-10
;; NUMBER OF SEQ ID NOS: 1226818
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 874650
;; LENGTH: 595
;; TYPE: DNA
;; ORGANISM: Homo sapien
US-10-301-480-874650

Query Match 2.3%; Score 70; DB 10; Length 595;
Best Local Similarity 62.6%; Pred. No. 5.4e-11;
Matches 109; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 2236 TTCAACATACCGCGCTGAGAGAACTATGCCCTCAGCTCGGAACTGACTTGCAG 2295
DB 27 TTCCGAATCTTCGCGCCGAGAGAACTATGCACTGAGAGCCGAGCGGTGATTTGAA 86
QY 2296 TTTCGATCTTAAACGGCTGACCTATGAGGGTGGCTGAGCTCACTGATATGGACCA 2355
DB 87 TTTCGAGCGGTCACTGCTGAGACATGAGGGTGGTGGAGTCCCTGCTGTTGCAACCG 146
QY 2356 GGAATGATGCTCGGACAAGACGAGAACTCTTGGGCACTTTGATGTTAATGAG 2409
DB 147 GATCAGAGGCTTGGCTCAGATGAACGTGCTTTGCTTGAATGAGCTTCAAGGTG 200

RESULT 12

US-10-301-480-874651
; Sequence 874651, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: In the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 874651
; LENGTH: 595
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-874651

Query Match 2.3%; Score 70; DB 10; Length 595;
Best Local Similarity 62.6%; Pred. No. 5.4e-11;
Matches 109; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 2236 TTCAACATACCGCGCTGAGAGAACTATGCCCTCAGCTCGGAACTGACTTGCAG 2295
DB 27 TTCCGAATCTTCGCGCCGAGAGAACTATGCACTGAGAGCCGAGCGGTGATTTGAA 86
QY 2296 TTTCGATCTTAAACGGCTGACCTATGAGGGTGGCTGAGCTCACTGATATGGACCA 2355
DB 87 TTTCGAGCGGTCACTGCTGAGACATGAGGGTGGTGGAGTCCCTGCTGTTGCAACCG 146
QY 2356 GGAATGATGCTCGGACAAGACGAGAACTCTTGGGCACTTTGATGTTAATGAG 2409

Db 147 GATCAGAGCTTGCTGCTCAGATGAACGTGCTTTGCTTTGATGCTTCAAGGTG 200

RESULT 13

US-09-925-065A-169264/C
Sequence 169264, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 169264
LENGTH: 608
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-169264

Query Match 2.3%; Score 70; DB 6; Length 608;

Best Local Similarity 62.6%; Pred. No. 5.5e-11;
Matches 109; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy 2236 TTCGAACATACCGGCTGAGAGAACTATGCGCTGCTGAGGAGTGTACTTGCAG 2295

Db 582 TTCGAATCTTCGTCGCGAGAGAACTATGAGTGAAGCCGAGCGGTGATTTTGA 523

Qy 2236 TTTGAGATCTTAAAGGCTGAGACTATGAGGCTGCGCTGAGCTCAAGCTGATATGACCA 2355

Db 522 TTTGAGAGGCTGCTGAGCAAGAGAGGTTGGTGAAGCGTCTGCTGTTGTCACCG 463

Qy 2356 GGAATGATGCTGAGCAAGAGAGAACTTTGGGCTTTGATGCTTACATGAG 2409

Db 462 GATCAGAGCTTGCTGCTCAGATGAAGTGCCTTGCTTTGATGCTTCAAGGTG 409

RESULT 14

US-09-925-065A-169265/C
Sequence 169265, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 169265

LENGTH: 608
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-169265

Query Match 2.3%; Score 70; DB 6; Length 608;

Best Local Similarity 62.6%; Pred. No. 5.5e-11;
Matches 109; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy 2236 TTCGAACATACCGGCTGAGAGAACTATGCGCTGCTGAGGAGTGTACTTGCAG 2295

Db 582 TTCGAATCTTCGTCGCGAGAGAACTATGAGTGAAGCCGAGCGGTGATTTTGA 523

Qy 2236 TTTGAGATCTTAAAGGCTGAGACTATGAGGCTGCGCTGAGCTCAAGCTGATATGACCA 2355

Db 522 TTTGAGAGGCTGCTGAGCAAGAGAGGTTGGTGAAGCGTCTGCTGTTGTCACCG 463

Qy 2356 GGAATGATGCTGAGCAAGAGAGAACTTTGGGCTTTGATGCTTACATGAG 2409

Db 462 GATCAGAGCTTGCTGCTCAGATGAAGTGCCTTGCTTTGATGCTTCAAGGTG 409

RESULT 15

US-10-750-185-28284
Sequence 28284, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMT GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 28284
LENGTH: 1761
TYPE: DNA
ORGANISM: Bovine
US-10-750-185-28284

Query Match 2.3%; Score 67.8; DB 8; Length 1761;

Best Local Similarity 62.9%; Pred. No. 5e-10;
Matches 105; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 2584 TTTGTACAGCTTGACACTTGTGTGGCCAAAAGCCAGGTTACATATGCGCAGAT 2643

Db 740 TTCAATACCTGTGTGAGCTGGAGTGGCTCAAGTGGGCAAGCTTGTGAAGAGAT 799

Qy 2644 GTGAATATCTGAAATATCTTCAACAATGTGTCTTTCAGAGGAGATATGAACATTTGC 2703

Db 800 GTGAGACCTTGAATATATTCACCATCTGTGCTTCAAGAGGGCTATGAACATTTGCC 859

Qy 2704 GTCAATATGAAGAGAGAGTGAAGTCACTGATACCAAGACCAAGCC 2750

Db 860 GTTAAACAATATGAGATATTCATCATGTGCTGAGCAAGAGCTTCC 906

Search completed: April 14, 2006, 15:56:41
Job time : 1274.5 secs

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QY 121 GAGTCAGCAAGACGTACACAGAGGCGCCGATATCATGATGTGTGCTGCTTTACTC 180
Db 10120 GAGTCAGCAAGACGTACACAGAGGCGCCGATATCATGATGTGTGCTGCTTTACTC 10179
QY 181 TGTCTTATTTGGCGGTTCTGGTGGGCAAGGGGGCTGTATGTATCTTACTCTGAGGGA 240
Db 10180 TGTCTTATTTGGCGGTTCTGGTGGGCAAGGGGGCTGTATGTATCTTACTCTGAGGGA 10239
QY 241 AACCAAGTAAAGATGTAAACAGCGGAAACATGAACAGCTCTCAAGAAATGTTCTGAG 300
Db 10240 AACCAAGTAAAGATGTAAACAGCGGAAACATGAACAGCTCTCAAGAAATGTTCTGAG 10299
QY 301 CTGATCAAAAAAAGACATCGGCAATGAGAACCGCGCGGTGATGACCCGATCGCACTAC 360
Db 10300 CTGATCAAAAAAAGACATCGGCAATGAGAACCGCGCGGTGATGACCCGATCGCACTAC 10359
QY 361 ACGAGAGATCATCATCAAGCTCCGAGGAACTGCTGAGGGAAATTCCTTCTGCGCTC 420
Db 10360 ACGAGAGATCATCATCAAGCTCCGAGGAACTGCTGAGGGAAATTCCTTCTGCGCTC 10419
QY 421 GCTGAACGTGTTCCGCAAAACGCAACGCAATATGTTCCATAAGAGAGAGCTTGAGGGG 480
Db 10420 GCTGAACGTGTTCCGCAAAACGCAACGCAATATGTTCCATAAGAGAGAGCTTGAGGGG 10479
QY 481 TTTATTTAAGTCGTCAACAGACGACACATCCAGGTAAGTCTCAAGATCAAGAAAGACTGG 540
Db 10480 TTTATTTAAGTCGTCAACAGACGACACATCCAGGTAAGTCTCAAGATCAAGAAAGACTGG 10539
QY 541 CAGCTGCTGGTCAAGACATCTACTCTCTTCAACCGCGTCTCAATCAAGTACGTGACCTG 600
Db 10540 CAGCTGCTGGTCAAGACATCTACTCTCTTCAACCGCGTCTCAATCAAGTACGTGACCTG 10599
QY 601 CAGAGAACCACTGCTCAGGAAACATGTTCCAGAGCGGAAAGAGCTGTACACACAGTG 660
Db 10600 CAGAGAACCACTGCTCAGGAAACATGTTCCAGAGCGGAAAGAGCTGTACACACAGTG 10659
QY 661 GCTGAATCTTCAACATCTGCTCAAGAGCCAGTACTTTGTAAGAGAGAAACAGACTTC 720
Db 10660 GCTGAATCTTCAACATCTGCTCAAGAGCCAGTACTTTGTAAGAGAGAAACAGACTTC 10719
QY 721 ATCTCTCCCAACGAAATTTGATTAAGTGTGCTGATTTATGCCAACAGAACAGAGTGT 780
Db 10720 ATCTCTCCCAACGAAATTTGATTAAGTGTGCTGATTTATGCCAACAGAACAGAGTGT 10779
QY 781 ACAGCAATTAACAGATGTACTCTCAAGTGTGGAAGAAAGAAAGAACACCTGAT 840
Db 10780 ACAGCAATTAACAGATGTACTCTCAAGTGTGGAAGAAAGAAAGAACACCTGAT 10839
QY 841 AAGAAACGCGACAAAGACAAAGAAATCCAGACGTCCTTAATGTAGCTTGTCTGAAGAG 900
Db 10840 AAGAAACGCGACAAAGACAAAGAAATCCAGACGTCCTTAATGTAGCTTGTCTGAAGAG 10899
QY 901 TTGTATCAAGTGGCTTTAACTTATTCGCTGCGAGAAACAGAACTGTGACAGATTTGT 960
Db 10900 TTGTATCAAGTGGCTTTAACTTATTCGCTGCGAGAAACAGAACTGTGACAGATTTGT 10959
QY 961 AAAGACAGGTTCTGGAAGAAATGTCAAGAACAGATGGGCAAAATTCGAGAGACCCAG 1020
Db 10960 AAAGACAGGTTCTGGAAGAAATGTCAAGAACAGATGGGCAAAATTCGAGAGACCCAG 11019
QY 1021 CTGACACTTCAGATAAATAGATCCGCGACAGCAAAATGTCTTGGCAACATTAATTGTAT 1080
Db 11020 CTGACACTTCAGATAAATAGATCCGCGACAGCAAAATGTCTTGGCAACATTAATTGTAT 11079
QY 1081 AGCAAGTTAGGTTGGAAGAGTAAAGCAATTAATCTGTGAAACTGCTGAAATTAAGGCC 1140
Db 11080 AGCAAGTTAGGTTGGAAGAGTAAAGCAATTAATCTGTGAAACTGCTGAAATTAAGGCC 11139
QY 1141 AAGATTATTGATATCCGTGAGAGAAATGCTGCTATGATTAAGTAAAGTCTTTTCGATGG 1200
Db 11140 AAGATTATTGATATCCGTGAGAGAAATGCTGCTATGATTAAGTAAAGTCTTTTCGATGG 11199
QY 1201 CATATGATCGACATCCCAACAAATGATGAAGAACTGTATCCGCTGCTGTGTGATATA 1260

Db 11200 CATATGATCGACATCCCAACAAATGATGAAGAACTGTATCCGCTGCTGTGTGATATA 11259
QY 1261 CAACGCAAGCGCGCGTCAATCGCTGCTTCCGACAAACTTCATCACTTCTGCGGAGA 1320
Db 11260 CAACGCAAGCGCGCGTCAATCGCTGCTTCCGACAAACTTCATCACTTCTGCGGAGA 11319
QY 1321 CATGAGCGTGTACATCTTCCGCTGCACTGACTCAAGCTCTGTGTGAAAGAGAGAAC 1380
Db 11320 CATGAGCGTGTACATCTTCCGCTGCACTGAGCTCTGTGTGAAAGAGAGAAC 11379
QY 1381 ATTGAGACAAAGATTAATGATGAAGATCTTAATCAATCTTGAAGACGACAGCTGAG 1440
Db 11380 ATTGAGACAAAGATTAATGATGAAGATCTTAATCAATCTTGAAGACGACAGCTGAG 11439
QY 1441 AAGATGACGTGTGAGAGAGGTTGAAGAGCCGACCCCTCAACGACGCTGTACACACC 1500
Db 11440 AAGATGACGTGTGAGAGAGGTTGAAGAGCCGACCCCTCAACGACGCTGTACACACC 11499
QY 1501 TTCTGTGCGGTCATGACTGAGAGGTCCGCGCTTTTGAGAGAGATCCTTATACATG 1560
Db 11500 TTCTGTGCGGTCATGACTGAGAGGTCCGCGCTTTTGAGAGAGATCCTTATACATG 11559
QY 1561 TCTTACGACACATCATAGCGAAGTCTGTGAGAAAGAGAGAGAGAGAGGGGTGGAG 1620
Db 11560 TCTTACGACACATCATAGCGAAGTCTGTGAGAAAGAGAGAGAGAGAGGGGTGGAG 11619
QY 1621 GAAGAGAGAGGGGTGGAGAGAGGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
Db 11620 GAAGAGAGAGGGGTGGAGAGAGGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 11679
QY 1681 CAAGAAATGAGAAACAAAGAGCTCTATTCCACCAAGCGCGCTGGCGAGCCGTGGGGTT 1740
Db 11680 CAAGAAATGAGAAACAAAGAGCTCTATTCCACCAAGCGCGCTGGCGAGCCGTGGGGTT 11739
QY 1741 GCCGAAATGAGTGTGCTGCACATCTCCGGTCCAAGGCTGCGCACGAGATGTCTAG 1800
Db 11740 GCCGAAATGAGTGTGCTGCACATCTCCGGTCCAAGGCTGCGCACGAGATGTCTAG 11799
QY 1801 AAGACTTTACAGCTCGGATTTAGTATACAGAGGGGGGGCAATTGATATACAGATGGGT 1860
Db 11800 AAGACTTTACAGCTCGGATTTAGTATACAGAGGGGGGGCAATTGATATACAGATGGGT 11859
QY 1861 ATGTTAACCACTTGAAGAGCAAGAAAGAGTGGGCTTCTTACGTCCATCGCGGCTC 1920
Db 11860 ATGTTAACCACTTGAAGAGCAAGAAAGAGTGGGCTTCTTACGTCCATCGCGGCTC 11919
QY 1921 ATGAATCTCTGCTCGGTGCTCGATCTTGAACGCTTGAAGAGAACCAAGGCTGAAGGT 1980
Db 11920 ATGAATCTCTGCTCGGTGCTCGATCTTGAACGCTTGAAGAGAACCAAGGCTGAAGGT 11979
QY 1981 CTGGGGGTGGGTCTGGAAGGTGGCGGGGAGAGAAATGATGAACGCCGAGTTCAAC 2040
Db 11980 CTGGGGGTGGGTCTGGAAGGTGGCGGGGAGAGAAATGATGAACGCCGAGTTCAAC 12039
QY 2041 TGGCACTCTTACAGTTCATTGAGCTCACTGTAAGAGACAACTTGAACCTGGCAGAAC 2100
Db 12040 TGGCACTCTTACAGTTCATTGAGCTCACTGTAAGAGACAACTTGAACCTGGCAGAAC 12099
QY 2101 TACCTGCGAATCTGAGCGGTAAACAGCAACAGTGAACGTGTCAATCTGACCGTCAAC 2160
Db 12100 TACCTGCGAATCTGAGCGGTAAACAGCAACAGTGAACGTGTCAATCTGACCGTCAAC 12159
QY 2161 TACCTGCTGCGGTGAGAGATCCATCAAGAGCTTACTGGGACATCTCAAGCAAGAGAA 2220
Db 12160 TACCTGCTGCGGTGAGAGATCCATCAAGAGCTTACTGGGACATCTCAAGCAAGAGAA 12219
QY 2221 CTGATGACCCCGCGCGCAAGGAACTTCTCAAGGCAATGAGCGCTTGCTTCCAGATGA 2280
Db 12220 CTGATGACCCCGCGCGCAAGGAACTTCTCAAGGCAATGAGCGCTTGCTTCCAGATGA 12279
QY 2281 TTCAACACCTCACTGAAGTCAATACAGGAGCTTGTATCCAGAAATCAGAGGCTTTGGCT 2340

Db	12280	TTCAACAACCCGTCATGTAAAGTCATACAGGAGCCTTTGTAACGGAATACGAGAGCTTTGGCT	123339
Qy	2341	CACCTCCAGGTTTGGGACGCTGTCGGTGGTTTCTGTTCTTATTTCCCAATGACAGAC	2400
Db	12340	CACCTCCAGGTTTGGGACGCTGTCGGTGGTTTCTGTTCTTATTTCCCAATGACAGAGC	123999
Qy	2401	AAGTTTTCGAAAGCACTGGTGGCAGGTGTGACCTGTGTAAGGAACCTCTCAATCTGCGAAG	2460
Db	12400	AAGTTTTCGAAAGCACTGGTGGCAGGTGTGACCTGTGTAAGGAACCTCTCAATCTGCGAAG	124599
Qy	2461	GACATGATATCCCATGATGCTGTCCATCTCTTGAAGAAATTTGTTAATGGTATCAATCGGC	2520
Db	12460	GACATGATATCCCATGATGATGCTGTCCATCTCTTGAAGAAATTTGTTAATGGTATCAATCGGC	125199
Qy	2521	AAGCAAAATGGTGAACACACTAGTAGAATCGGCTCCACCTGGAACCTGATCTCTGAATAAC	2580
Db	12520	AAGCAAAATGGTGAACACACTAGTAGAATCGGCTCCACCTGGAACCTGATCTCTGAATAAC	125799
Qy	2581	TTCCGACATGTTCTCTCAAGCTGGAAGAACCTGACCTCCAGGCCCAGCTTCCAGGAGATTTGAT	2640
Db	12580	TTCCGACATGTTCTCTCAAGCTGGAAGAACCTGACCTCCAGGCCCAGCTTCCAGGAGATTTGAT	126399
Qy	2641	GCCAAATACGACGGCTGGGTGCTGCGCCAGAGACCTTCAAGGAGAAAAATGGAACAACAGAG	2700
Db	12640	GCCAAATACGACGGCTGGGTGCTGCGCCAGAGACCTTCAAGGAGAAAAATGGAACAACAGAG	126999
Qy	2701	AGTTATATCTCCCGAAGAAATCGAAGTTCTCTCTAGCTTCTGCGAGACGAACCAACGACGC	2760
Db	12700	AGTTATATCTCCCGAAGAAATCGAAGTTCTCTCTAGCTTCTGCGAGACGAACCAACGACGC	127599
Qy	2761	AAGTTAAGCTACATCGGTTTCTGCGACCGTTTTCACAGACCTGCGCAAGAGATCGGGTTT	2820
Db	12760	AAGTTAAGCTACATCGGTTTCTGCGACCGTTTTCACAGACCTGCGCAAGAGATCGGGTTT	128199
Qy	2821	AACTTGGCCGGTACTAGCTAACTTGTCTGAACTATGTCGGAACATATGCGAAGAGCCTAGATTGGCA	2880
Db	12820	AACTTGGCCGGTACTAGCTAACTTGTCTGAACTATGTCGGAACATATGCGAAGAGCCTAGATTGGCA	128799
Qy	2881	CGTTTCTCTGAGACGCGAGGTTTCAGTCTGTGAACCTACTTTCGAAACCATATTCCTGGCCGTATC	2940
Db	12880	CGTTTCTCTGAGAGCGGACGGTTCAGTCTGTGAACCTACTTTCGAAACCATATTCCTGGCCGTATC	129399
Qy	2941	GAGATCATGGCGGCTCCAAAGCCGATGAGCGTGTCTACTTGGAGATCAAGAGTCTAAT	3000
Db	12940	GAGATCATGGCGGCTCCAAAGCCGATGAGCGTGTCTACTTGGAGATCAAGAGTCTAAT	129999
Qy	3001	A 3001	
Db	13000	A 13000	
RESULT 2			
US-10-668-767-145			
Sequence 145, Application US/10668767			
Publication No. US2004017114A1			
GENERAL INFORMATION:			
APPLICANT: Caspar, Timothy			
APPLICANT: Cordova, Daniel			
APPLICANT: Guteridge, Steven			
APPLICANT: Raun, James			
APPLICANT: Smith, Rejane			
APPLICANT: Tao, Yong			
APPLICANT: Wu, Lihong			
TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors			
FILE REFERENCE: B01533 US NA			
CURRENT APPLICATION NUMBER: US/10/668,767			
CURRENT FILING DATE: 2003-09-23			
PRIOR APPLICATION NUMBER: 60/412,795			
PRIOR FILING DATE: 2002-09-23			
PRIOR APPLICATION NUMBER: 60/4427,324			
PRIOR FILING DATE: 2002-11-18			
NUMBER OF SEQ ID NOS: 149			
SOFTWARE: PatentIn version 3.1			

[illegible]

Db	10756	AAAGAACGCGACAAAGACAAAGAGTCCAAAGGTCCTTAATGTATGCTTGTCTAAAGAGG	10815
Qy	901	TTGTTTACAGTTGGCCTTAACCTAATTCGCTGGCAGAGAACAAAGACTGGTCAGACATTTG	960
Db	10816	TTGTTTACAGTTGGCCTTAACCTAATTCGCTGGCAGAGAACAAAGACTGGTCAGACATTTG	10875
Qy	961	AAAGACAGGTTCTCGAAGAAAAATGTGAGAACAGATGTGGCAAGAAATTCGGAAGACCCAG	1020
Db	10876	AAAGACAGGTTCTCGAAGAAAAATGTGAGAACAGATGTGGCAAGAAATTCGGAAGACCCAG	10935
Qy	1021	CTGACACTTCAGATTAATAATAGATCCGGCAGACGAAATGTCTTGCCAACTTACTGTAT	1080
Db	10936	CTGACACTTCAGATTAATAATAGATCCGGCAGACGAAATGTCTTGCCAACTTACTGTAT	10995
Qy	1081	AGCAAGTTAGGTTGCGAAGAGTAAGAGCAATTAATGTGAAACTGTGAAATTAAGGCC	1140
Db	10996	AGCAAGTTAGGTTGCGAAGAGTAAGAGCAATTAATGTGAAACTGTGAAATTAAGGCC	11055
Qy	1141	AAAGTTATTTAGTATACCGTTCGAGAAATCGTCCGCTATGATTAAGTTCCTTTCGATTTG	1200
Db	11056	AAAGTTATTTAGTATACCGTTCGAGAAATCGTCCGCTATGATTAAGTTCCTTTCGATTTG	11115
Qy	1201	CATATGATTCGACATCCCCCAACAAATGATTAAGAAACGTATACCGGTGGGTGTGTGATTA	1260
Db	11116	CATATGATTCGACATCCCCCAACAAATGATTAAGAAACGTATACCGGTGGGTGTGTGATTA	11175
Qy	1261	CAAGCAAGCGCGCGCTCATCGCCTGCTTCGCAAACTTCACTACATTCCTGTCGCGAGA	1320
Db	11176	CAAGCAAGCGCGCGCTCATCGCCTGCTTCGCAAACTTCACTACATTCCTGTCGCGAGA	11235
Qy	1321	CATCGAGCGTGTAAATCTTGTGCTTCGACGTACTACGAGCTCTGTGTGAAGAGAGAAC	1380
Db	11236	CATCGAGCGTGTAAATCTTGTGCTTCGACGTACTACGAGCTCTGTGTGAAGAGAGAAC	11295
Qy	1381	ATTGGAACAAGAAATGATTAAGAAATCTTAATCAATCAATTCGAAAGACGAGACTGAAG	1440
Db	11296	ATTGGAACAAGAAATGATTAAGAAATCTTAATCAATCAATTCGAAAGACGAGACTGAAG	11355
Qy	1441	AAAGATGACGTGTGAGAGAGTGAAGAGCTGACCCCTCAGCAGAGCTGTGACCAACC	1500
Db	11356	AAAGATGACGTGTGAGAGAGTGAAGAGCTGACCCCTCAGCAGAGCTGTGACCAACC	11415
Qy	1501	TTCTGTGCGGTGTCATGACTGAGAGGTCCGGCGCTTTCGAGAGAGATCCTTAATACATG	1560
Db	11416	TTCTGTGCGGTGTCATGACTGAGAGGTCCGGCGCTTTCGAGAGAGATCCTTAATACATG	11475
Qy	1561	TCTTAACGCAACATCATATGCGAAGTCTCTGTGGAAGAAAGAAAGGGGGTGGGAG	1620
Db	11476	TCTTAACGCAACATCATATGCGAAGTCTCTGTGGAAGAAAGAAAGGGGGTGGGAG	11535
Qy	1621	GAAGAGAGAGGGGTGAGAGAGAGGCTGAAGACGAGAGCAGAGCAGATTAACAGAA	1680
Db	11536	GAAGAGAGAGGGGTGAGAGAGAGGCTGAAGACGAGAGCAGAGCAGATTAACAGAA	11595
Qy	1681	CAGAAGATGAGAAACAAAGCTCTTAATCCAGCAAGCGCGCTGGCGAGACCTGTGGGTT	1740
Db	11596	CAGAAGATGAGAAACAAAGCTCTTAATCCAGCAAGCGCGCTGGCGAGACCTGTGGGTT	11655
Qy	1741	GCCGAATGTGTGTGCTGACATTCGCGCTCAGAGGCTGCCAGCGAGATGTCAATG	1800
Db	11656	GCCGAATGTGTGTGCTGACATTCGCGCTCAGAGGCTGCCAGCGAGATGTCAATG	11715
Qy	1801	AAAGCTTACAGCTCGGATTAATGATTAATGAGGGGCGGCAATATTGATTAACAGATGGGT	1860
Db	11716	AAAGCTTACAGCTCGGATTAATGATTAATGAGGGGCGGCAATATTGATTAACAGATGGGT	11775
Qy	1861	ATGTTGAACCACTTGAAGACAAAGAAAGACGTGGGCTTCTTAAGTCCATCGCGGCTC	1920
Db	11776	ATGTTGAACCACTTGAAGACAAAGAAAGACGTGGGCTTCTTAAGTCCATCGCGGCTC	11835
Qy	1921	ATGAACCTCTGCTCGGTGCTGATCTTGAAGCTTCGAGAGAGAACACCAAGGCTGAAGGT	1980
Db	11836	ATGAACCTCTGCTCGGTGCTGATCTTGAAGCTTCGAGAGAGAACACCAAGGCTGAAGGT	11895
Qy	1981	CTGGCGGTGGGTCTGGAAGGTGGCGGGAGAGAAACATGATGACGCGGATTCACC	2040
Db	11896	CTGGCGGTGGGTCTGGAAGGTGGCGGGAGAGAAACATGATGACGCGGATTCACC	11955
Qy	2041	TGGCACTCTTCAGGTTCAATTCAGCTCAGCTGTGAAGAGACAACTTGAATGGCAGAAC	2100
Db	11956	TGGCACTCTTCAGGTTCAATTCAGCTCAGCTGTGAAGAGACAACTTGAATGGCAGAAC	12015
Qy	2101	TACCTGGAACCTAGGCGGGTAAACAGACAAAGTGAAGTGGATCTGACACGCTGAC	2160
Db	12016	TACCTGGAACCTAGGCGGGTAAACAGACAAAGTGAAGTGGATCTGACACGCTGAC	12075
Qy	2161	TACCTGTGCGGTGCGAGAGTCCATCATGAGCTTCTACTGTGCACTTCAAGCAAGAA	2220
Db	12076	TACCTGTGCGGTGCGAGAGTCCATCATGAGCTTCTACTGTGCACTTCAAGCAAGAA	12135
Qy	2221	CTGATCGACCCGGCGCGCAAGCGAACTTCTCAAGGCCATTGGCGTGGCTTCCAAATA	2280
Db	12136	CTGATCGACCCGGCGCGCAAGCGAACTTCTCAAGGCCATTGGCGTGGCTTCCAAATA	12195
Qy	2281	TTGAACACCTCTCATGAAGTCAACAGGACCTTGTACGAGAAATCAGACAGGCTTGGCT	2340
Db	12196	TTGAACACCTCTCATGAAGTCAACAGGACCTTGTACGAGAAATCAGACAGGCTTGGCT	12255
Qy	2341	CACCTCAGGTTGTGGACGCTGTGGGTGTTCTGTCTTAATTCCTCAATGACAGAC	2400
Db	12256	CACCTCAGGTTGTGGACGCTGTGGGTGTTCTGTCTTAATTCCTCAATGACAGAC	12315
Qy	2401	AAATTGTGAAAGCATGTGTGCGAGGTGACCTGCTGAAGAACTCTCAATTCGCAAG	2460
Db	12316	AAATTGTGAAAGCATGTGTGCGAGGTGACCTGCTGAAGAACTCTCAATTCGCAAG	12375
Qy	2461	GACATGATCCCAATGATGCTGTGCAATGCTTGAAGAAATGTTTAATGTTAAATCGCG	2520
Db	12376	GACATGATCCCAATGATGCTGTGCAATGCTTGAAGAAATGTTTAATGTTAAATCGCG	12435
Qy	2521	AAAGCAATGGTGAACACACTAGTAGAATGGGCTCCACAGTGAACCTGTAATAC	2580
Db	12436	AAAGCAATGGTGAACACACTAGTAGAATGGGCTCCACAGTGAACCTGTAATAC	12495
Qy	2581	TTGCAATGTTCTCTCAAGCTGAAGAACCTGACCTCAGCGCCAGCTTCCAGAGATTTGAT	2640
Db	12496	TTGCAATGTTCTCTCAAGCTGAAGAACCTGACCTCAGCGCCAGCTTCCAGAGATTTGAT	12555
Qy	2641	GCCAAATTAAGAGCGGTGGGTGCTGCCAAGGAACTTGAAGAGAAATGGAACAAAGAG	2700
Db	12556	GCCAAATTAAGAGCGGTGGGTGCTGCCAAGGAACTTGAAGAGAAATGGAACAAAGAG	12615
Qy	2701	AGTTATTAATCCCGAAGAAATCGAGTCTCTTAAGCTTGTGCGAGACGAAACGACCGG	2760
Db	12616	AGTTATTAATCCCGAAGAAATCGAGTCTCTTAAGCTTGTGCGAGACGAAACGACCGG	12675
Qy	2761	AAATTAGACTACATCGGTTTCTGCGACCGTTTCAAGAGCTGCGAAGAGATCGGGTTT	2820
Db	12676	AAATTAGACTACATCGGTTTCTGCGACCGTTTCAAGAGCTGCGAAGAGATCGGGTTT	12735
Qy	2821	AACTTGGCGGTGTTACTGACTTAATCTGTCTGAACATATGCGGAAGAGGCTTAATGGCA	2880
Db	12736	AACTTGGCGGTGTTACTGACTTAATCTGTCTGAACATATGCGGAAGAGGCTTAATGGCA	12795
Qy	2881	CGTTTCTGGAAGCGGCAAGTCAAGCTGAAGCTTGAAGCAATTCCTCGGCGGTATC	2940
Db	12796	CGTTTCTGGAAGCGGCAAGTCAAGCTGAAGCTTGAAGCAATTCCTCGGCGGTATC	12855
Qy	2941	GAGATCATGGCGGCTCAGAGGCAATGAGCGTGTCTACTTGAAGTCAAGAGTCTAAT	3000
Db	12856	GAGATCATGGCGGCTCAGAGGCAATGAGCGTGTCTACTTGAAGTCAAGAGTCTAAT	12915
Qy	3001	A 3001	
Db	12916	A 12916	

RESULT 3
US-10-668-767-1
Sequence 1, Application US/10668767
Publication No. US20040171114A1
GENERAL INFORMATION:
APPLICANT: Caspar, Timothy
APPLICANT: Cordova, Daniel
APPLICANT: Gutierrez, Steven
APPLICANT: Rauh, James
APPLICANT: Smith, Rejane
APPLICANT: Tao, Yong
APPLICANT: Wu, Lihong
TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
FILE REFERENCE: B01533 US NA
CURRENT APPLICATION NUMBER: US/10/668,767
PRIOR FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: 60/412,795
PRIOR FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 60/427,324
PRIOR FILING DATE: 2002-11-18
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 15679
TYPE: DNA
ORGANISM: Heliothis virescens
FEATURE:
NAME/KEY: CDS
LOCATION: (251)..(15676)
OTHER INFORMATION:
FEATURE:
NAME/KEY: misc feature
LOCATION: (5515)
OTHER INFORMATION: n = c or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (13000)
OTHER INFORMATION: n = a or t
US-10-668-767-1
Query Match 97.2%; Score 2917.4; DB 7; Length 15679;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 2964; Conservative 0; Mismatches 37; Indels 15; Gaps 1;
QY 1 CAGTTCTCTGTCGACAGATCGCTGACCAATCTTTGGAAAGCCCAAGACATTAATGCG 60
DB 10277 CAGTTCTCTGTCGACAGATCGCTGACCAATCTTTGGAAAGCCCAAGACATTAATGCG 10336
QY 61 AAAATGGAACAATGATCCGACGCTGAGACGATCTTAAGCGAGTGAACCAATTGCGT 120
DB 10337 AAAATGGAACAATGATCCGACGCTGAGACGATCTTAAGCGAGTGAACCAATTGCGT 10396
QY 121 GAGTCAGACAGACGTACAGACGAGCGCGCATATCATGATGATGTCGCTTACTC 180
DB 10397 GAGTCAGACAGACGTACAGACGAGCGCGCATATCATGATGATGTCGCTTACTC 10456
QY 181 TGTCTTATTTGCGCTTGTGTGGGACAGAGGGGCTGATTAATGTTACTCTTAATGCGGGA 240
DB 10457 TGTCTTATTTGCGCTTGTGTGGGACAGAGGGGCTGATTAATGTTACTCTTAATGCGGGA 10516
QY 241 AAACACGTAAACAATGTTAAACAGCGGACACATGAAACGATCTCTTAAGAAATGTTTGAAG 300
DB 10517 AAACACGTAAACAATGTTAAACAGCGGACACATGAAACGATCTCTTAAGAAATGTTTGAAG 10576
QY 301 CTCTCAAAAAGAAACATCGGCAATGAGAAACGCGCGTGAATGACCGGATCGCCACTAC 360
DB 10577 CTCTCAAAAAGAAACATCGGCAATGAGAAACGCGCGTGAATGACCGGATCGCCACTAC 10636
QY 361 ACGCAGACATCATCATCAACAGCTCCGAGAACTGCTGAAGGATTCCTTCTGCGGCTC 420
DB 10637 ACGCAGACATCATCATCAACAGCTCCGAGAACTGCTGAAGGATTCCTTCTGCGGCTC 10696

QY 421 GCTGAACGTGTTCGCAACCGCACGACATATGTTCCATTAAGAGAGAGCTTGAGGCGG 480
DB 10697 GCTGAACGTGTTCGCAACCGCACGACATATGTTCCATTAAGAGAGAGCTTGAGAGGG 10756
QY 481 TTTATTTAATGCTGTCAACAGACAGACATCCAGGTAAAGTCTCAATTAAGAAAGACTGG 540
DB 10757 TTTATTTAATGCTGTCAACAGACAGACATCCAGGTAAAGTCTCAATTAAGAAAGACTGG 10816
QY 541 CAGCTGCTGGTCAGAGACATCTACTCTTCTTACCCGCTGCTCATCAATGATAGTGCACCTG 600
DB 10817 CAGCTGCTGGTCAGAGACATCTACTCTTCTTACCCGCTGCTCATCAATGATAGTGCACCTG 10876
QY 601 CAGAGAAACCACTGGCTCAGAAACAATGTTCCAGAGCGGAGAGAGCTGTACAACACCTG 660
DB 10877 CAGAGAAACCACTGGCTCAGAAACAATGTTCCAGAGCGGAGAGAGCTGTACAACACCTG 10936
QY 661 GCTGAATTTCTCAACATCTGTGTCAAGACGATCTTTGTAAGAGAGAAACGAATTC 720
DB 10937 GCTGAATTTCTCAACATCTGTGTCAAGACGATCTTTGTAAGAGAGAAACGAATTC 10996
QY 721 ATCTCTGCAACGAAATTTGATTAATGATGCTGCTGATTAATGCAAGCAACGAAGAGT 780
DB 10997 ATCTCTGCAACGAAATTTGATTAATGATGCTGCTGATTAATGCAAGCAACGAAGAGT 11056
QY 781 ACACAGTTAACAGATGTAATCTCTCAAGGTGTGGAAGAAAGAAAGAACACCGTAT 840
DB 11057 ACACAGTTAACAGATGTAATCTCTCAAGGTGTGGAAGAAAGAAAGAACACCGTAT 11116
QY 841 AAGAAAGCGCAACAAAGCAAGAAAGTCCAGCGTCTTAATGTTAGTCTTGTGAAGAG 900
DB 11117 AAGAAAGCGCAACAAAGCAAGAAAGTCCAGCGTCTTAATGTTAGTCTTGTGAAGAG 11176
QY 901 TTGTTACAGTTGSCCTTAACCTATTTGCTGGGAGAGAAACGAAGCTGGTCAATGTT 960
DB 11177 TTGTTACAGTTGSCCTTAACCTATTTGCTGGGAGAGAAACGAAGCTGGTCAATGTT 11236
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DB 11237 AAAGACAGTTCCTGAGAGTGAAGGAGCCCTCAAGAAATGTCAAGAACAAAGTGTGGCAGAA 11296
QY 1006 TTGCGAAGACCGACGTGACATCTTCAGATTAATTAATGATCCGCGACGAATGTTTGG 1065
DB 11297 TTGCGAAGACCGACGTGACATCTTCAGATTAATTAATGATCCGCGACGAATGTTTGG 11356
QY 1066 CAACATTAATCTGTATACAGTTAGTGTGGAAGAGTAAGCAATTAATCTGTGAAGT 1125
DB 11357 CAACATTAATCTGTATACAGTTAGTGTGGAAGAGTAAGCAATTAATCTGTGAAGT 11416
QY 1126 GCTGAATAAAGGCGCAAGATTAATGATGATACCGTCGAGAGAAATCGTGTATGATTA 1185
DB 11417 GCTGAATAAAGGCGCAAGATTAATGATGATACCGTCGAGAGAAATCGTGTATGATTA 11476
QY 1186 GTGCTTTTGGATTCATATGATGATGACATCCCAACAATGATTAAGACGTGACCG 1245
DB 11477 GTGCTTTTGGATTCATATGATGATGACATCCCAACAATGATTAAGACGTGACCG 11536
QY 1246 TCGGTGTGTGATTAACAGCAAGCGCGCGCTATTCGCTGCTTCCGACAACTTCACTA 1305
DB 11537 TCGGTGTGTGATTAACAGCAAGCGCGCGCTATTCGCTGCTTCCGACAACTTCACTA 11596
QY 1306 CATTCCTGCGGAGACATCGACGCTGTAACTCTTCCTGCGACGTAACGACTCTG 1365
DB 11597 CATTCCTGCGGAGACATCGACGCTGTAACTCTTCCTGCGACGTAACGACTCTG 11656
QY 1366 TTGGAAGAGAGAACTTGAACAAGATTAATGATTAAGATCTTAATCAATCAATTCGAA 1425
DB 11657 TTGGAAGAGAGAACTTGAACAAGATTAATGATTAAGATCTTAATCAATCAATTCGAA 11716
QY 1426 GAGCAGAGCTGAAGAGAGAGTGTGTGAAGAGAGTGAAGAGCTGAGCCCTCAGC 1485
DB 11717 GAGCAGAGCTGAAGAGAGAGTGTGTGAAGAGAGTGAAGAGCTGAGCCCTCAGC 11776

1486 CAGCTGGTACACCACTTCTGTGCGGTGSCATGACTGAGAGTCCGGGCTTTGCAAGAG 1545
11777 CAGCTGGTACACCACTTCTGTGCGGTGSCATGACTGAGAGTCCGGGCTTTGCAAGAG 11836
1546 GATCCTTATATCATGTCTTACGACACATCATAGGAGTCTGTGAGAGAGAGAA 1605
11837 GATCCTTATATCATGTCTTACGACACATCATAGGAGTCTGTGAGAGAGAGAA 11896
1606 GAAAGGGGTGGGAG 1665
11897 GAAAGGGGTGGGAG 11956
1666 GCCAGTATACAGCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAGAG 1725
11957 GCCAGTATACAGCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAGAG 12016
1726 GCGGACCGTGGGGTGGCGGAAATGGTGTGCTGACATCTCGGCTCCAAAGGCTGCC 1785
12017 GCGGACCGTGGGGTGGCGGAAATGGTGTGCTGACATCTCGGCTCCAAAGGCTGCC 12076
1786 AGCGAGATGTCTATGAGAGACTTTTACAGCTCGGTATTTAGTATATGAGGGGCGCAATATT 1845
12077 AGCGAGATGTCTATGAGAGACTTTTACAGCTCGGTATTTAGTATATGAGGGGCGCAATATT 12136
1846 GATATACAGAGGGGTATGTTGAACCACTTGAAGAAAGAAAGAGAGAGAGAGAGAGAGAG 1905
12137 GATATACAGAGGGGTATGTTGAACCACTTGAAGAAAGAGAGAGAGAGAGAGAGAGAG 12196
1906 TCCATCGCGGGCTCATGAGACCTCTGCTCCGTGCTCATGATCTTGAAGAGAGAGAGAG 1965
12197 TCCATCGCGGGCTCATGAGACCTCTGCTCCGTGCTCATGATCTTGAAGAGAGAGAGAG 12256
1966 ACCAAGGCTGAGAGTCTGAGGCGTGGTCTGGAAGGTGGGCGGAGAGAGAGAGAGAGAG 2025
12257 ACCAAGGCTGAGAGTCTGAGGCGTGGTCTGGAAGGTGGGCGGAGAGAGAGAGAGAGAG 12316
2026 GAGCCCGAGTTCACCTGCGCATCTCTCAAGTTCATTCAGGCTCACTCTGAGAGAGAGAGAG 2085
12317 GAGCCCGAGTTCACCTGCGCATCTCTCAAGTTCATTCAGGCTCACTCTGAGAGAGAGAGAG 12376
2086 TTGGAAGTGGCAGAGACTACCTGCGAGACTACGAGCGGTAACAGAGAGAGAGAGAGAGAG 2145
12377 TTGGAAGTGGCAGAGACTACCTGCGAGACTACGAGCGGTAACAGAGAGAGAGAGAGAGAG 12436
2146 ATCTGACCGTGCATCTACCTGCTGCGGTGCGAGAGAGTTCATGAGACTTCTACTGCGAC 2205
12437 ATCTGACCGTGCATCTACCTGCTGCGGTGCGAGAGAGTTCATGAGACTTCTACTGCGAC 12496
2206 TACTCAAGCAAGAGAACTGATGAGACCCGCGCGGCAAGAGAGAGAGAGAGAGAGAGAGAG 2265
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2266 GTGGCTTCCCAAGTATCAACACACCTCACTGAATCTTACAGAGAGAGAGAGAGAGAGAGAG 2325
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2326 CAGGAGGCTTTGGCTCACTCCAGGTTGTGGAGCGCTGTGGTGGTTCCTGTTCTTATTC 2385
12617 CAGGAGGCTTTGGCTCACTCCAGGTTGTGGAGCGCTGTGGTGGTTCCTGTTCTTATTC 12676
2386 TCCCAATGCAAGAGAAAGTTGTGAGAGCACTGTGCGAGGTGAGACTCTGAGAGAGAGAGAG 2445
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2446 CTCAATCTGCAAGAGAGAGATGATCCCATGATGCTGTCTGATGAGAGAGAGAGAGAGAGAG 2505
12737 CTCAATCTGCAAGAGAGAGATGATCCCATGATGCTGTCTGATGAGAGAGAGAGAGAGAGAG 12796
2506 AATGTGTAATCTGCAAGAGAGAAATGTGAGAGCACTAGTAGAATGCGCTCCAAAGTGGAA 2565
12797 AATGTGTAATCTGCAAGAGAGAAATGTGAGAGCACTAGTAGAATGCGCTCCAAAGTGGAA 12856
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12857 CTGATCTGTAATCTTCTGACATGTTCTCAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 12916
2626 TTCAGAGAGATTTGATGCAATTAACAGAGCGCTGGGTGCTGCCAAGAGAGAGAGAGAGAG 2685
12917 TTCAGAGAGATTTGATGCAATTAACAGAGCGCTGGGTGCTGCCAAGAGAGAGAGAGAGAG 12976
2686 ATGAGACACAGAGAGATTTACTCCCGAAGAAATGAGAGTTCTCTTACTGCTGTGGAG 2745
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2746 ACGAACCAGAGCGGCAAGTATGACTATGCTGTTGCGAGACGTTTCCAGAGAGAGAGAGAG 2805
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13097 AAGAGATCGGCTTTAATCTGCGGCTTACTGACTTACTGAGAGAGAGAGAGAGAGAGAGAG 13156
2866 GAGCCTGATTTGACAGTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2925
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13217 TTCTCGGCGGTATCGAGATCATGAGCGGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 13276
2986 ATCAGAGAGTCTAATA 3001
13277 ATCAGAGAGTCTAATA 13292

RESULT 4
US-10-668-767-129
; Sequence 129, Application US/10668767
; Publication No. US2004017114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutierrez, Steven
; APPLICANT: Raub, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: B1513 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; PRIORITY FILING DATE: 2003-09-23
; PRIORITY FILING DATE: 2002-09-23
; PRIORITY FILING DATE: 2002-09-23
; PRIORITY FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 15405
; TYPE: DNA
; ORGANISM: Heliothis virescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(15402)
; OTHER INFORMATION:
; FEATURE:
; OTHER INFORMATION: PXL-Hv2
US-10-668-767-129

Query Match 94.8%; Score 2846.4; DB 7; Length 15405;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2920; Conservative 0; Mismatches 81; Indels 15; Gaps 1;

1 CAGTTCTCTGCTGTAAGAGAGATGCTGACATTTCTTTGAGAGAGAGAGAGAGAGAGAGAGAG 60
10003 CAGTTCTCTGCTGTAAGAGAGATGCTGACATTTCTTTGAGAGAGAGAGAGAGAGAGAGAGAG 10062

Oy	61	AAAATGGAAACAATGCAATGCCGACGCTAAGAGAAGATCTCTTAAAGGAGAGTGTGACCAATTTCCGG	120
Db	10063	AAAATGGAAACAATGCAATGCCGACGCTAAGAGAAGATCTCTTAAAGGAGAGTGTGACCAATTTCCGG	101222
Oy	121	GAGTCAGACAAGACGTATGCAACGAGAGGCGCGCATATCATCATGATGTGGTGTGCTTAACTC	180
Db	10123	GAGTCAGACAAGACGTATGCAACGAGAGGCGCGCATATCATCATGATGTGGTGTGCTTAACTC	10182
Oy	181	TGTTCTTAAATTTGCGGTTCTGTGTGGGCAACAGGGGCTGATTAATGTATCTCTACTGCGGGA	240
Db	10183	TGTTCTTAAATTTGCGGTTCTGTGTGGGCAACAGGGGCTGATTAATGTATCTCTACTGCGGGA	10242
Oy	241	AACCACTTAACATGTGTACAGCGGGAACAATATACACAGCTCTCTCAAGAAATGTTCTGAAG	300
Db	10243	AACCACTTAACATGTGTACAGCGGGAACAATATACACAGCTCTCTCAAGAAATGTTCTGAAG	10302
Oy	301	CTCATTAAGAAAAGAACATGGCAGATGAGAAACGCGCGGTGATGACCGGATCCGACACTAC	360
Db	10303	CTCATTAAGAAAAGAACATGGCAGATGAGAAACGCGCGGTGATGACCGGATCCGACACTAC	10362
Oy	361	ACGACGACGATCATCATCAACAGCTCCGAGAACTGTGAGGATTCCTTCCGCGCTC	420
Db	10363	ACGACGACGATCATCATCAACAGCTCCGAGAACTGTGAGGATTCCTTCCGCGCTC	10422
Oy	421	GCTGAACGTGTTCGCAACAACGACGACATATGTTCTCATAGAGAGAGCTTTGAGGGG	480
Db	10423	GCTGAACGTGTTCGCAACAACGACGACATATGTTCTCATAGAGAGAGCTTTGAGAGGG	10482
Oy	481	TTTATTAAGTCGTCAACAGACGACATCCAGATGAGTCAGTACAGAAAGACTGG	540
Db	10483	TTTATTAAGTCGTCAACAGACGACATCCAGATGAGTCAGTACAGAAAGACTGG	10542
Oy	541	CAGCTGCTGGTCAGAGACATCTACTCTTCAACCGCTGCTCAACATGACTGCACCTG	600
Db	10543	CAGCTGCTGGTCAGAGACATCTACTCTTCAACCGCTGCTCAACATGACTGCACCTG	10602
Oy	601	CAGAGAAACACTGGCTCAGGAACAATGTTCCAAGGCGAGAGGCTGTACACCACTGG	660
Db	10603	CAGAGAAACACTGGCTCAGGAACAATGTTCCAAGGCGAGAGGCTGTGTACACCACTGG	10662
Oy	661	GCTGAATCTTCAACATCTGTGTGAAGAGCGCACTTCTTGAAGAGGAACAAGAACTTC	720
Db	10663	GCTGAATCTTCAACATCTGTGTGAAGAGAGCGCACTTCTTGAAGAGGAACAAGAACTTC	10722
Oy	721	ATCTCTGCAACGAAATTTGATTAACAATGTGCTGATTAATGCGAACACAAACAAGAAAGTG	780
Db	10723	ATCTCTGCAACGAAATTTGATTAACAATGTGCTGATTAATGCGAACACAAAGAAAGTG	10782
Oy	781	ACAGCAGTTAACAGATGTACTCTCTCAAGGTGTGGAAGAAAGAAAGAAAGACCCGTAT	840
Db	10783	ACAGCAGTTAACAGATGTACTCTCTCAAGGTGTGGAAGAAAGAAAGAAAGACCCGTAT	10842
Oy	841	AAGAAACGCGACAAAGACAAAGAAAGTCGAAGCGTCCCTTAATGTAGCTTGTCTGAAGG	900
Db	10843	AAGAAACGCGACAAAGACAAAGAAAGTCGAAGCGTCCCTTAATGTAGCTTGTCTGAAGG	10902
Oy	901	TTGTTTACAGATGGCCCTTAACCTATTGCGTGGCAAGAAACAABAACGTGGCGACATGT	960
Db	10903	TTGTTTACAGATGGCCCTTAACCTATTGCGTGGCAAGAAACAABAACGTGGCGACATGT	10962
Oy	961	AAAGACAGATTCCTG-----AAGAAATGTCAAGAACAAAGTGTGCAGAA	1005
Db	10963	AAAGACAGATTCCTGAAAGTAAAGGAGCCCTCAAGAAATGTCAAGAACAAAGTGTGCAGAA	110222
Oy	1006	TTTGGCAAGACCAAGCTGACATTCACAGATTAATTAATATGATCCGCGACAGAAATGCTTGG	1065
Db	11023	TTTGGCAAGACCAAGCTGACATTCACAGATTAATTAATATGATCCGCGACAGAAATGCTTGG	11082
Oy	1066	CAACATTACTTGTATACAGATTAATGTTTCAAGATGAAGTAAAGCAATTAATCTGTGAATCT	1125
Db	11083	CAACATTACTTGTATACAGATTAATGTTTCAAGATGAAGTAAAGCAATTAATCTGTGAATCT	11142

QY	1126	GCTGAAAATPAAAGCCAAAGTATATGTAATGATACCGTCGAGAAAGATGTCGTAATGATGATA	1185
Db	11143	GCTGAAAATPAAAGCCAAAGTATATGTAATGATACCGTGTAAAGATGTCGTAATGATGATA	11202
QY	1186	GTGCTTTTCGAAATGTCATATGATCGACCAATCCCAACAATAGATPAGAAGCTGTACCGG	1245
Db	11203	GTGCTTTTCGAAATGTCATATGATCGACCAATCCCAACAATAGATPAGAAGCTGTACCGG	11262
QY	1246	TCGGTGTGTGCATPACACGCAAGCCGCCGTATCGCTCTCCGACAACTTCACATA	1305
Db	11263	TCGGTGTGTGCATPACACGCAAGCCGCCGTATCGCTCTCCGACAACTTCGCTA	11322
QY	1306	CATTCTCTGCCCGAGACATCGAAGGTGTAACTCTTCGTCGACAGTAACTAGAGCTCGG	1365
Db	11323	CATTCTCTGCCCGAGACACCGAAGGTGTAACTCTTCGTCGACAGTAACTAGAGCTCGG	11382
QY	1366	TTGGAGAAGAGAAACATTTGGAACAAGATPATAATGATGAAAGATCTTAATCAATTCGAA	1425
Db	11383	TTGGAGAAGAGAAACATTTGGAACAAGATPATAATGATGAAAGATCTTAATCAATTCGAA	11442
QY	1426	GACGCAAGCTGAAGAAAGATGACGTGTGTGAAGAAAGTGAAGACTGACCCCTCACG	1485
Db	11443	GACGCAAGCTGAAGAAAGATGACGTGTGTGAAGAAAGTGAAGAGCCGACCCCTCACG	11502
QY	1486	CAGCTGTGCACACACTTCTGTCCGCGTCATGACTGAGAAGGTCCGCGCCTTTGAGAGAG	1545
Db	11503	CAGCTGTGCACACCTTCTGTCCGCGTCATGACTGAGAAGGTCCGCGCCTTTGAGAGAG	11562
QY	1546	GATCCTCTATACATGTCTTACGCAACATCATPAGCAAGTCTCTGTGTGAAGAAAGAGAA	1605
Db	11563	GATCCTCTATACATGTCTTACGCAACATCATPAGCAAGTCTCTGTGTGAAGAAAGAGAA	11622
QY	1606	GAAAGGGGTGTGGAGAGAAAGAGGGGGTGTGAAGACAGAGGCTTGAAGACGAAGGCAGA	1665
Db	11623	GAAAGGGGTGTGGAGAGAAAGAGGGGGTGTGAAGACAGAGGCTTGAAGACGAAGGCAGA	11682
QY	1666	GCCAGTATACACCAACAAGAAATGTGAAGAAACAAAGCTCTTATTCACCAACGCGGCTG	1725
Db	11683	GCCAGTATACACCAACAAGAAATGTGAAGAAACAAAGCTCTTATTCACCAACGCGGCTG	11742
QY	1726	GCGAGCGGTGGGGGTGGCCAAATAGATGTGTCTGCAATCTCCGCGTCCAAAGGCTGCCC	1785
Db	11743	GCGAGCGGTGGGTGGCCGAAATGTGTGTCTGCAATCTCCGCGTCTPAAAGGCTGCCC	11802
QY	1786	AGCGAGATGTGCATGAAGACTTTACAGCTCGGTGATTAGTATCTGAGGGGCGCAATTT	1845
Db	11803	AGCGAGATGTGCATGAAGACTTTACAGCTCGGTGATTAGTATCTGAGAGAGGCAATTT	11862
QY	1846	GATATPACAGATGGGTATGTGAAACCACTTGAAAGACAAAGAAAGCTGGGCTTCTTACG	1905
Db	11863	GATATPACAGATGGGTATGTGAAACCACTTGAAAGACAAAGAAAGCTGGGATTTCTTACG	11922
QY	1906	TTCATTCGCCCGGCTCATGAACCTCTGCTCCGTCGATCTTGAAGGCTTGTGAAGAGAAC	1965
Db	11923	TTCATTCGCCCGGCTCATGAACCTCTGCTCAAGTCTGAAGCTTGAAGGCTTGTGAAGAGAAC	11982
QY	1966	ACCAAGGCTGAAGGTCTGGGCGTGTGGGTGTGAAAGTGTGCGGCGGAGAGAAAGACATGCAT	2025
Db	11983	ACCAAGGCTGAAGGTCTGGGCGTGTGGGTGTGAAAGGCGCGAGAGAGAAAGACATGCAT	12042
QY	2026	GAGCGCGAGTTTCACTTGCAGACTCTTCAAGTTCAATCACTCACTCTGTGAAGACACAC	2085
Db	12043	GAGCGCGAGTTTCACTTGCAGACTCTTCAAGTTCAATCACTCACTCTGTGAAGACACAC	12102
QY	2086	TTTGAATGTGGAGAACTACCTGTGCGAACTCAAGCCGGTAAACAGACACATGAACTGTGTC	2145
Db	12103	TTTGAATGTGGAGAACTACCTGTGCGAACTCAAGCCGGTAAACAGACACATGAACTGTGTC	12162
QY	2146	ATCTGCAACCGTGCATCTCTGTGCGGCTTGCAGAGTCCATCATGAGACTTCTACTGTGCAC	2205
Db	12163	ATCTGCAACCGTGCATCTCTGTGCGGCTTGCAGAGATCCATCATGAGACTTCTACTGTGCAC	12222
QY	2206	TACTCAGCAAGAACTGATGCACCGGCGCGCAAAAGCAATTTCTTACAGGCAATTGGC	2265


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Db 12223 TACTCTGACAGAGAACTGATGACCCGCGCGCAAGGAATTTCTTCAAGGCCATTGGC 12282
Qy 2266 GTGGCTTCCCAAGATTCAACACCCCTCACTGAAGTCATACAGGAGACCTTGTACGAGAT 2325
Db 12283 GTGGCTTCCCAAGATTCAACACCCCTCACTGAAGTCATACAGGAGACCTTGTACTCAAGAC 12342
Qy 2326 CAGAGAGCTTTGGCTCACTCCAGGTTGTGGAGCGCTGTGGTGTCTTCTTCTATTC 2385
Db 12343 CAGAGAGCTTTAGCTCACTCTAGGTTATGGAGCGCTGTGGTGTCTTCTTCTATTC 12402
Qy 2386 TCCCAATGACAGCAAGTTTGTGAAGCACTGTGTGAGGAGACCTGTGAAGAAATGTTGT 2445
Db 12403 TCCCAATGACAGCAAGTTTGTGAAGCACTGTGTGAGGAGACCTGTGAAGAAATGTTGT 12462
Qy 2446 CTCAATCTGACAGAGCAATGATCCCAATGATGCTGTCTCAATGATGATGATGATGAT 2505
Db 12463 CTCAATCTGACAGAGCAATGATCCCAATGATGCTGTCTCAATGATGATGATGATGAT 12522
Qy 2506 AATGATCAATCGGCAAGCAAAATGTGAGCACTAGTATGATGATGATGATGATGATGAT 2565
Db 12523 AATGATCAATCGGCAAGCAAAATGTGAGCACTAGTATGATGATGATGATGATGATGAT 12582
Qy 2566 CTGATCTGAAATATCTTGTGACATGTTCTCAAGCTGAAGGACCTGACCTCCAACTGTGAA 2625
Db 12583 CTGATCTGAAATATCTTGTGACATGTTCTCAAGCTGAAGGACCTGACCTCCAACTGTGAA 12642
Qy 2626 TTCCAGAGATTGATGCAATTAACAGCGCTGGGTGCTGCCAAGACCTTCAAGAGAA 2685
Db 12643 TTCCAGAGATTGATGCAATTAACAGCGCTGGGTGCTGCCAAGACCTTCAAGAGAA 12702
Qy 2686 ATGGAACAACAGAGATTATATCTCCGAGAGAAATGATGATGATGATGATGATGATGAT 2745
Db 12703 ATGGAACAACAGAGATTATATCTCCGAGAGAAATGATGATGATGATGATGATGATGAT 12762
Qy 2746 ACGAACAACAGAGATTATATCTCCGAGAGAAATGATGATGATGATGATGATGATGATGAT 2805
Db 12763 ACGAACAACAGAGATTATATCTCCGAGAGAAATGATGATGATGATGATGATGATGATGAT 12822
Qy 2806 AAGAGATCGGATTATATCTTGGCGGTGATCTGAATCTTGTGAACATATGCGGAC 2865
Db 12823 AAGAGATCGGATTATATCTTGGCGGTGATCTGAATCTTGTGAACATATGCGGAC 12882
Qy 2866 GAGCTTGAATTGAGACGTTTCTGAGAGCGGAGGATCTGAATCTTGTGAACATATGCGGAC 2925
Db 12883 GAGCTTGAATTGAGACGTTTCTGAGAGCGGAGGATCTGAATCTTGTGAACATATGCGGAC 12942
Qy 2926 TTCTGTGGCGGTATCGAGATGATGAGGCGCTCCAAAGGCAATGAGGCTTATCTTGAAG 2985
Db 12943 TTCTGTGGCGGTATCGAGATGATGAGGCGCTCCAAAGGCAATGAGGCTTATCTTGAAG 13002
Qy 2986 ATCAAGAGTCTAATA 3001
Db 13003 ATCAAGAGTCTAATA 13018

RESULT 5
US-10-668-767-143
; Sequence 143, Application US//10668767
; Publication No. US2004017114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Guttridge, Steven
; APPLICANT: Raub, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yung
; APPLICANT: Wu, Li-hong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US//10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIORITY APPLICATION NUMBER: 60/412,795
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; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 143
; LENGTH: 15429
; TYPE: DNA
; ORGANISM: Helicobacter virescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(15429)
; OTHER INFORMATION:
; FEATURE:
; OTHER INFORMATION: pXL-Hv3
US-10-668-767-143
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Query Match 94.8%; Score 2844.8; DB 7; Length 15429;
Best Local Similarity 96.8%; Pred. No. 0; Mismatches 82; Indels 15; Gaps 1;
Matches 2919; Conservative 0;

Qy 1 CAGTTCCTCTGCTGAACAGATGCTGACCATTTCTTGGAGCCCAAGACATATATGAG 60
Db 10027 CAGTTCCTCTGCTGAACAGATGCTGACCATTTCTTGGAGCCCAAGACATATATGAG 10086
Qy 61 AAAATGGAACATATGATGCTGACGCTGAGACGATCTTAAAGGAGGTGACCAATTCGTG 120
Db 10087 AAAATGGAACATATGATGCTGACGCTGAGACGATCTTAAAGGAGGTGACCAATTCGTG 10146
Qy 121 GATTCAGACAGACGATGACAGAGGCGCGCATATGATGATGATGATGATGATGATGATGAT 180
Db 10147 GATTCAGACAGACGATGACAGAGGCGCGCATATGATGATGATGATGATGATGATGATGAT 10206
Qy 181 TGTTCCTTATTTGCGTTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
Db 10207 TGTTCCTTATTTGCGTTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10266
Qy 241 AACCATGTAACATATGATGACAGGGAACATATGATGATGATGATGATGATGATGATGATGAT 300
Db 10267 AACCATGTAACATATGATGACAGGGAACATATGATGATGATGATGATGATGATGATGATGAT 10326
Qy 301 CTATCAAAAAGAAACATGCGCAATGAGAACGCGCGGTGATGATGATGATGATGATGATGATGAT 360
Db 10327 CTATCAAAAAGAAACATGCGCAATGAGAACGCGCGGTGATGATGATGATGATGATGATGATGAT 10386
Qy 361 ACGCAGATCATCATCAACAGCTCCGAGAACTGCTGAGGATTCCTTCTGCGGCTC 420
Db 10387 ACGCAGATCATCATCAACAGCTCCGAGAACTGCTGAGGATTCCTTCTGCGGCTC 10446
Qy 421 GCTGAACGTGTTCGAAACGCAAGCAATATGTTCAATAGGAGAGAGAGCTTGAAGGGG 480
Db 10447 GCTGAACGTGTTCGAAACGCAAGCAATATGTTCAATAGGAGAGAGAGCTTGAAGGGG 10506
Qy 481 TTTATTAAGTCGTCACACAGACACATCCAGGTGAGTTCAGATTAACAAGAAAGCTGG 540
Db 10507 TTTATTAAGTCGTCACACAGACACATCCAGGTGAGTTCAGATTAACAAGAAAGCTGG 10566
Qy 541 CAGCTCTGGTCAAGACATCTACTCTTCTACCCGCTGCTCATCAAGTACGTGACCTG 600
Db 10567 CAGCTCTGGTCAAGACATCTACTCTTCTACCCGCTGCTCATCAAGTACGTGACCTG 10626
Qy 601 CAGAGAACCACTGGCTCAGAAACATATGTTCCAGAGCGGAGAGCTGTACCAACACGTTG 660
Db 10627 CAGAGAACCACTGGCTCAGAAACATATGTTCCAGAGCGGAGAGCTGTACCAACACGTTG 10686
Qy 661 GCTGAATCTTGAACATCTGTCGAGAGACCGAGTACTTCTTGAAGAGAGAAAGAACTTC 720
Db 10687 GCTGAATCTTGAACATCTGTCGAGAGACCGAGTACTTCTTGAAGAGAGAAAGAACTTC 10746
Qy 721 ATCTGCAAGAAATGATTAACATGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 780
Db 10747 ATCTGCAAGAAATGATTAACATGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 10806
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QY 781 ACAGCAGTAAACAGATGTACTCTCCAGAGTGTGAAAAAGAAAGAGACCGTAT 840
Db 10807 AACAGAGTAAACAGATGTACTCTCCAGAGTGTGAAAAAGAAAGAGACCGTAT 10866
QY 841 AAGAAACCGCAACAGAGAGTCCAGAGTCCCTTAATGTAGCTTTGTGAAGAG 900
Db 10867 AAGAAACCGCAACAGAGAGTCCAGAGTCCCTTAATGTAGCTTTGTGAAGAG 10926
QY 901 TTGTTACAGTGTGGCTTAACTAATTCGTGACAGAGAACAGAACTGGTGACAGATGT 960
Db 10927 TTGTTACAGTGTGGCTTAACTAATTCGTGACAGAGAACAGAACTGGTGACAGATGT 10986
QY 961 AAGAAGAGTCTG-----AAGAAATGTCAAGAACAGATGTGACAGAA 1005
Db 10987 AAGAAGAGTCTGAGAGTAGAGACCTCAAGAAAAATGTCAAGAACAGATGTGACAGAA 11046
QY 1006 TTGCGGAAGACCCAGCTGACATTCAGATTAATATGATCCGCGACAGAGAAATGTCTTGG 1065
Db 11047 TTGCGGAAGACCCAGCTGACATTCAGATTAATATGATCCGCGACAGAGAAATGTCTTGG 11106
QY 1066 CAACATTACTTGATAGCAAGTTAGTTGAGAGAGTGAAGCAATTAATCTGTGAAACT 1125
Db 11107 CAACATTACTTGATAGCAAGTTAGTTGAGAGAGTGAAGCAATTAATCTGTGAAACT 11166
QY 1126 GCTGAAAAATAGCCAGATTAATTAATGATACCTGACAGAGATCGTCTATGAGTAA 1185
Db 11167 GCTGAAAAATAGCCAGATTAATTAATGATACCTGATGAAAGATGCTGCTATGAGTAA 11226
QY 1186 GTGCTTTTGGATTGATATGATGCAACATCCCAACAAATGATTAAGAGCTGTACCGG 1245
Db 11227 GTGCTTTTGGATTGATATGATGCAACATCCCAACAAATGATTAAGAGCTGTACCGG 11286
QY 1246 TCGGTGTGTGCAATCAACGCAAGCGCGCTCATCGCTGCTTCCGACAACTTCACAT 1305
Db 11287 TCGGTGTGTGCAATCAACGCAAGCGCGCTCATCGCTGCTTCCGACAACTTCACAT 11346
QY 1306 CATTCCTGCGCAGACATCGAGCGTGTAACTCTTCGCTGCGACGTACTACAGAGCTGAG 1365
Db 11347 CATTCCTGCGCAGACATCGAGCGTGTAACTCTTCGCTGCGACGTACTACAGAGCTGAG 11406
QY 1366 TTGGAAGAGAGAACATTTGGAACAGAGTAAATGATTAAGAGATCTTAATCAATCTTCCAA 1425
Db 11407 TTGGAAGAGAGAACATTTGGAACAGAGTAAATGATTAAGAGATCTTAATCAATCTTCCAA 11466
QY 1426 GACGCAAGCTGAAGAGAGTACGTGTGAGAGAGAGTGAAGAACCTCGAACCTTCACG 1485
Db 11467 GACGCAAGCTGAAGAGAGTACGTGTGAGAGAGAGTGAAGAACCTTCACG 11526
QY 1486 CAGCTGTGTCAACACCTTCTGTGCGGGTGCATGACGTAAGAGGTCCGGCGCTTTACAGAG 1545
Db 11527 CAGCTGTGTCAACACCTTCTGTGCGGGTGCATGACGTAAGAGGTCCGGCGCTTTACAGAG 11586
QY 1546 GATTCCTTAATACATGTCTTACGACACATCATAGCGAGTCTGTGAGAGAGAGAGAA 1605
Db 11587 GATTCCTTAATACATGTCTTACGACACATCATAGCGAGTCTGTGAGAGAGAGAGAA 11646
QY 1606 GAAAGGGGTGTGAG 1665
Db 11647 GAAAGGGGTGTGAG 11706
QY 1666 GCCAGTATACAGAAACAAGAAATGAGAAACAAAGGCTCTAATTCACCAACGCGGGCTG 1725
Db 11707 GCCAGTATACAGAAACAAGAAATGAGAAACAAAGGCTCTAATTCACCAACGCGGGCTG 11786
QY 1726 GCGGACCGTGGGTGTGCGAAATGTGTGTGTCACATCTCCGCGTCCAAAGCGTGC 1785
Db 11767 GCGGACCGTGGGTGTGCGAAATGTGTGTGTCACATCTCCGCGTCCAAAGCGTGC 11826
QY 1786 AGCGAGATGTGTCACTGAAGCTTTACAGCTCGGTATTAATGATACCTGAAGAGAGAGAGAG 1845
Db 11827 AGCGAGATGTGTCACTGAAGCTTTACAGCTCGGTATTAATGATACCTGAAGAGAGAGAGAG 11886
QY 1846 GATATATACAGATGGGTATGTGAACCACTTGAAAGACAAAGAAAGAGCGTGGCTTCTTACG 1905

Db 11887 GATATATACAGATGGGTATGTGAACCACTTGAAAGACAAAGAAAGAGCGTGGATTCCTTACG 11946
QY 1906 TCCATTCGCGGCTCACTGAATCTCTGCTCCGCTGCATCTTTAGCGCTTTGAGAGAGAC 1965
Db 11947 TCCATTCGCGGCTCACTGAATCTCTGCTCAATGTCTGATCTTGAACGCTTTGAGAGAGAC 12006
QY 1966 ACCAAGCTGAAGGTGTGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGAGAGAGAGAT 2025
Db 12007 ACCAAGCTGAAGGTGTGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGAGAGAGAT 12066
QY 2026 GACCGGAGTTACCTGTGCACTCTTCAAGTTCAATTCAGCTCACCTGTGAAGACACAC 2085
Db 12067 GACCGGAGTTACCTGTGCACTCTTCAAGTTCAATTCAGCTCACCTGTGAAGACACAC 12126
QY 2086 TTGACCTGGCAGAACTACCTGCGAACTCAGGCGCGGTAAACAGAGAACAGTAAGTGTG 2145
Db 12127 TTGACCTGGCAGAACTACCTGCGAACTCAGGCGCGGTAAACAGAGAACAGTAAGTGTG 12186
QY 2146 ATCTGACCGTGCATACCTGCGGTGAGAGAGTGCATATGAGATCTTCACTGAGAC 2205
Db 12187 ATCTGACCGTGCATACCTGCGGTGAGAGAGTGCATATGAGATCTTCACTGAGAC 12246
QY 2206 TACTCAAGCAAGAACTGATGACCCGCGCAAGGCAATCTTCAAGGCAATGGC 2265
Db 12247 TACTCAAGCAAGAACTGATGACCCGCGCAAGGCAATCTTCAAGGCAATGGC 12306
QY 2266 GTGCTTCCCAAGATTAATCAACACCTTCATGAAATGATACAGAGAGCTTTGACAGAGAT 2325
Db 12307 GTGCTTCCCAAGATTAATCAACACCTTCATGAAATGATACAGAGAGCTTTGACAGAGAT 12366
QY 2326 CAGCAGCTTGGCTCACTCCAGGTGTGAGAGCTGTGCTGTGCTTCTGCTTCAATTC 2385
Db 12367 CAGCAGCTTGGCTCACTCCAGGTGTGAGAGCTGTGCTGTGCTTCTGCTTCAATTC 12426
QY 2386 TCCCAATGACAGACAAAGTTGTGAGACATCGTGCAGAGTGAACCTGCTGAAGAGACTC 2445
Db 12427 TCCCAATGACAGACAAAGTTGTGAGACATCGTGCAGAGTGAACCTGCTGAAGAGACTC 12486
QY 2446 CTCAATCTGCAAGAGACATGATCCCATGATGCTGTCTCAATGCTTTGAAGAGAAATGTTGT 2505
Db 12487 CTCAATCTGCAAGAGACATGATCCCATGATGCTGTCTCAATGCTTTGAAGAGAAATGTTGT 12546
QY 2506 AATGCTAACATCGGCAAGCAATGATGAGACACTGATGAAGATGAGCGCTTCCAAAGTGA 2565
Db 12547 AATGCTAACATCGGCAAGCAATGATGAGACACTGATGAAGATGAGCGCTTCCAAAGTGA 12606
QY 2566 CTGATCTGAATACTTGCACATGTTCTCAAGCTGAAGAGACTGACCTTCAGCGCCAGC 2625
Db 12607 CTGATCTGAATACTTGCACATGTTCTCAAGCTGAAGAGACTGACCTTCAGCGCCAGC 12666
QY 2626 TTCCAGAGATTTGATGCAATTAAGACGCGTGTGTGCTGCGCCAGAGACTTCAAGAGAGAA 2685
Db 12667 TTCCAGAGATTTGATGCAATTAAGACGCGTGTGTGCTGCGCCAGAGACTTCAAGAGAGAA 12726
QY 2686 ATGGAACCAAGAGAGTATTAATCTCCGAGAAATGAGATCTCTCTAGCTTGTGCTGAG 2745
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Db 12787 ACGAACCAAGACGCAAGTATGACATTCGTTTCTGCAACGTTTCCAGAGACTGCGC 12846
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Db 12847 AAGAGATCGGTTTAATTTGCGCGTGTTAATGACATTAATGTTGTGAACATATCCGAAC 12906
QY 2866 GAGCTGATGTGCAAGCTTCTGAGAGCGGCAAGTCAAGCTGAATCACTTGAAGACCA 2925
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QY 2926 TTCCCTGAGCGTATCGAGATCATGCGCGCTCAAGCGCATGAGCGTGTCTACTTGAAG 2985

Db 12967 TTCTGGCCGCTATGAGATCATGGGCGGCTCTTAAGCGCATCGAGGAGTCTACTTGAG 13026
Qy 2986 ATCAAGAGTCTAATA 3001
Db 13027 ATCAAGAGTCTAATA 13042

RESULT 6
US-11-097-143-22562
; Sequence 22562, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: C1000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22562
; LENGTH: 15606
; TYPE: DNA
; ORGANISM: DROSOPHILA
; US-11-097-143-22562

Query Match 57.3%; Score 1718.2; DB 10; Length 15606;
Best Local Similarity 73.9%; Pred. No. 0;
Matches 2236; Conservative 0; Mismatches 753; Indels 36; Gaps 3;

Qy 1 CAGTTCTCTTGTGACAGAGATGCTGACCAATCTTTGAAAGCCCAAGACATATATGAG 60
Db 9922 CAGTACTGCTGCTCAACGATATGCGGATCACTCACTGAGGCGCAGACATATATGATC 9981
Qy 61 AAAATGGAACANTGATGAGCCGACGCTAAGACATCTTAAGCGAGTGCAGACATTTGCTG 120
Db 9982 AAGATGAGAGCTGTATGCAAAATCTTGAAGACCAATTCGCGAGAGTGCAGACATTTGCTG 10041
Qy 121 GAGTCAGACAGAGCTGACAGAGGCGCGCATATCATGATGATGATGCTGCTTACTC 180
Db 10042 GAGTCGACAGACATTAAGATGCGCTCATATATGACGATGATGCTGCTGCTTACTC 10101
Qy 181 TGTTCCTATTTGCGCTTGTGTGAGCAGAGGCGCTGATTAATGTTACTCTTACTGGCGGA 240
Db 10102 TGCGCTATCTAACGTTTGTGTGCTCCAGGGAACGATTAATGTCAGTCCACAGTGGC 10161
Qy 241 AACCACTGAACATGCTGAACGCGGAACACATGAACGATCTCTCAAGAAATGTTCTGAG 300
Db 10162 AACCACTGACATGCTGAACGCGGATCAATGAATCGTTGTGCGAAATGTCTTAAA 10221
Qy 301 CTCATCAAAAAGAACATCGGCAATGAGAACGCGCGTGAATGACCCGACCTGAC 360
Db 10222 ATGATCAAGAAAGACATTTGGCAGATTAACGCGCTTGAATGATCTGCGATTTGCCCTAT 10281
Qy 361 ACGAGACGATCATCATCAACAGCTCCGAGGAATGCTGAGGAAATTCCTTCTGCGCGCTC 420

Db 10282 ACGAGACGATTTATCACTCAATACGTCGAGAGAGTGTCTCAAGATCCGTTCTTGCCCTG 10341
Qy 421 GCTGAACGTGTTCGCAACGACGAGCAATATGTTCCATTAAGAGAGAGCTTGAGGGG 480
Db 10342 GCGAGCGGTGAAAGAGCCGACCTGAGACATGCTGCAAGAGAGACAGATCTGAGGA 10401
Qy 481 TTTATTAAGTCTCAACAGACACATCCAGGTAGAGTCTCAGATACAGAAAGCTG 540
Db 10402 TTGATCAAGTCTGCGCAAGACACTTCCAGGTGAGACCCAGCTGCGAGAGAGCTG 10461
Qy 541 CAGTGTGCTGTCAGAGACATCTACTCTTTTACCCGCTGCTCATCAAGTACGTGACCTG 600
Db 10462 AATCTGCTAATGCGAGACATATCTCGTTATCTCCCTGCTCATCAAGTACGTGAGCTG 10521
Qy 601 CAGAGAACACATGCGCTCAAGAACAAATGTTCCAGAGCGGAGAGAGCTGTCAACACAGT 660
Db 10522 CAGGAAACCATGCGCTGAAAGACACATACCGAGGCGAGAGGCTCTTCAACACATGTG 10581
Qy 661 GCTGAATCTTCAACATCTGCTGAGAGAGCAGTACTTCTTGAAGAGAGAACAGACTTC 720
Db 10582 GCAAGATCTTCAATATATGTCTTAAGAGCAGTACTTCTTGAAGAGAGAGACTTC 10641
Qy 721 ATCTTCCCAACGAATTTGATTAACATGTGCTGATTAATGCAACAGCAACAGAGAGT 780
Db 10642 ATCTTCCCAATGATGATGACCAATGCGCTTGTATCTATGCAACTGCAACAGAGAGT 10701
Qy 781 ACAGCAGTAAACAGATGATCTCCCTCAAGAGT---TGAAAGAAAGAAAGAGCAGCT 837
Db 10702 GCCATCTCGAAGAGTCTCTGCTGTGAGTGGAGGATTAAGAGAGAGAGAGAGAG 10761
Qy 838 GATTAAGAAAGCGACCAAGAACAGAGAGTCAAGCGTCCCTAATGTAGTGTCTGAG 897
Db 10762 GACAAAGAGGCGGCAAGAGCAAGAGAGTCAAGCGCAGTCTGATGATGATGATGATGAT 10821
Qy 898 AGGTTGTTACGATGTCCTTAACCTATTTGCTGAGAGAGAACAGAACTGTGTACAGAT 957
Db 10822 CGCTCTTACCGGTGATGAAATCTGTTGCGCGGTGAGAGAGAGAACTGTGTGAGCAG 10881
Qy 958 TGTAAAGACAGGTTCTCGAAGAAATGTGAGAAACAGATGTGAGAAATCGCAAGAC 1017
Db 10882 TGCAAGATGCTGATCTGAGAGAGATGCCAGATGATGATGATGATGATGATGATGAT 10941
Qy 1018 CAGCTGACCTTCAGATTAATAATAGATCCGAGAGAGCAAGAAATGTCTTGGCAACTTACTG 1077
Db 10942 CAGCTGACCTTCGAGATTAAGTGAACCGTCCGAGAGAGATGATGATGATGATGATGAT 11001
Qy 1078 TATAGCAAGTTAGTTCGA-----AGAGTAAAGACATATTAAT 1116
Db 11002 TACTCAAAAGCTGGGCAAGAGAGAGAACCGGTGAGAGCAAGAGCGCTGAGAGAGGCAAT 11061
Qy 1117 GTGGAACCTGCTGAAAATAAGCCAGATTAATGATGATGATGATGATGATGATGATGATGAT 1176
Db 11062 GTTAACTCAACAG 11121
Qy 1177 ATGAGTAAAGTGTCTTTCGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 1236
Db 11122 ATGGCAAGGTTGTTGCTGCTGCAATATGATGATGATGATGATGATGATGATGATGATGAT 11181
Qy 1237 GTGTAACGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1296
Db 11182 GTCTACAGAGAGCTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 11241
Qy 1297 ACTTCACTAATCTGCGCGAGACATGAGAGGTTAATCTTTCGCTGCGAGTACTAC 1356
Db 11242 ACATGCTGATTTCTTCCAGACATGCGGCTGCAACATCTTTCGACATGATGATGATGAT 11301
Qy 1357 GAGCTCTGTTGGAAGAGAGACATTTGACAAAGAAATTAAGATTAAGATTTTACTCA 1416
Db 11302 GAGGAGTGTGCGAG 11361
Qy 1417 TCATTCAGAGAGCAGAGCTGAAG 1476

Db 11362 AGCTTCAGAGACTCCGAGAAATCCAAAGAGAGGCGAGAGACGGAACGACACGACCGGAT 11421
Qy 1477 CCCCTCAGCAGCTGGTGCACCACTTCTGTGCGGGTGCATGATGAGAGTCCGGCCT 1536
Db 11422 CCGCTACCCCACTGGTTACCACTTCTGTGCGGGTGCATGATGAGAGTCCGGCCT 11481
Qy 1537 TTGCAGAGAGTCTCTATACATGTTCTTACGCAATCATAGCAAGTCTCTGTGAGAA 1596
Db 11482 CTCGAGAGAGATCTGCTCTACATGTTCTTATGCCAGATGCGGGCAGATCCAGGGCAAG 11541
Qy 1557 GAGAGAGAGAGAGGGGGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1656
Db 11542 GAGAGAGAGAGAGGGGGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 11589
Qy 1657 GAGAGAGAGAGAGAGAGATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1716
Db 11580 GCGGAGAGAGAGAGAGATCCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 11649
Qy 1717 GCGCGGCTGGCGGAGCGTGGGGTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1776
Db 11650 GCAAGCTCTCTCCATCTGTGGCGTTGCCGAAATGGTGGTGGCACTTTCCGCTCCAA 11709
Qy 1777 GAGCTCCGAGAGAGATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1836
Db 11710 GGTATACCTTCGAGAGATGGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 11769
Qy 1837 GGCATATTTGATATACAGATGGGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1896
Db 11770 GGCACATGAGATCAAAATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 11829
Qy 1897 TTCTTTACGTCATCGCGGCTCTCATGAACTCTCTGCTGCTGCTCATCTTGAACGCTTC 1956
Db 11830 TTCTTTACGTCATCGCGGCTCTCATGAACTCTCTGCTGCTGCTCATCTTGAACGCTTC 11889
Qy 1957 GAG 2016
Db 11890 GAGCGAAACACCAAG 11949
Qy 2017 AACATGAG 2076
Db 11950 AACATGAG 12009
Qy 2077 GAG 2136
Db 12010 GAG 12069
Qy 2137 AACATGAG 2196
Db 12070 AACATGAG 12129
Qy 2197 TACTGAG 2256
Db 12130 TACTGAG 12189
Qy 2257 GGCATGAG 2316
Db 12190 GGCATGAG 12249
Qy 2317 ACAG 2376
Db 12250 ACCGCAATGAG 12309
Qy 2377 TTCTTATTTCTCCCACTGAG 2436
Db 12310 TTCTTATTTCTCCCACTGAG 12369
Qy 2437 AAG 2496
Db 12370 AAG 12429
Qy 2497 AATGTTGTTAATGTTAATGTTAATGTTAATGTTAATGTTAATGTTAATGTTAATGTTAAT 2556
Db 12430 AATGTTGTTAATGTTAATGTTAATGTTAATGTTAATGTTAATGTTAATGTTAATGTTAAT 12489

Qy 2557 AACGTGAG 2616
Db 12490 AATGTTGAG 12549
Qy 2617 AGCGGAG 2676
Db 12550 TCGGCGAG 12609
Qy 2677 AAG 2736
Db 12610 AAG 12669
Qy 2737 TGCTGAG 2796
Db 12670 TGCTGAG 12729
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Qy 2857 ATGCCGAG 2916
Db 12790 ATGCCGAG 12849
Qy 2917 TTGAG 2976
Db 12850 TTGAG 12909
Qy 2977 TACTTCGAG 3001
Db 12910 TACTTCGAG 12934

RESULT 7
US-10-668-767-9
; Sequence 9, Application US/10668767
; Publication No. US2004017114A1
; GENERAL INFORMATION:
; APPLICANT: Casper, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutierrez, Steven
; APPLICANT: Raun, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, LiHong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: B0153 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 16363
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15850)..(15890)
; OTHER INFORMATION: n = a, c, g, or t
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(15327)
; OTHER INFORMATION:
; US-10-668-767-9

Query Match 57.3%; Score 1718.2; DB 7; Length 16363;
Best Local Similarity 73.9%; Pred. No. 0;
Matches 2236; Conservative 0; Mismatches 753; Indels 36; Gaps 3;

QY 1 CAGTTCCTCTGCGTGAACAGATCGCTGACCATCTTTGGAAGCCCAAGACATATGCG 60
DB 9928 CAGTACTGCTGCTCAACCGATATGCGGATCACTACGAGAGCCGACGACATATGCTC 9987
QY 61 AAAAGGAAACATGCAATGCCGACGCTAAGACGATCTTAAGGAGAGTGAACCAATTCGTG 120
DB 9988 AAGATGGAGAGCTGATGCGCAATCTAAGACCATCTCCGAGAGTGAACCAATTCGTG 10047
QY 121 GAGTCAGACAGACGCTAACAAGAGGCGCGCATATCATGATGTGTGCTGCTTTATCTC 180
DB 10048 GAGTCGACACAGACATATGATATGCGCTCATATTTATGACGTATCTCTGCGCTGCTT 10107
QY 181 TGTCTTATTTTCCGCTCTGCTGAGGACAGGGGCTGATATGTTATCTCTAATGAGGGA 240
DB 10108 TGGCGCTATCTACCGCTTTTGTGTGTCCAGAGGACCGGATTAATGTCAATGCCACAGTGGC 10167
QY 241 AACCCGCTAACATATGCTAACAGCGGAAACATGAAACAGCTCTCTAAGAAATGTTCTGAAG 300
DB 10168 AACCCGCTAACATATGCTAACAGCGGAAACATGAAATCGGTTGCGAAATGTGCTTAAA 10227
QY 301 CTGATCAAAAAGAAACATCGGCAATGAGAACGCGCGCTGATGACCCGCGATCGCCACTAC 360
DB 10228 ATGATCAAGAAAGACATTTGGCAAGATTAACGCTTGTGATGATCTCGATTTGCCCTTAT 10287
QY 361 ACGCAGACATCATCATCAACAGCTCCGAGGAACTCTGAGAGGATTCCTTCTGCGCTC 420
DB 10288 ACGCAGACATTTATCATCAATACGTCCGAGGAGCTGCTCAAGGATCCGTTCTTGCCTG 10347
QY 421 GCTGAACGTGTTCGAAACGACGGAACAATATGTTCCATTAAGAGAGAGCTTGAAGGGG 480
DB 10348 GCGGAGCGGTGAAAGACGCACTGAGAACTGCTGCAAGAGAGGACAGCATCGAGGA 10407
QY 481 TTTATTAAGTGGTCAACAGACGACACATCCAGAGTAGATCGATACAGTAAGAAAGCTG 540
DB 10408 TTTATTAAGTGGTCAACAGACGACACATCCAGAGTAGATCGATACAGTAAGAAAGCTG 10467
QY 541 CAGCTGCTGATCAAGACATCTAATCTCTTCAACCGCTGCTCATCAAGTACGTGACCTG 600
DB 10468 AATCTGCTGATGCGAGACATATTAATCGTTATCCCTGCTCATCAAGTACGTGACCTG 10527
QY 601 CAGAGGAAACCACTGCTCAAGAACATTTCCAGAGCGGAGAGCTGTAACAACAGT 660
DB 10528 CAGAGGAAACCACTGCTCAAGAACATTAACGAGGCGGAGAGCTTCAACAACATG 10587
QY 661 GCTGAATCTTCAACATCTGATCGAAGGCGAGTACTTCTGAAGAGGAAACAGAACTTC 720
DB 10588 GCAAGATCTTCAATATATGATCTTAAGGCGAGTACTTCTGAAGAGGAAACAGAACTTC 10647
QY 721 ATCTCTGCGCAACGAATTTGATTAACATGCTGATTAATGCGAACAGCAACAGAAAGT 780
DB 10648 ATCTCTGCGCAACGAATTTGATTAACATGCTGATTAATGCGAACAGCAACAGAAAGT 10707
QY 781 ACAGACGTAACAGATGTAATCTCTCAAGTGG---TGAGAAAGAAAGAAAGACCCGT 837
DB 10708 GCCATCTCGAAGGAGTCTCTGCTGTGGGTGCAAGGTAAAGAAAGAAAGAAACAGG 10767
QY 838 GATAAGAAAGCGCAACAAAGACAGAGTCCAGAGTCCCTAAGGTAGCTTGTCTGAAG 897
DB 10768 GACAAGAAAGCGCAACAAAGACAGAGTCCAGAGTCCCTAAGGTAGCTTGTCTGAAG 10827
QY 898 AGGTGTTTACAGTGTGGCTTAATCTAATCGCTGCGAGAGAACAGAACTGCTGACAT 957
DB 10828 CGCTCTTACCGCTTGAATCTGATCTGTTGCGGGTGAAGAGAGAACTGCTGACATC 10887
QY 958 TGTAAAGACAGGTTCTGAGAGAAATGTCAAGACAAAGATGTGCAAGATTCGAGAAC 1017
DB 10888 TGTAAAGACAGGTTCTGAGAGAAATGTCAAGACAAAGATGTGCAAGATTCGAGAAC 10947
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QY 1078 TATAGCAAGTTAGTTGCA-----AGAGTAAGACCAATATTAAT 1116
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DB 11068 GTTAATCTCAACGAAAGGCGCAAGAACAAACCGAGAGACAGTGAATGCAATGTGCG 11127
QY 1177 ATGATTAAGTGTCTTTCGATTTGATATGATGACCATCTCCCAACAAATGATTAAGAC 1236
DB 11128 ATGGCCAAAGGTCTGTTTGGCTGACATATGATGACCATCAACAGACAGAGAAAT 11187
QY 1237 GTTACCGGTGCTGATGATCAACGCAAGCGCGCTGATCGCTGCTTCCGACAA 1296
DB 11188 GTTACAGAGAGCTGTGTGATGATCAAGAGAGGCTGCTAATCGCATCTTCCGACAG 11247
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DB 11248 ACATCGCTGATTTCTTACCCAGACATCGGCGCTGCAACATCTTCCGACGATGTA 11307
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QY 1477 CCGCTCAACGACGTGTGACACCTTCTGTGCGGTGCTTATGATGAGAGTCCGCGCT 1536
DB 11428 CCGCTCAACGACGTGTGACACCTTCTGTGCGGTGCTTATGATGAGAGTCCGCGCT 11487
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DB 11548 GAGAGAGAGAGAGGAGGCGGCGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 11595
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DB 11836 TTCTTAAAGTCAATGCGCGGCTCATGAACTCTGCTCGGTGCTGATCTTGAAGCTTC 11895
QY 1957 GAGAGAGACCAAGAGCTGAGAGTCTGAGGAGTGTGAGAGAGTGTGAGAGAGAGAG 2016
DB 11896 GAGAGAGACCAAGAGCTGAGAGTCTGAGGAGTGTGAGAGAGTGTGAGAGAGAGAG 11955
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DB 11956 AATGATGAGAGCGGAGTCACTGCGGACCTTCAAGTTCACTTCAAGTTCACTTGTGA 12015
QY 2077 GAGCAACATTTGAG 2136
DB 12016 GAGCAACATTTGAG 12075
QY 2137 AAGTGTATCTGACAGCTGACATCTGCTGCGGCTGAGAGAGTCAATGACATCT 2196

Db	12076	AGGTGGTCACTCTGACTGTGAGATTAATTTCCTTCGTCTGAGAGATTCATCAGACTTC	12135
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Qy	2257	GCCATTGGCGTGGCTTCCCAAGTATTCACAACCCCTCACTGAAAGTCATACAGGACCTTGT	2316
Db	12196	GCCATTCAGATGTGGCTAGCCCAAGATATTTTAAACCCCTCACTGAAATCATCAGGGTCTCTGT	12255
Qy	2317	ACGCAAGATCAGCAGGCTTTGGCTCACTCCAGGTGTGGGACGCTGTCCGTTGGTTTCTTG	2376
Db	12256	ACCTCAATCAGCAGGCTTTGGCACTCCAGGTTGTGGGATGCAATTGGTGGCTTCTCTC	12315
Qy	2377	TTCTTATTTCCCATGACAGACAAGTTGTGAAAGCACTCGTGGAGGTGACCTGTCTG	2436
Db	12316	TTCTGTTTTCCCATGACAGACAAGCTGTCAAAGCACTCCAGCMAAGTTGATCTGTCTC	12375
Qy	2437	AAGCAATCTCTCAATCTGCAAGAGACATGATCCCACTGATGCTGTCTCATGCTTTAAAGA	2496
Db	12376	AAGCAATCTCTCAATCTGCAAAAGACATATCACTGATGCTTTCATGCTGAAAGGA	12435
Qy	2497	AATGTTGTATAGGTATCAATCCGGCAAGCAATGGTGAACAACATGATGAATCCGGCTCC	2556
Db	12436	AATGTTGTATAGGTATCTATTTGGCAAGATGGTGGACCGCTGTGAGTCTGCTCAGC	12495
Qy	2557	AACGTGAACTGATCTCTGAATACTTTCGACATGTTTCTCAAGCTGAAAGACTGACCTCC	2616
Db	12496	AATGTGAGCTGATCTTTAAGTACTTTCGACATGTTTCTGAAGCTCCGCGCATTTATCGAA	12555
Qy	2617	AGCCCAAGCTTCCAGAGATTTGATGCCATTAACAACGGCTGGTGTCTGCCCAAGACTTC	2676
Db	12556	TCGCCCAAGCTTCCAGAGTGAATGAAAGACGAGGGTTGGGTGAACCCCAAGACTTT	12615
Qy	2677	AAGGAGAAATATGGAACAACGAAAGTTATATCTCCGAGAAATTCAGTCTCTCTAGCT	2736
Db	12616	AGGAGAAATATGAGAGCAATCCAGAACTACACCCGGAAGAAATGATTTCTTTGGCC	12675
Qy	2737	TGCTGCAAGACGAACCAACGACGGCAATTAGACTACATCCGTTTCTGCGACCGCTTTCAC	2796
Db	12676	TGCTGCAAGACGCAACCAAGAGGCAATATGATTAACGGGCCCTTCGTGAGGACTTCCAC	12735
Qy	2797	GAGCTTGCAGAGAGATCGGGTTTAATCTGGCCGTGTACTGATCAATCTTGTCTGAACAT	2856
Db	12736	GAACTATCAAAAGAGATCGGTTTCAACTGGCTGTGCTCTGACCAACTCCACAGCAAC	12795
Qy	2857	ATGCGCAACGAGCCTAATTTGGCACCTTTCCTGGAAGCGCAGGTTCAAGTCCGAACTAC	2916
Db	12796	ATGCGCAACGAGCCGCGCTGGCCGCTCTCTGGAAGCCCGCGCTCGGTGCTCAACTAC	12855
Qy	2917	TTGCAACATTTCTGGGCGGTATGAGATCAATGGGCGGCTTCAAGCGCATCGAGCGTGTCT	2976
Db	12856	TTGCAAGCTTCTCTGGGCGGATGAGATTTCTCGGCACTCTCAAGCGCATCGAGCGGTT	12915
Qy	2977	TACTTCAGATCAAGAGTCTTAATA 3001	
Db	12916	TACTTCAGATCAAGAGTCTGAACA 12940	
RESULT 8			
US-10-668-767-7			
/ Sequence 7, Application US/10668767			
/ Publication No. US2004017114A1			
GENERAL INFORMATION:			
/ APPLICANT: Caspar, Timothy			
/ APPLICANT: Cordova, Daniel			
/ APPLICANT: Gutierrez, Steven			
/ APPLICANT: Raub, James			
/ APPLICANT: Smith, Rejane			
/ APPLICANT: Tao, Yong			
/ APPLICANT: Wu, Linhong			
/ TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors			

	FILE REFERENCE:	BB1533 US NA
	CURRENT APPLICATION NUMBER:	US/10/668,767
	CURRENT FILING DATE:	2003-09-23
	PRIOR APPLICATION NUMBER:	60/412,795
	PRIOR FILING DATE:	2002-09-23
	PRIOR APPLICATION NUMBER:	60/427,324
	PRIOR FILING DATE:	2002-11-18
	NUMBER OF SEQ ID NOS:	149
	SOFTWARE:	PatentIn version 3.1
	SEQ ID NO 7	
	LENGTH:	15413
	TYPE:	DNA
	ORGANISM:	Peregrinus falco
	FEATURES:	
	NAME/KEY:	misc feature
	LOCATION:	(1264)
	OTHER INFORMATION:	n = a,c,g, or t
	FEATURES:	
	NAME/KEY:	CDS
	LOCATION:	(117)..(15397)
	OTHER INFORMATION:	
	US-10-668-767-7	
Query Match	52.6%	Score 1578.6; DB 7; Length 15413;
Best Local Similarity	71.2%;	Pred. No. 0;
Matches 2142;	Conservative 0;	Mismatches 829; Indels 36; Gaps 3;
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QY	61	AAAATGGAACAATGCATGCCAGCGGTAGAGCGATTTGAGGAGGTGACCAATTCG 120
DB	10073	GGAATGGAAGAATCAATGCGCAACTTTAAGCACATTTTGAAGATGATCACTTTGTA 10132
QY	121	GAGTCAGAACAGAGCTGACACAGAGCGCGCATATCATGCATGATGTGGTCTGCTTACTC 180
DB	10133	GAGTCGATTAATAACCATAACATGACCTCATATTTAGTAGTAGTAATGCAATGCTA 10192
QY	181	TGTTCTTATTTGCCGTTCTGTGTGGGCAACAGGGCGCTGATTAATGTTACTTACTGCGGA 240
DB	10193	TGCTCTATTTGCTGCTGTTGTGTGAATCAAAGACCTGATTAATGTGCTCTCACTGCCGA 10252
QY	241	AACACGTAACATGTGTAACAGCGGGAACATGAAACCACTCTCCAAGAAATGTCGAA 300
DB	10253	AATTAATGTCACACAGGTGACGAGTGAACATGTAATCACTTTAAAGATGTACTCAA 10312
QY	301	CTCATCAAAAAAGAACATCGGCATGAGAAACGCGCGGTGATGACCCGATCCCACTTAC 360
DB	10313	ATGATTAAGAAAATATTGAAATGAAAGGCTCCATGATGATGATGATGATGATGATGAT 10372
QY	361	ACGCAGACGATCATCATCAACAGCTCCGAGAACTGCTGAGGATTCCTTCTGCCGCTC 420
DB	10373	ACACACAAATTAATTAATCACTCTTGGAGAGATGTTGTAAGATGCATCTCCCATATG 10432
QY	421	GCTGAAGCTGTGGCAAAAGCAAGGCAAAATTTCCATTAAGAGAGAGAGCTTGAAGGGGG 480
DB	10433	GCTAAGAGAGTGAAGAAAGCAAGCTGATGATGATTTTCAATAAGAGGAATCACTCAGGGGA 10492
QY	481	TTTATTAAGTGTCAACAGACGACATCTCCAGGTAGCTCAGATTAACAAGAGACTGG 540
DB	10493	TTTCAATAATGCGCTCTGATGACATTTCTCAATTTGAAGCGAAATTTCAAGAAATGG 10552
QY	541	CAGCTGCTGTCAGAGACATCTAATCTCTTACCCGCTGCTCATCAATGATGCTGACCTG 600
DB	10553	CAACTCTTGTGAGATATCTACTCATTTCAATCCACTTCTCATCAAGTACGTTGACTTG 10612
QY	601	CAGAGAAACACTGCGCTCAGAAACATGTTCAGAGCGGGAAGAGCTGTAACAACAACGCG 660
DB	10613	CAAGGAATCATGTGTGAAGAAATTAATTTTGAAGCTGAAACATTTGATTAATCATGTA 10672
QY	661	GCTGAATCTTCAACATCTGTGTGAAGAGCACTTCTTGAAGAGGAAACAGAACTTC 720

Db 10673 GCAGAAATCTTCATATACCTTGGTCGAAGTCTCAATATTTCTCTCAAGAAAGAACAGAACTTC 10732
Qy ATCTGCGCAACGAATATTGATTAACATGGTGTGATTTATGCCAACAGAACAGAGAGTG 780
Db 10733 ATTCGGGGAATGAATTTGATTAATGGTTCTCATCATGCCACGGCTATCGAGGAAGT 10792
Qy 781 ACAGCATGTAACGA-----TGGTACTCTCTCAAGGTGTGTGAAGAAAAGAAAGAAC 834
Db 10793 GCCGTAGTCAAGTGAAGTGTCTCTCCCTGGAGGCAAGCGGTAAAGAAAAGAAAGAAC 10852
Qy 835 CGGTAAAGAAACGGGCAAGAAAGCAAGAGTCCAGAGTCCCTTAATGGTAGCTTGTCTG 894
Db 10853 AGAGAAAGAAAGAGGACAAAGAACAAAGCTTCAAGCAAGTAAATGATGTTGCTTGTG 10912
Qy 895 AAGAGTGTGTTACGAGTTGGCTTAACTTAATCGTGGCAGAGAACAAAGAACTGGTCAG 954
Db 10913 AAGAGCTGTCTTCCGTGGTGGTTGAATCTTTGTGTGAACAGAAACAAAGAACTGGTTAG 10972
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Qy 1255 TCGATCAACGCAAGCGCGCGTCATCGCTGCTTCGCAAACTTCACTCATTTCTGTG 1314
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Db 11378 GAGAAATTTGGAACCGAGGTTTGAATTAAGACCTCACGCAATCATTTGAAGATGTGA 11437
Qy 1435 CTGAAGAAAGATGACGTGTGAGAGAGGTGAGAACCTTGAACCCCTTCACGACGTGTC 1494
Db 11438 CTCAAGAAACAGATGAAGAAAGTGAATGAAGGAAGTGAATCCGCTGACACAGTTGTG 11497
Qy 1495 ACCACTTCTGTGCGGTGTCATGACTGAAGAGTCCGCGCTTTGGCAGAGAGATCTCTA 1554
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Qy 1555 TACATGCTTTACGCAACATCATATGCGAAGTCCGTGTGAGAAAGAAAGAGAAAGGGGT 1614
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Db 11618 GATGAAGAGAAAGAGAGAGAAAGAAACAG-----GTGCTTCAATA 11662
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Db 11663 CACGAAACAAGAAATGAGAAACAGAGCTGCTTTCATCATCAATCAAGACTGGCTAAATGA 11722
Qy 1735 GGGGTGGCCGAATGCTGTGCTGACATCTCCGCTGCAAAAGCCTGCCAGAGAGATG 1794
Db 11723 GGGGTGGCAGAGATGCTGTATTTGACATTTCCGCTTGCAATGCTGTTCAAAGTGAATG 11782

Qy 1795 GTCATGAAGACTTTACAGCTCGGTATTAATGATCTGAAGGGCGGCAATATGATATACAG 1854
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Db 11843 ATGGAAATGCTGAATCACTTAAAGAAAGAAAGATGTGGATTTTATCACTATGCT 11902
Qy 1915 GGCCTCAATGAATCTCTCTCGGTCTGATCTTGAATCTTGAAGCCCTTCGAGAGAAACCAAGCT 1974
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Qy 2455 CAGAAAGCATGATCCCATGATGTGTCCATGCTTGAAGAAATGTTTAAATGTACA 2514
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Qy 2575 AAATATCTTCAACATGTTCTTCAAGCTGGAAGACCTGACCTGACGCGCACTTCAGAG 2634
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Qy 2695 CAGAAAGATTATCTCCGAGAAATGAGTTCTCTTACCTTGTCTGCGAGAACAC 2754
Db 12683 CAAAGAGCTATACACAGAAAGAAATAGCTTATGCTGACAGTGTGTGAATTAATCAC 12742
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Qy	2935	
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Db	12923	
Qy	TCTAATA 3001	
Qy	2995	
Db	TCAATA 12989	

RESULT 9
US-10-66

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1 Sequence, Application US/10668767
2 Publication No. US20040171114A1
3
4 GENERAL INFORMATION:
5 APPLICANT: Caspar, Timothy
6 APPLICANT: Cordova, Daniel
7 APPLICANT: Gutteridge, Steven
8 APPLICANT: Rauh, James
9 APPLICANT: Smith, Rejane
10 APPLICANT: Tao, Yong
11 APPLICANT: Wu, Lihong
12
13 TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
14
15 FILE REFERENCE: BB1533 US NA
16 CURRENT APPLICATION NUMBER: US/10/668,767
17 CURRENT FILING DATE: 2003-09-23
18 PRIOR APPLICATION NUMBER: 60/412,795
19 PRIOR FILING DATE: 2002-09-23
20 PRIOR APPLICATION NUMBER: 60/427,324
21 PRIOR FILING DATE: 2002-11-18
22 NUMBER OF SEQ ID NOS: 149
23
24 SOFTWARE: PatentIn version 3.1
25
26 SEQ ID NO 5
27
28 LENGTH: 15315
29
30 TYPE: DNA
31
32 ORGANISM: Periplaneta americana
33
34 FEATURE:
35 NAME/KEY: CDS
36 LOCATION: (1)..(15112)
37
38 OTHER INFORMATION:
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40 US-10-668-767-5

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Query Match	49.6%	Score 1489.6	DB 7	Length 15315
Best Local Similarity	69.3%	Pred. No. 0		
Matches 2083	0	Mismatches 894	Indels 27	Gaps 3

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Db	10027	AGATGGAGGACATATGCTCTACTTGAAACTGTATTAATGAAAGTTGACAGATTGTC	10086
Qy	121	GAGTCAGCAAGACGTTCACAGAGGCGCGCATATCATGCATGGGCGCTGCTTACTC	180
Db	10087	GAATCAGAAAAACATATGCTGATGCACTTCACATTATGATGTATTTTACCTTTATTG	10146
Qy	181	TGTTCTTATTTGCCGTTCTGGTGGGACAAGGGGCTGTATATGTTTACTCTACTGGCGGA	240
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Qy	241	AACACGTAAACAATGGTAAACAGCGGAAACAATGAACAGCTCCCAAGATGTTCTGAAG	300
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Db	10267	TTAATTAATAAAAAATATTGGAAAGATATATGCCCTTGGATGACACAAATAGCAGCTTAT	10326

QY	361	ACGAGCAGAGTATCATATCAACAGACTCCGAGAACTCTGACGGAATTCCTTCGCGCTC	420
Db	10327	ACACACAAATTAATTAATTTCTTGAGAAAGATTATTAAGATCCATTTCTTACACTT	10386
QY	421	GCTGAACGTGTGCGAAACGCACGACAAATATGTTTCATTAAGAGAGAGCTTGAAGGGG	480
Db	10387	GCAGAAACGAGTTAAAAAAGCTACAGAAACATTATACATTAAAGAAATCATTAAGAGGA	10446
QY	481	TTTATTTAAGTCGTACACAGACACATCCCAAGTGAAGTCTCAGATACAGAAAGACTGG	540
Db	10447	TTTATATAAAATCATCTATGATGTATAGTCCCAATGGAAGCACAATATACAAAGATTGG	10506
QY	541	CAGCTGCTGTGACAGACATCTACTCCTCTACCCGCTGCTCATCAAGACGTCGACCTG	600
Db	10507	CAATTGGTGTGTAGGGAATTTATGCTTTTATCCACTCTCTATTAATAATACGTGATCCT	10566
QY	601	CAGAGAAACCACTGCTCAGGAAACAATGTTCCAGAGCGGAAGAGCTGTACACACAGTG	660
Db	10567	CAAGGCAATACCTGCTACGTATATACATATCAAAAGCTGAAGATTATATACATATGTC	10626
QY	661	GCTGAAATCTTCAACATCTGTCTGAAGAGCCAGTACTTTGAAGAGGAAGAACTTC	720
Db	10627	TCTGAATATTTAAACATTTGCTCAATCGCAATACCTTTTTCGTGAAGAACAAACTTT	10686
QY	721	ATCTCTCCCAACGAATATGATTAACATGTGCTGATTAATGCCAACAGCAACAAAGAGTG	780
Db	10687	ATATCTGCAAAATGAATATGATTAACATGATATCTTATATGCAACGGCAACTCGAGATCG	10746
QY	781	ACAGCAGATTAACAGATGTACTCCTCAAG---TGGTGAAAGAAAAGAAAGAACCCGT	837
Db	10747	GCTGTATATACGAAACTCTGTTAGAGAGGTCACTCGAAAGAAAAGAAAACACAGG	10806
QY	838	GATTAAGAAACGCAACAAGACAGAAAGTCCAAAGCTCCCTAATGATGACTTGTCTGAG	897
Db	10807	GATTAATAAACGTGCAAAAGAAAAGAAATTCAAAGCTTCAATGATGCTGTCTGTAA	10866
QY	898	AGGTTGTACCACTGTGGCCTTAACATTCCTGCTGGAAGAAACAAGATGCTGACGAT	957
Db	10867	CGATTACTGCGACGTGTATTAATTTGTTGCGCGGAAGAAACAAATAATTAATTCACAT	10926
QY	958	TGTAAAGACAGGTTCTCGAAGAAATGTGAGAAACAAGATGTGAGCAATTCGCGAAGCC	1017
Db	10927	TGCAAGATATGATTTCTTAAAAAAATGCCAGATTATGATGTATACAAATTTGTCAAAAT	10986
QY	1018	CAGCTGACACTTCGAGTAAATAGATCCGCGAGAGAAATGCTTTGGCAACTTACTTG	1077
Db	10987	CAATTGACATTAACCGATTAATTAAGACCGAGCTGAGAAATGCTCGGACGACTATTTA	11046
QY	1078	TATATGCAATTTAGGTTGGAAGAGTAAGCAATTAATCTGTGAAACTGCTGAAATTAAG	1137
Db	11047	TACTCCAAAGTTAGAGCAAAA-----AAGGAATCTGAATTTAA	11088
QY	1138	GCCAAAGTTATATATGATACCCGTGAGAGAAATGCTGCTATAGATTAATGCTTTCCGA	1197
Db	11089	CCACAACAAGTGCACGAGTAGGAGATAGATATGTGCTATGCTTAAATTTCTTATGSA	11148
QY	1198	TTGCATATGATCAACCATCCCAACAATATGATPAAGACGTGTACCCGTGTGATGTCG	1257
Db	11149	TTGCATATGATATATCTCTCAAGCTTCAAGAGAAAGCGACTTATGATCTGTGTATG	11208
QY	1258	ATTAACAACGACGCGCGCTCATCGCTGCTTCCGAAACTTCACTACATTTCTGCGCG	1317
Db	11209	ACGCAACGTAAGAGAGCGTAATTTGCTGTTTCCGAAACTCTCACTCCACCTTTGAC	11268
QY	1318	AGACATGACGCTGTACATCTTCGCTGCGACGTATAGAGGCTCGTGTGAAGAGGAG	1377
Db	11269	AGAACCCGTGATTAATATATTCGTCGTTGCTTTACGAATTTGGCTTCAAGATGA	11328
QY	1378	AACATTTGACAAGATATATATAGAAAGATCTTAATCAATCTTGCAAGACGCAAGCTG	1437
Db	11329	AATATTTGACAAGATATATATATGATTAAGATCTCAGACAAATCAATTTGAAGACGGAACTT	11388
QY	1438	AAGAAGATGACGTGTGAGAGAAAGGTGAGAACCTTGACCCCTCAGCAGACTGCTCAC	1497

Matches 2062; Conservative 0; Mismatches 915; Indels 27; Gaps 3;

QY 1 CAGTCTCTGCTGTAAGAGATGCTGCACTCTCTTGGAAAGCCCAAGACATATGAG 60
DB |||||
10243 CAATATTCATTCTTAATGATTCCTGTAGTACTATGGAAGCTCAAGATTAATGCA 10302
QY 61 AAATGGAACATATGATGCGGACGCTAGAGCATCTTAAGCGAGGTGGACCAATTCGTG 120
DB |||||
10303 AGAAGGAAGGCACTATGCCCCACTTGGAAACGATTAATTAACGAAGTTGATCAGTTATTC 10362
QY 121 GAGTCAGACAGAGCTACAGAGAGCGCGCATATCATGATGTGTGCTGCTTACTC 180
DB |||||
10363 GAATCAGAAAAACATATACAGACCGCACCATATCATGTATGATGTATTTTGCTATGTTG 10422
QY 181 TGTCTTATTTGCGGTGCTGTGGGACAGAGGCGCTGATTAATGTACTCTTACCTGAGCGGA 240
DB |||||
10423 TGTCTATCTTACCGTACTGAGGGAAGAGGTCAAGTAAATGTGCTCTTACACAGAGT 10482
QY 241 AACCACTTAACATATGTAACAGCGGACATGAACAGCTCCTCAAGATGTTCTGAAG 300
DB |||||
10483 AATCATGTCATATGTTGACTAGTGAACATATGAACCTGTCTATGAAAAATGTTTAAA 10542
QY 301 CTCTCAAAAAAGACATCGGCAATGAACCGCGCGGTGATGACCGGATCGCCACTAC 360
DB |||||
10543 TTAATTAATAAAAAATATGGGAACGATTAATGCTCTTGATGACCAATATGCAAGCTTAT 10602
QY 361 ACGCAGCATCATCATCAACGCTCCGAGAACCTGAGGAGATTCCTTCTGCGCGTC 420
DB |||||
10603 ACACAAACAATTAATTAATTAATCTTCAAGAAATTAATTAAGATTCATCTTACACATT 10662
QY 421 GCTGAACGTTTCGCAAAACGACGCAATATGTTCCATTAAGAGAGAGCTTGAAGGAG 480
DB |||||
10663 GCGGAACAGATTAAAAACGTAACAAACGTTGTAACATTAAGAAAGATTCGTTAAGAGA 10722
QY 481 TTTATTAAGTGTCAACAGACGACATCCAGGTAGAGTCTCAGATTAACAAGACATGG 540
DB |||||
10723 TTTATTAATCATCTACGACGATACATCCCAATTTGAAGCCCAATTAACAAGAAATGGG 10782
QY 541 CAGCTGCTGTCAAGACATCTACCTCTTACCCGCTGCTCATCAATAGTGTGACCTG 600
DB |||||
10783 CAATTAAGTTGTAAGGATTAATATGCAATTTTACCACTCTCATTAATAACGTGATCTT 10842
QY 601 CAGAGGAACACTGTGCTCAGAACATGTTCCAGAGCGGAAGAGCTGTACACACGCTG 660
DB |||||
10843 CAAGCAATCACTGTTACGTATAGCATATCAATATGCTGAAGATTTTATACATACGTA 10902
QY 661 GCTGAATCTTCAACATCTGTGTGAAGACGATCTTCTGAAGAGAGAACAGAACTTC 720
DB |||||
10903 TCTGAATATTTCAACATATGCTCAAAATCTCAATCTTTTACAGAAAGAACAAATCTT 10962
QY 721 ATCTTGTCCAAAGAAATTTGATTAACATGTGTGATTAATGCTCAACGCAACAAAGAGTG 780
DB |||||
10963 ATTTCTGGAAATGAATTTGACAAATGATTAATTTATGCTCAACGCTACACGAGATCG 11022
QY 781 ACAGAGTAACAGATGTACTCTCAAGG---TGTGGAAGAAAGAAAGAAAGACACCT 837
DB |||||
11023 GCTGTCAATTCAGAAATCTCGTTAGAGGATCAACAGAAAGAAAGAAAGAAAGAAAG 11082
QY 838 GATAAGAAACGCAACAAGACAGAGAGTCCAAAGGCTCCCTAATGTAGTGTCTGAAG 897
DB |||||
11083 GATAAAAAACGTATAGGAAAGAAAGAAATTCAMGCAATCTGATGCTGTCTTAAA 11142
QY 898 AGGTGTATACAGTTGGCTTAACTATTTCTGTGCAAGAACAAAGACTGTGTGACAT 957
DB |||||
11143 CGATTATTTGCGAGTTGTTAAATTTGTTGCGAAGAAAGAGCAAGAAATTAAGTTACAC 11202
QY 958 TGTAAAGACAGGTTCTGGAAGAAATGTCAAGAACAGATGTGGCAGAAATTCGCGAAGAC 1017
DB |||||
11203 TGCAGAGATAGATTTTAAAGAAAGATGCGAGCTATGACGTATACGATTTGTCAAATTT 11262
QY 1018 CAGCTGACACTTCAGATTAATAATAGATCGGCAAGCAAAATGTCTTGGCAACATTAAGT 1077
DB |||||
11263 CAATTGACATTAACGACAAATTTGAGCCAGCTGACGAATGTCTGTGCAACACTATTTA 11322

QY 1078 TATAGCAAGTTAGGTTGGAAGATGAAGCAATATACTGTGAAACTGTGAAATTAAG 1137
DB |||||
11323 TACTCAAGCTAGGAGCAAAA-----AAGGACCTCCGAAATTTAAA 11364
QY 1138 GCCAAGATTAATATGATACCGTGCAGAGAAATCGCTATAGATGAAGTCTTTTGGGA 1197
DB |||||
11365 CCTCAACAGATGACAGAGTTGCCGATATGAAATTTGTCTATAGGCTTAAAGTTCTTAAATGA 11424
QY 1198 TTGCAATATGATGACATATCCCAACAAATAGTAAAGACGTATACCGGTGCGTGTGTCG 1257
DB |||||
11425 TTGCAATGATATGATCATCTCAGCTTCAAGCAAGGCGATTTATCATACAGTTGTATCG 11484
QY 1258 ATTAACGCAAGCCCGCGCTCATGCTGCTTCCGACAACTTCACTACATTCCTGCGG 1317
DB |||||
11485 ACGCACTGAAGAGACCGTAAATGCTTTGTTCCGACAACTCTCACTCAACGCTTGAAC 11544
QY 1318 AGACATGAGCGGTAAATCTTTCGCTGCGACGTAATCAAGCTCTGGTTGGAAGAGAG 1377
DB |||||
11545 AGACACGTCAGATTAATTAATTTGTTGCTGTTTACGAACCTTGGCTTCAAGATGAA 11604
QY 1378 AACATGGAACAAGATTAATATGAAGATTTTACTAATCATTCGAAGACGACGCTG 1437
DB |||||
11605 AATATGCGCAAGAGATGATGATTAAGATCTACGCAATCGTTTGAAGACGGAACCTT 11664
QY 1438 AAGAAGAGTACGTGTGGAAGAGATGAAGAGCTGACCCCTCAGCAGCTGTGACAC 1497
DB |||||
11665 AAAAACTGACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 11724
QY 1498 ACCTTCTGTGCGGTGCCATGATCAGAGAGTCCGAGCTTTGACAGAGAGATCTCTATAC 1557
DB |||||
11725 ACCTTGTGCGAGGTGCTATGATCAGAGAGAGTGTGTCTTTAACAAGAGAACCTCTTAT 11784
QY 1558 ATGTCTTAACGACATCATATGCGAAGTCTCTGTGGAAGAAAGAAAGAAAGAGGAGTGG 1617
DB |||||
11785 ATGTCTTAATGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 11844
QY 1618 GAGGAAGGAAGGAGGAGGTGGAAGAGAGAGCTGAAGCAAGGACAGGACAGATATAC 1677
DB |||||
11845 GAAAGAGAGTTTACTGTGTATCGA-----GAAAGAGAGGCGGCGCTTATACAC 11898
QY 1678 GAACAAGAAATGAGAAACAAAGCTCTTATTCACCAAGCGGCTGTGGCGAACGTTGG 1737
DB |||||
11899 GAACAAGAAATGAGAAACAAABACGTGTGTTTACCAAGCTGATATGGCCAAACGTTGT 11958
QY 1738 GTTCCGGAATATGTGTGTCTGACATCTCCGCTCAAAAGGCTGCCAGGAGATGCTC 1797
DB |||||
11959 GTCCAGAAATGTATTTGTTACATATCACTTGCACAAAGGTATACGAGGGAATGTT 12018
QY 1798 ATGAAGACTTACAGCTCGGTATTAATATCTGAGGAGGCGCAATATTAATATCAATG 1857
DB |||||
12019 ATGAAGACGTTCAATTTGGAATCGAGATCTTACGTGTGTATTTAAGAAATTCAAATG 12078
QY 1858 GGTATGTTGAACCACTTGAAGAACAGAAAGACGTGGCTCTTATAGCTCATCGCGGC 1917
DB |||||
12079 GGTATGTTAAATCAATTTAAAGAAAGAAAGAAAGATTTTAACTTCACTGCTGTGT 12138
QY 1918 CTATGAATCTCTGCTGCTGCTGATCTTGAAGCTTTCAGAGAGAACCAAGCTGAA 1977
DB |||||
12139 TTAATGAACCTGTGCAAGGTTCTGATTTGGAACCTTTTGAAGAAATATCAAGAACGGA 12198
QY 1978 GGTCTGGGCGGAGGTGGAAGAGTGGCGGGAAGAAAGCAATGATGACAGCGGAGTT 2037
DB |||||
12199 GGTATGAGAGTGAAGTGAAGAGTGTGTGTGTGAAGAAATATGACAGATGCGGAATTT 12258
QY 2038 ACTGCGCACTTTCAAGTTCAATTCAGCTCACTGTGAAGACAACTTGAAGTGGCAG 2097
DB |||||
12259 ACGTATCTTATTCAGATTTATTCATCTGTAAGAGCAATATTTAAGATGGAACAA 12318
QY 2098 AACTTACTGCAATCTCAGCGCGGTAAACAGACAACTGGAACGTGTGATCTGTGACCGTC 2157
DB |||||
12319 AATTAATTAAGAACACAGAGGAAATACACGACTGTAAATGTGTATTTGTATACAGTG 12378

QY	2158	GACATCCGCGCGGCTCAGAGGACATCACTGACCTTACCTGACGACCTACCAACAG	2217
Db	12379	GATTTATTTACTTAGGCTTCAGGAATCTATATGGAATTTTATTTGCACTTATTCAGACAA	124338
QY	2218	GAACCTGATCGACCCCGGCGAAGCGAATCTTCTTCAAGGCCATTTGGCGCTTCCAA	2227
Db	12439	GAGCTAAATTTGACCCAGCAGGAAAAAGCAATTTCTTCAAAACCAATCGGTGAGCAACCTTA	12498
QY	2278	GTAATTCACACCCCTCACTGAAGTATACAGGACCTTGTAAGAGAAATCGACGAGGCTTGG	2337
Db	12489	GTTTTTATACGCTATCCGAAGTAAATTCAMGACCGGTGACTCAAAATCAACAGGCCCTT	12558
QY	2338	GCTCATCTCAGAGTTGTGGAGCGCTGTCCGTGGTTCCTGTCTCTATTCCTCCACATGCA	2397
Db	12559	GCTCATCTCAGATTTGTGGAGTGCCTGTGGAGGGTTTTTGTTTTGTTTTCAACATGCA	12618
QY	2388	GACAAAGTTGTGGAAACACTCGTCCGAGGTGACCTGCTGAAAGAACTTCCATATCTGCA	2457
Db	12619	GATAAATTTGAAACCAATTTAGTCAAGTGAATTTATTTGAAAGAACTTTTAAATTTTACA	12678
QY	2458	AAGGACATGATCCCATGATGCTGTCCATGCTTGAAGAAATGTTGTATATGTGACATTC	2517
Db	12679	AAAGATATGATTTACGATGATGCTGTCCATGTTGAAGAAAGAACTGTATATGGAACATTT	12738
QY	2518	GGCAAGCAATGTGTGACACATATGTAATTCGGCTTCCACGTGAATGATCTTGAA	2577
Db	12739	GGTAAACGAGTGGTTGACACTTATGTAGAAATCGCGCTCAATGTCCGATGATTTTGAA	12798
QY	2578	TACTTCGACATGTTCTCTCAAGCTGAAGACCTGACCTCCAGGCCAGCTTCCAGAGATTT	2637
Db	12799	TATTTTCGACATGTTCTCTGAACTTAAAGATTTTAACTATGTTCAACAAAGCTTTTACGAAATTT	12858
QY	2638	GATGCCAATTAACGACGCTGGGCTGCTCCCAAGACTTCAAGAGAAATGGAACAAACAG	2697
Db	12859	GACCCCAACATGATGTTGGGTATCATCCAAAGATTTTAAAGAAAAATGGAACAAACA	12918
QY	2698	AAAGATTATATCTCCGAAAGAAATGGAATTTCTCTCTAGCTTGTGCGAGCGAACACACAC	2757
Db	12919	AAAAGTTACATCGACAGGAAATGGAATTTATGTTTCAATGTTGTGAATTTATATCAAGAT	12978
QY	2758	GGCAAGTTAGCTACATCGGTTTTCTGCGACCGTTTCCACGAGCCTGCCAAGAGATCGG	2817
Db	12979	GGGAAATATGATTTACATTTGGTTTACCGACATCAATCCAGGCGCATCCAAAGAAATTTGAT	13038
QY	2818	TTTAACTTTGGCCGTGTTTACTGACTTAACTTGTCTGGAATATATGCCAACAGACTTGAATTTG	2877
Db	13039	TTTCAATCTTGGCCGTTTTTGTGTAACCTTATCAAGAACATGCGCAATGAACTTAGTTTA	13098
QY	2878	GCAAGTTTCTCGAGAGACGACAGGTTCAAGTCTGTAACATCTTGAAACCAATTCCTGGGCGGT	2937
Db	13099	ACGAGATTTCTTGAAGAACAGCTAGAGAGTGTTTGAATTTTTCAGGCAATTCCTTGGAGAA	13158
QY	2938	ATCGAGATCATGGCGGCTCCAGACGATGAGGTGTCTTACTTGAGATCAAGAGTCT	2997
Db	13159	ATTGAAATTTCTCGAGAGAAATGTAACGATATGAAACGGGTGTACTTTGAAATTAAGAAATCA	13218
QY	2998	AATA 3001	
Db	13219	AAAA	
Db	13222	AAAA	

RESULT 11
 US-10-887-553A-489
 : Sequence 489, Application US/10887553A
 : Publication No. US2005008546A1
 : GENERAL INFORMATION:
 : APPLICANT: Garza, Dan
 : APPLICANT: Li, Hao
 : TITLE OF INVENTION: Method to treat conditions associated
 : WITH OF INVENTION: with insulin signaling dysregulation
 : FILE REFERENCE: 4-33262
 : CURRENT APPLICATION NUMBER: US/10/887, 553A
 : CURRENT FILING DATE: 2004-07-08

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? PRIOR APPLICATION NUMBER: 60/485,883
? PRIOR FILING DATE: 2003-08-07
? NUMBER OF SEQ ID NOS: 1208
? SOFTWARE: FASTSEQ for Windows Version 4.0.
? SEQ ID NO: 489
? LENGTH: 15359
? TYPE: DNA
? ORGANISM: human
US-10-887-553A-489

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Query Match	25.7%	Score 771.8;	DB 9;	Length 1535;
Best Local Similarity	56.5%;	Pred. NO. 9.2e-22;		
Matches 1691;	Conservative	0;	Mismatches 1187;	Indels 117; Gaps 9;

OY	38	TGMAAGCCCAAGCATTAATGCAAAAATGGAAACAATGCAATGCGAAGCTGAGAGACAATCT	97
Db	9819	TGGGGCTCCCAACAGTGTGAGAGAAATGTGTCCGACATCCGGTGTGAGCCGCTCA	9878
OY	98	TAGCCGAGGTGAACCAATTCTGAGTCAACAAGACGTACAAAGAGCGCGGCATATCA	157
Db	9879	TGGCAGACATTGGGAGGGCTGGCCGAAATCAGTGTCCCGCTACACAGAGATGCGCATGTCA	9938
OY	158	TCGATGTGAGTGCCTTAACTCTGTCTTAAATTGACCGTTCTGTGTGGGACAAGGGGCTGT	217
Db	9939	TCGAGATCAGCTGTCCCATGTCTATGCACTTCTGTCCCGATGTGTGGAGCCGGGGCCCG	9998
OY	218	ATAATGTTACTCTACT-----GGCGGAAACACGTAAACATGTGTAAACAGCG	265
Db	9999	AGGCACCCCTTCGCGCTGCCGCTGCCGCGGCGCCCCACCTGTGACAGCTGTCACTCTG	10058
OY	266	AACACATGAACCAAGCTCTCCAGAAATGTTCTGAAGCTCATCAAAAAGACATCGGAAATG	325
Db	10059	ACCACTCAATCTCCGTCTGTGGGAAATCCTGAAATCATGTCAACAACCTGGGCATTTG	10118
OY	326	AGAACGCGCCGTGATGACCCCGCATCGCACTTACAGAGAGATCATCATCAACGCT	385
Db	10119	ACGAGGCTCTCTGAGATGAAGCGGCTGGCTGTGTGTGCAACAGCCCATTTGAGCCGTGAC	10178
OY	386	CCGAGGAATCTGTGAGGAAATCTTCTTCGCGCTCGCTGAAGTGTGTGCGAAACGCAACG	445
Db	10179	GCGCGAGCTCTGCAAGTCCCATTTATCCCACTATCGGGCGGCTGCCAAGAAGGCAAG	10238
OY	446	ACAATATGTTCCAAATGAAGAGAGAGCTTGAAGGGGGTTTATTAAAGTGTGTCAACAGACGA	505
Db	10239	GGAAGGTGTGTCCGAGAGAGAGACGTGCTGCTGAAGGCAAGGCG-----GAGG	10289
OY	506	CATCCAGATGAAGTCTCAGATACAAAGAACTGGCAGCTGTGTGACAGACATCTACT	565
Db	10290	CCGAGGAGGGCAGAGCTGTGTGTGCGGGAAGATTTCTGTGTGCTGTGCGGAGCTCTACG	10349
OY	566	CTTTTACCCGCGTCTCATCAAGTACTGACCTGTGAGAGAAACCATGGCTCAAGAAACA	625
Db	10350	CCCTGTATCCGCTGTCTATCCGCTACGTGACAAACAACAGGGCGCAGTGGCTGAAGAGCC	10409
OY	626	ATGTTCCAGAGCGGAAAGACTGTACAAACACGTGGCTGAAATCTTCAACATCTGGTCA	685
Db	10410	CGAATCCAGCGCGGAGAGAGCTGTTACAGATGTGTGGCGAGATCTTCACTACTGTGCA	10469
OY	686	AGAACCAATGATCTTCTTGAAAGAGAAACAGAACTTCACTCTGTCCCAACGAAATTGATPACA	745
Db	10470	AGTCCCAACAATTCMAAGCGCGAGAGACAAATTTGTGTGTCCAGATGATCAACAACA	10529
OY	746	TGGTGTGATTAATGACCAACGAAACAAGAAAGTGAACGACATTAACATGTGTACTCTCTC	805
Db	10530	TGTCTTCTCTGACTGCTGACAAACAAAGCAAAATGGCTTAAGCGGAGATATA-----C	10583
OY	806	AAGGTGTGGAAGAAAGAAAGAAAGCAACGTGATTAAGAAACGCAACAAGACAAGAAAG	865
Db	10584	AGTCCGATGGCTGGACCAAGAAACGCAACAAGAAAGAGCGGGGGGACCGGTACTCTG	10643
OY	866	TCCAAAGCTCTCCCTTAATGTGTAGCTGTGTCTGAAGAAGGTTTACCATGTTGGCTTAACTAT	925
Db	10644	TGCAAGCTCACTGAATCTGTGCGCAACTGAAGAAAGATGTCTTCAATCGGCTCTGAATATGT	10703

926 TCGCTGGAGAGAACAGAACTGCTGACATTTGTAAGACAGTTCCGTAAGAAATGT 985
10704 GTGCCCCCAGACCAAGACCTCATACGCTGGCCAGACCGTTTACCGCCCTGAAGACA 10763
986 CAGAACAAAGATGTGGCAGAAATTCGGAAGACCCAGCTGACATTCAGATTAATATGATC 1045
10764 CAGATGAGAGAGGTCCGGGAAATTCGACAAACCTTCACTTCAGGGAAAGGTGCAAG 10823
1046 CGGACAGAGAAATGCTTTGGCAATTAATTGTATGCAAGTTAGTTGCAAGATTAAGA 1105
10824 GCTCCCCCTCTCTGCTGGCAGATGAGCTGTACCG----- 10860
1106 GCAATATACTGTGAAACTGCTGAAATTAAGGCCAAGTTATTGATGATCCGTGAGA 1165
10861 -----GGGCGTCCCCGGGTCCGAGAGAGACCGAGTGAACCCGAGAAATCGTGCCA 10913
1166 GAATCGTGTATGATGAAAGTGTCTTTGGAATGCAATATGATGACATCCCAACAA 1225
10914 GAGTCCAGGAAGTGTCAAGCGGTGTCTACTACCTGACAGACGAGACCCCTTACAAAT 10973
1226 TGAATGAACCTGTACCGGTGTGTGTGATACAAAGCAAGCGCCCGCTCATGCGCT 1285
10974 CTAAAGAGCGGTGTGGCACAAGCTTTTGTCCAAACAGCGCGGCGGCAATCGTGGCT 11033
1286 GCTTCGCAAACTTCACTACATTTCTGTGCGAGACATGAGCGGTGATCATCTTCGCTC 1345
11034 GTTTCGATATGACGCGCCCTGTACAACTGTCCACGACCGGCAATGTAACTATGCTGG 11093
1346 GCACTGATCTACGAGCTGTG---TTGGAAGAGAGAAACATTTGCAAAAGTATGATAG 1402
11094 AGAGCTACAAAGCTGTGATGATCTGTGATGAGAACCAAGTTTGAAGACCGCAGTAG 11153
1403 AAGATCTTACTCATATTCATTCGAAAGCAGAGCTGAAGAGATGACGTGTGAGAGAG 1462
11154 ATGACCTT-----TCAAAAGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 11204
1463 GTGGAAGACCTGACCCCTCAGCAGCTGTGACCACTTCTGTGCGGTGACAGATG 1522
11205 AGAAGAACCCAGACCCCTCAGCAGGTGTGTCTGTCACTTCAAGCCGCACTGCTGAGCG 11264
1523 AGAGGTCCGCGCTTTGCGAGAGATCTCTATATGATGTTTACGCAACATCATAGCGA 1582
11265 ABAAG---AGCAAACTGTATGATGATTACTGTATATGCGCTATGTATATCATGGCAA 11321
1583 AGTCTGTGAG 1642
11322 AGAGCT-----GCCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 11354
1643 CAGAGGCTGAAAGACAGAGCAGAGCGCATGATACAGAACAAAGATGAGAAACAAAGC 1702
11355 GTGAAGCTGAAAG 11414
1703 TCCATTTCCACCAAGCGCGCTGTGCGAGACCGTGGGGTTGCGGAATGGTGTGCTGACA 1762
11415 TCTTTACAG 11474
1763 TCTCCGCTCCAAAGCGCTGCCAGAGAGATGATGAAGACTTTACAGCTCGGTATTA 1822
11475 TCAAGGCTGCAAG 11534
1823 GTATATCTGAG 1882
11535 CCATCTCTCAATGAG 11594
1883 AGAAG 1942
11595 AGAAG 11654
1943 ATCTTGAAGCTTTCAG 2002
11655 ATCTCAATGCTTTGAG 11714

2003 CGGCG-----GAG 2044
11715 GCACTGTCAATATGCGAG 11774
2045 CACTTTCAGATTCAATGACTACCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2104
11775 ACTGTTCCTCAATGCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 11834
2105 TGGAG 2164
11835 TACGAG 11894
2165 TGCTGCGGCTGAG 2224
11895 TCTGCGGCTGAG 11954
2225 TCGACCGGCGGAG 2284
11955 TTGAAG 12014
2285 ACACCTTCACTGAG 2344
12015 ACAGCTTCACTGAG 12074
2345 CCAGGTTGAG 2404
12075 GTGCGATATGAG 12134
2405 TGTGAAAGACTGTGCGAG 2464
12135 TCGCTCAG 12194
2465 TGATCCCAAG 2524
12195 TGTGTGAG 12254
2525 AATGTGTGAG 2584
12255 AGATGTGTGAG 12314
2585 ACATGTGTCTCAAG 2644
12315 ACATGTGTCTCAAG 12374
2645 ATTAAG 2704
12375 ATCCCGGTGCTCATCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 12434
2705 ATACTCCGAG 2764
12435 TCAAGCGTCCAG 12494
2765 TAGACTACATCGGTTTCTGCGACCGTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2824
12495 TCACTGAG 12554
2825 TGGCGGTGTTACTGATTAATCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2884
12555 TGGCGGTGTTACTGATTAATCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 12614
2885 TCTGAG 2944
12615 TCTGAG 12674
2945 TCATGAG 2999
12675 TCATGAG 12729

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 4960
LENGTH: 15359
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIMILAR
LOCATION: (131)..(15244)
OTHER INFORMATION: 100% homologous to Homo sapiens skeletal muscle ryanodine
OTHER INFORMATION: receptor, accession number U48508, Smith-Waterman Score=26424.
US-10-450-763-4960

Query Match 25.7%; Score 771.8; DB 9; Length 15359;
Best Local Similarity 56.5%; Pred. No. 9.2e-222;
Matches 1691; Conservative 0; Mismatches 1187; Indels 117; Gaps 9;

QY 38 TGAAGGCCAAGACATTAATGCAAAAATGAAACATGATGCCAGCTGAACGATCT 97
DB 9819 TGGGGCTTCCCAACAGTGTGAGAGATGTGTCCGACATCCCGGTGTGAGGGCTCA 9878
QY 98 TAGCGAGAGTGAACCAATTCGTGAGTCAAGAACGTACAGAGCGCGCATATCA 157
DB 9879 TGGCAGACATTGGGGGGGCTGGCCGAGTCAAGGTGCCCGCTACAGAGATGCGATGTCA 9938
QY 158 TCGATGTGTGCTGCTTACTCTGTCTTATTTTGGCGTTCTGTGGCAGAGGGCTGTG 217
DB 9939 TCGGATACACGCTGCTCCATGTCTATGCAAGCTACCTGCCGATGTGGAGCGCGGGCCG 9998
QY 218 AATAATGTTACTCTACT-----GGCGGAAACAGTAACAATGTGTACAGCGG 265
DB 9999 AGGACCCCTTCGCGCTGCCCGCGCGCCCCCAACCTGTGACAGCTGTCACTCTG 10058
QY 266 AACCATGAACAGCTCTCTCAAGATGTTCTGAAGCTCATCAAAAAGAACATCGGCATG 325
DB 10059 ACCACCTCACTCTGCTGGGGAATTCGTGAATATCATGTCAACAACCTGGGCAATTG 10118
QY 326 AGAAGCGCGGTGATGACCGCATCGCACCTTACAGCAGCAGATCATCAACAGCT 385
DB 10119 ACGAGGCTCTCTGATGAAAGCGGCTGTGTGTGCAACGCCATGTGTGAGCGGTGAC 10178
QY 386 CCGAGGAATGCTGAGGGATTCCTTCCGCGCTCGGACGATGTTGCGAAAGCAAGCGG 445
DB 10179 GGGCGAAGCTCTGATGCCATTCCTTCACTCACTATCGGGCGCTGGCAAGGGGAG 10238
QY 446 ACAATATGTTCCATTAAGAGAGAGCTTGAAGGGGTTTATTATGCTGTCAACAGACCA 505
DB 10239 GGAAGGTGTGTCCAGAGAGAGAGCGCTGCGCTGAGAGGCCAAGGCG-----GAGG 10289
QY 506 CATCCAGGTGATGATCTCAATACAGAAAGCTGGCAGCTGTGCTGACAGACATCTACT 565
DB 10290 CCCAGAGAGGAGAGCTGTGTGTGGGAGCGAGTTCTGTGTCTGTGCGCGGACCTTACG 10349
QY 566 CTTTCTACCGGCTGTATCAAGTACGTGACCTGCGAGAGAAACATGGGTCTGAGAA 625
DB 10350 CCTGTATCCGCTGTATTCGCTACGTGACAAACAAGGGCCGAGGTGACGAGC 10409
QY 626 ATGTTCCAGAGCGAAGAGCTGTACACACAGTGTGAATTTCAACAATCTGTGTGA 685
DB 10410 CGAATCCAGGCGGAGAGAGTGTTCAGAGATGTGGGAGATTTTCACTACTGTGTCA 10469

QY 686 AGAGCCGTAATCTTCTTGAAGAGGAACAGACTTCACTCTGCCAACGAATTTGATACA 745
DB 10470 AGTCCCAACATCTTCAAGCGGAGAGCAAACTTTGTGTCCAGAAATGATACAAACA 10529
QY 746 TGTGCTGATTTATGCCAAGCAAGCAAGAAAGCTGACAGATTAACATGTGTACTCTC 805
DB 10530 TGTCTTCTGACTGCTGACCAACAAAGCAAAATGTGTTAAGGGGAGATTA-----C 10583
QY 806 AAGGTGTGAAAGAAAGAAAGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 865
DB 10584 AGTCCGTGTGCTGGACACAGAAACGACCAAGAAAGAGCGCGGGGAGACCGGTACTCTG 10643
QY 866 TCCAGAGCTCTCAATGT 925
DB 10644 TGCAGAGCTCATGTATGT 10703
QY 926 TCGGTGGCAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 985
DB 10704 GTGGCCCAACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 10763
QY 986 CAGAACAGATGTGTGCAAGATTCGCAAGAACCCAGCTGACATTTCCAGATTAATGATC 1045
DB 10764 CAGATGAGAGGTCCGGGAATTTCTGCAACAACCTTCACTTCAAGGAAAGTGTGAG 10823
QY 1046 CCGCAGCAAGAAATGTCTTGCAACATTTCTGTATGCAAGTTAGTTGCAAGATTAAG 1105
DB 10824 GCTCCCGCTCTGCGCTGGCAGATGAGCTTGTACG----- 10860
QY 1106 GCAATTAATCTGTGAACCTGTGAAGAAATGAAGCCAAAGATTAATGATACCGTCA 1165
DB 10861 -----GGCGCTCCGGGTGCGAGAGAGAGCCCAATGACCCGGAATGTGCGCA 10913
QY 1166 GAATGTGTGTATGATGAATGAATGCTTTTGGATGTGATGATGACATCCCAACAA 1225
DB 10914 GAGTCCAGAAAGTGTGACCGCTGTCTTACTTACCTGACCAAGACCACTTACAAAGT 10973
QY 1226 TGAATGAAGACGTGTACCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1285
DB 10974 CTAAAGAGGCGGTGTGCAACAGCTTTTGTCCAAACAGCGCCGCGGGGAGTGTGGCT 11033
QY 1286 GCTTCCGAACAACTTCACTACATTTCTGTCCGAGCATGAGGGGTGAACCTTGTGCTC 1345
DB 11034 GTTTCGTGTAGACGCCCTGTACACCTGTCCACGACCGGGCATGTACATGTTCTGTG 11093
QY 1346 GCACTACTACGAGCTGTG---TTGAAGAGAGAACTTGAACAAGATATGATAG 1402
DB 11094 AGAGCTTAAAGGTGTGATGTATCTGATGAAACCAAGTTTGAAGACCGCATGATAG 11153
QY 1403 AAGATCTTACTCAATCATTTGAAAGACGAGACTGAAGAAAGTGAACGTGTGTGAAG 1462
DB 11154 ATGACCTT-----TCAAAAGCTGGGAGAGCAAGAGAGAGAGAAAGAGTGTGAAG 11204
QY 1463 GTGAGAAAGCTGACCCCTTCAAGCAGCTGTGTCAACCTTCTGTGCGGGTCCATGCTG 1522
DB 11205 AGAAGAGCCAGACCCCTTGTACAGCTGTGTCTGTGACCTTCAAGCCGACCTGTAGCG 11264
QY 1523 AGAGGTCCGCGCTTTGACAGAGAGATCTTATACATGTCTTACGCAACATCATAGCG 1582
DB 11265 AAAAG---AGCAAACTGTATGAGATTACTGTACATGTGCTGTATCATGTGCA 11321
QY 1583 AGTCTGTGTGAAGAAAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1642
DB 11322 AGAGCT-----GCCACCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 11354
QY 1643 CAGAGCTGAAG 1702
DB 11355 GTAAAGCTGAAG 11414
QY 1703 TCTTATTCACCAAGCGCGCTGTGCGAACCGTGGGGTTGCCAAGATGTGTGTGTGTGT 1762
DB 11415 TCTTGTACAG 11474
QY 1763 TCTCCGCTTCAAAGGCTGTGCCAGAGAGATGTATGAAGCTTTACAGCTCGGTATTA 1822

Db 11475 TCAGGCTCTGCAAGAGAGACAGGTCATGTGTCTCCACCTCGAAGCTGGCATCT 11534
Qy 1833 GATATCTGAGGGGCGGCATATTTGATATACATAGGATATGTTGAACCACTTGAAAGCA 1882
Db 11535 CCATCTCTCATATGAGGCAATGCTGAGTCCAGCAGAAATATGCTGATATATCTTAAAGCA 11594
Qy 1883 AGAAAGAGTGGGCTTCTTTACATGTCATGCGGGCTCATGAACTCTGCTCGTGTG 1942
Db 11595 AGAAGAGATTTGGCTTCTTCCAGAGATATCAGGCACTGATGCAAAATATCAGGCTCTGG 11654
Qy 1943 ATCTTGAAGCTTTCGAGAGAAACCAAGGCTGAAAGTCTGGGCTGTGAAAGTG 2002
Db 11655 ATCTCAATGCTTTTGAAGAGCAAAACAGGCGGAGGCTGGGCAATGGAATGAGATG 11714
Qy 2003 CGGCG-----GAGAGAGAAATGATGATACCCGAGTTCACTCG 2044
Db 11715 GCATCTGATCAATCGCCAGAACGAGAGAAAGTCAATGCGGATGATGATTCACACAG 11774
Qy 2045 CACTCTTCAAGTTCAATTCAGCTCACCTGTGAAGGACACAACTTGAGCTGGCAGATCAC 2104
Db 11775 ACCTGTTCCGATTTCTACATTTGCTGTGAGGGGCAATATATGTTTCCAGAACTACC 11834
Qy 2105 TCGGAATCAGGCGCGTAAACAGACAAACAGTAAAGTGTCTATCTGACCGTCACTACC 2164
Db 11835 TACGACACAGACAGGAAACAGACCACTATTAATCATCATTTGCACTGTGCACTACC 11894
Qy 2165 TGTGCGGCTGCAAGATCTCATATGAACTTTACTGCGCACTACTCAAGACAGAACTGA 2224
Db 11895 TCTCTCGGCTGCAAGATCTCATACAGCACTTACTGTGATCACTCGGCAAGAGATGCA 11954
Qy 2225 TCGAACCGGCGGCAAGGAACTTCTCAAGGCAATGGGCGGCTTCCAGATTTCA 2284
Db 11955 TTGAAGAGAGGCGCAAGAGAACTTCTCAAGGCAATGGGCGGCTTGAAGAGTGTCTCA 12014
Qy 2285 ACAACCTCACTGAAGTCAATACAGGAACTTTGATCGCAAGATGAGAGGCTTTGGCTCACT 2344
Db 12015 ACAGCTCACTGAATCAATCCAGGGGCTCTGCAAGGAGAAACAGAGAGGCTGGGCACTA 12074
Qy 2345 CCAAGTTTGGGACGCTGTGGGTGTTCTGTCTCTATTTCTCCCATGACAGAACAT 2404
Db 12075 GTGCGCTATGAGGACCAAGTGTGGGATTCCTGCACTGTTCGCCCACTGAAGATGAAGC 12124
Qy 2405 TGTGAGAGCACTGCTGCAAGTGAACCTGTGAAGAACTCTCTCAATCTGCAAGAGACA 2464
Db 12135 TCGCTCAAGACTCAAGCCAGATCGAGCTGCTGAAGAGCTGTGATCTGCAAGAGACA 12194
Qy 2465 TGATCCCAATGATGCTGTCATGCTTGAAGAAATGTTGTAATGATCAATCGGCAAGC 2524
Db 12195 TGGTGGTGAATGTTGCTGTGCTGCTAATGAAGGAACTGTGTAACGGCATATCGCCGCG 12254
Qy 2525 AAATGGTGAACACTAGTGAATGGGCTTCAAGCTGGAACCTGATCTGAATATCTTG 2584
Db 12255 AGATGGTGAACATGCTGTGAGATCTTCAATATGTAAGATGATCTCAAGTCTTCTG 12314
Qy 2585 ACATGTTCTTCAAGCTGAAGACCTGACCTCAAGCGCCAGTTTCAAGAGATTTGATGCA 2644
Db 12315 ACATGTTCTTGAACCTCAAGGACATTTGGGCTCTGAAGCTTTCAGAGCTACGTAACG 12374
Qy 2645 ATAAAGACGCTGGGCTGCGCCCAAGACTTCAAGAGAAATGGAACAAAGAGATTT 2704
Db 12375 ATCCCGTGGCTCATCTCCAAAGAGACTTTCAGAGGCACTGAGACGCGAGAGCAT 12434
Qy 2705 ATACTCCCGAAGAAATCGAGTTCTCTAGCTTGTGAGAGCAACACAGCGCAAGT 2764
Db 12435 TCAGCGGCTCAAGAAATCCAGTTCTGTCTTGTGCTCCGAAACGAGATGGAAGCAAGTA 12494
Qy 2765 TAGACTCAATCGTTTCTGCGACCGTTTCAAGAGCTGCGCAAGAGATCGGGTTAAT 2824
Db 12495 TCAACTGCGAAGATTCGCAACCGCTTCAAGAGACAGCAACGCACTCGGCTTCAAG 12554
Qy 2825 TGGCGGTGTTACTGACTAATCTGTCTGAACATATGCGCAACGAGCTATGATTTGACGTT 2884

Db 12555 TGGCGGTGCTGACCAACTGTGAGCATGTCGCGCATGACCTTCGCTGCAACT 12614
Qy 2885 TCTGAGAGAGGCAAGTTCACTCCGAACTACTTCAACCAATTCCTGGGCGGATTCGAGA 2944
Db 12615 TCTGAGACTGGCGAAGACATCTTGAATGTAATTCGCGCCCTTACTGGGCGCATTCGAGA 12674
Qy 2945 TCATGGGCGGCTCCAAAGCAGCTGATGCTTCTGAGATCAAGAGATCTTA 2999
Db 12675 TCATGGGCGGCTCAACGCGCATTCGAGGCGCATCTTCTGAGATCTCAAGAGCAAA 12729

RESULT 13
US-10-276-774-500
; Sequence 500, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Yang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 500
; LENGTH: 15359
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-500

Query Match 25.7%; Score 770.2; DB 7; Length 15359;
Best Local Similarity 56.4%; Pred. No. 2.8e-221;
Matches 1690; Conservative 0; Mismatches 1188; Indels 117; Gaps 9;

Qy 38 TGAAGCCCAAGACATTAATGCAAAATGGAACAAATGATGAGCGGACGTAGACGATCT 97
Db 9819 TGGGCTCTCCCAACAGTGTGAGAGAGATGTTCCGACATCCGATGTGAGCGGCTCA 9878
Qy 98 TAGCGAGGTGGAACCAATTCGTGAGTCAACAAGACGTACAAAGAGCGCGGATATCA 157
Db 9879 TGGCAGACATTTGGGGGCGTGGCCGATCAGGTGCCCCGTACACAGAAATGCGGATGCA 9938
Qy 9939 TCGAGATCAAGCTGCCCATGTATGACAGCTACTGCCCCGATGAGTGGAGCGCGGCGG 9998
Qy 218 ATATATGTTATCTCACT-----GCGGAAACCAAGTAAACATATGTAACAGGG 265
Db 9999 AGGCAACCCCTTCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCACTCTG 10058
Qy 266 AACCATGAACCAAGTCTCTCAAGATGTTTGAAGCTCATCAAAAAGAACATCGCAATG 325
Db 10059 ACACCTCAATCTCTGTTGGGAAATATCTGAAGATATGTCAACAACTCGGGCAATG 10118
Qy 326 AGAAGCGCGGTGAATGACCCGCAATCGGCACTTCAACGAGCAATCATCAACAGCT 385
Db 10119 ACGAGGCTCTCTGATGAAAGGGGCTGGCTGTGTTGCAACAGCCCATGTGAGCGGTGCA 10178
Qy 386 CCGAGGAATGCTGAGGATTCCTTCCCTGCGCGCTGCTGGAACGTTTTCGAAAGGCAAG 445
Db 10179 GCGCGAGCTCTTGAAGTCCCACTTCACTCAATCAGTATCGGCGGCTGCGCAAGAGG 10238
Qy 446 ACAATATGTTCAATTAAGAGAGAGCTTGAAGGGGTTTATTAATGCTCAACAGACGA 505
Db 10239 GGAAGTGTGTCGAGAGAGAGAGAGAGCTGGGCTCTGAGAGCCAAAGCG-----GAGG 10289
Qy 506 CATCCAGTGAAGTCTCAATCAAGAAAGCTGAGAGCTGCTGCTCAAGACATCTACT 565
Db 10290 CCGAGAGGGGAGAGCTGTGCTGGGAGAGAGTTCTGTGCTCTGCGGAGACCTTACG 10349

OY 566 CTTTCTACCCGCTGCTCATCAAGTACGTGACCTGCAAGAGAACCACTGGCTCAGAGACA 625
DB 10350 CCTGTATTCGCTGTCTCATTCGCTACGTGAGCAACAAGCGCGAGTGGCTGACGAGGC 10409
OY 626 ATGTTTCCAGAGCGGAGAGAGCTGTACAAACACGTGGCTGAAATCTTCAACATCTGTGTGA 685
DB 10410 CGAAATCCCAAGCGCGAGAGAGCTGTACAGGATGTGTGGCGAGATCTTCACTTACTGTGTCA 10469
OY 686 AGAGCAGTACTTCTTGAAGAGAGAACAACTTCACTGTGCGCAAGAAATTTGATACA 745
DB 10470 AGTCCACAACCTTCAAGGCGGAGAGAGAACTTGTGTGTCCAGATGAGTCAACAACA 10529
OY 746 TGTGTCTGATTTATGCGCAACAGCAACAAGAGTGAACAGACGTAAACATAGTGTACTCTC 805
DB 10530 TGTCTTCTGTACTGTCTGACAAACAAAGGAAATGTGCTAAGCGGAGATATA-----C 10583
OY 806 AAGGTGTGAGAAAGAAAAGAAAGAACCGGTATAGAAAACGCGACAAAGACAAAGAGAG 865
DB 10584 AGTCCGATGGCTCGGACCAAGAACCGCACCAAGAAAGACGCGGGGGGACCGGTACTCTG 10643
OY 866 TCCAGCGTCCCTATATGTAGCTTGTCTGAAGAGTTTATACAGTTGGCTTTAACTAT 925
DB 10644 TGCAGACGTCACTGATCGTGGCACACTGAAGAAAGATCTGCGCCATGCGCTGATATGT 10703
OY 926 TCGCTGGCAGAGAACAAAGACTGTGACAGATTGTAAAGACAGGTTCTTGAAGAAAATGT 985
DB 10704 GTGCGCCCAACCGAACACACCTCATCAGCTGGCCAAACCGCTTATCCGCTGAAAAGACA 10763
OY 986 CAGAACAAAGATGTGGCAGAAATTCGCGAAAGACCAGCTGACACTTCCAGATAAATAGATC 1045
DB 10764 CAGATGAGAGAGGTCCGGGAATTTCTGCACAAACACTTCACTTCAAGGAAAGGTCCGAMG 10823
OY 1046 CGGACAGAGAAATGTCTTGGCAACATTACTTGTATAGCAAGTTAGTTTGAAGAGTAA 1105
DB 10824 GCTCCCGCTCTCTGGCTGGCAGATGCGCTCTGTACG----- 10860
OY 1106 GCAATATATACTGTGAAAATCTGCTGAAAATAAGGCCAAGATTATGATGATACCGTCCAGA 1165
DB 10861 -----GGGGGTCCCGGGGTGGCGAGAGAACGCCAGTAGCCCGAGAAAATCGTGGCCA 10913
OY 1166 GAATGCTGTCTATGTGTAAGTGTCTTTTGGATTGCAATATGATGACATCCCAACAA 1225
DB 10914 GAGTTCAGAGAAAGTGCACGCCGTCTTACTACTGTGACCAAGACCCAGACCCCTTATCAAGT 10973
OY 1226 TGAGTAAAGAAAGTGTACCGGTGCGTGTGTGATACAAAGCAAGCGCGCTCATTCGCT 1285
DB 10974 CTAAAGAAAGCGGTGTGGCACAAGCTTTGTCCAAACAGCGCGCGGGCAAGTCTGTGGCT 11033
OY 1286 GCTTCCGACAAACTTCACTACATTTCTGCGAGACATCGACGCTGTAAACATTTCTGCTC 1345
DB 11034 GTTTCCTGTATGACGCGCTGTATCAACCTGCCAAGCACCGGGCAATGTAACTGTTCCTGG 11093
OY 1346 GCACTACTACGAGCTCTGG---TTGAAAGAGAGAACATTTGGACAAAGTAATGATAG 1402
DB 11094 AGAGCTACAAAGCTGTGATGTCTGTACTGAAGACCAAGTTTGAAGACCGCATGATAG 11153
OY 1403 AAAGTCTTACTCAATTCATTCGAAGCGCAGAGCTGGAAGAAGAGTGTGTGAGAGAG 1462
DB 11154 ATGACCTT-----TCAAAAGCTGGGAGACAGAGAGAGAGAGAGAGAGGTGAGAG 11204
OY 1463 GTGAGAACCTGACCCCTCAACGACAGCTGTCAACCACTTCTGTGCGGGTCCCATCTG 1522
DB 11205 AGAAGAAACCAAGACCCCTGTGACACAGTTGGTCTGTGCACTTCAAGCGCACCTGCCCTGACGG 11264
OY 1523 AGAGGTCCGGCGCTTGTGACAGAGGATCTTATACATGTCTTACGCAACATCATAGCGA 1582
DB 11265 AAAAG---AGCAAACTGGATGGATTACTGTATCATGGCTTACTAGTGTGCAA 11321
OY 1583 AGTCTGTGTGAGAAAGAGAGAGAGGGGGTGGGAGAGAGAGAGAGGGGGTGTGAGAG 1642
DB 11322 AGAGCT-----GCCACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 11354

OY 1643 CAGAGCTGAAGACGAAGCAGAGCCAGTATACAGAACAAAGAAATGAGAAAACAAAGC 1702
DB 11355 GTGAAGCTGAAGAGAGAGTGTGAAGTCTCTTTGAGAGAAAACAGATGAGAGAGAGAGC 11414
OY 1703 TCTAATTCACCAAGCCCGCTGGCGGACCGTGGGGTTGCCGAAATGTGTGTGTGCA 1762
DB 11415 TCTTGTACAGCAGACACCGCTGTACACCGGGGGGGGGCGAGATGTCTGTGAGATGA 11474
OY 1763 TCTCCGCGTCAAAAGGCTGCCAGAGAGTGTGATGAAGACTTTACAGCTCGGTATTA 1822
DB 11475 TCAGTGCTGTGAAGAGAGAGACAGGTGCATGTGTCTCTCAACCTTAAGCTGGGACTCT 11534
OY 1823 GTATATCTAGAGGGCGCAATATTGATATACAGATGGGTATGTGAACCACTTGAAGACA 1882
DB 11535 CCATCTCTCAATGTGAGCAATGTGTGAGGTCCAGCAGAAAATGTGTGAAATTATTAAGACA 11594
OY 1883 AGAAAGCGTGGGCTTTTAACTCCATGCGCGGCTCATGAACCTCTGCTCGGTGTG 1942
DB 11595 AGAAGAAATTTGGCTTTCAGAGTATCCAGGCACTGAATGCAAACATGCAAGCGTCTTG 11654
OY 1943 ATCTGAAGCTTTCAGAGGAAACCAAGGCTGAAGGTCTGGGCGTGGAGAGTG 2002
DB 11655 ATCTCAATGCTTTGAGAGACAAAACAGGCCCGAGGGCTGGGCAATGTGAATGAGAGATG 11714
OY 2003 CGGCG-----GAGAGAAAGAACATGATGACGCCAGTTCACCTGCG 2044
DB 11715 GCATGTATCAATTCGCCAGAACGAGAGAAAGGTCAATGGCGAATGATGAATTCACACAG 11774
OY 2045 CACTCTTCAGATTCAATTCAGCTCACTGTGTGAAGACAACTTGGACTGGCAGAACATACC 2104
DB 11775 ACCGTGTCGCAATTCATCAATTTCTCTGTAGAGGGCACAAATTAATGATTTCCAGAACTAAC 11834
OY 2105 TGCACATCAGGCGCGGTACACGACAAACAGTGAACGTGTATCTGCAACGCTGCATACC 2164
DB 11835 TAGGACACAGACAGGAGAACGACACATTAATCATCATTTGTGACGTGTGACATACC 11894
OY 2165 TGCTGCGGCTGCAGAGATTCATCATGTGACTTTCATGCGCACTACCTCAAGCAAGACATGA 2224
DB 11895 TCTGCGGGCTGCAGAAATTCATCAGCGACTTATCTGTACTCTGCGGCAAGGATGTCA 11954
OY 2225 TCGACCGGCGCGGCAAGCGAACTTCTTGAAGCCATTTGGCGTGGCTTCCCAAGTATTA 2284
DB 11955 TTGAAGACAGGGCAGAAAGAACCTTCCAAACCAATGTGGGTCTTAAGCAGGTGTCA 12014
OY 2285 ACAACCTCACTGAAGTATCAAGGAGACTTGTACGCAAGATACAGAGGCTTTGGCTCACT 2344
DB 12015 ACAGCTCACTGATGATCATCAGGTTCTGTGCACCGGAAACAGCAGAGAGCTGGCGACA 12074
OY 2345 CCAAGTTTGGGACGCTGTGGTGTCTGTCTTCTTATTTCTCCACATGCAAGACAAGT 2404
DB 12075 GTGCGCTATGGGACGCAGTGTGGGATTCCTGTGACGHTGTTCCGCCACATGATGATGAAGC 12134
OY 2405 TGTGCAAGCACTGTGCGCAGAGTGAACCTGTGAAGGAACCTCTCAATTTGCAAGAGACA 2464
DB 12135 TCGCTCAGACCTCAAGCCAAATGAGCTGTGAAGAGCTGTGAGATCTGCAAGAGGACA 12194
OY 2465 TGAATCCCATGATGTCTGTCACTGTGAAGAAATGTTGTAATGTGAACATCGGCAAGC 2524
DB 12195 TGGTGTGATGTGTGTGTCTGTACTGTAGAGGAAACGTGTGAACCGGCAATATGCGCCGGC 12254
OY 2525 AAAATGTGACACACTAGTAAATCGGCTTCAACGTGAACTGATCTGAAAATCTTGG 2584
DB 12255 AGATGTGTGACATGTGTGTGAATTCATTCATGATGTGAGATGATCTCAAGTTCTTGG 12314
OY 2585 ACATGTCTCTCAAGCTGAAGACCTGACCTTCAGCGCCAGCTTCCAGAGATTTGATGCCA 2644
DB 12315 ACATGTCTCTGAACCTCAAGAGAAATGTGTGGCTCTGAAGCTTCCAGGACTTACGTAAACGG 12374
OY 2645 ATAAAGCGGCTGGGTGCTGCCAAGGACTTCAAGAGAAATGGAACAACAGAAAGTT 2704
DB 12375 ATCCCGGTGGCTCATGTCTCAAGAGAGACTTTCCAGAAAGGCAATGACAGCAGAGAGCT 12434
OY 2705 ATACTCCGAAGAAATGCAATGATCTCTTACTTGTCTGCGAGACGAACAGACGGCAAGT 2764

Db 12435 TCAGCGGTCCAGAAATCCAGTTCCCTGCTTCGTCGCCAAGCGGATGAGAACGAATGA 12494
Qy 2765 TAGACTATATCGGTTTCTGCGACCGTTTCCAGACCTGCGCAAGAGATTCGGTTTACT 2824
Db 12495 TCACATGCGAAGAGTTCCGCAACCGCTTCCAGAGACCGACGCGACATCCGCTTCAACG 12554
Qy 2825 TGGCGGTGTTACTGACTAATCTGTCTGAACATATGCGCAAGAGCGCTAGATTGCGACGTT 2884
Db 12555 TGGCGGTGCTGTGACCACTGTGTGAGACATGTCCGCAATGACCTCGCCGTGCAACT 12614
Qy 2885 TCTTGAGACCGGACAGTTCACTGTGAACTACTTGAACCAATCTCTGAGCGGATGAGA 2944
Db 12615 TCTTGAGACTGGCCGAGAGACATCTTGAGTACTTCCGCCCTTACTGAGCGGATGAGA 12674
Qy 2945 TCATGGGGGGCTCCAGAGCGCATCGAGCGTGTACTTGTGAATGCAAGAGTTCTTA 2999
Db 12675 TCATGGGGCGCGTCAAGCGCGCATGAGCGCATCTACTTGTGAATGTCAGAGACCA 12729

RESULT 14

US-10-276-774-552
Sequence 552, Application US/10276774
Publication No. US20040053245A1
GENERAL INFORMATION:
APPLICANT: Hybex, Inc.
APPLICANT: Tang, Y., Tom et al
TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
CURRENT APPLICATION NUMBER: US/10/276,774
CURRENT FILING DATE: 2002-11-18
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: Cuihom
SEQ ID NO 552
LENGTH: 14302
TYPE: DNA
ORGANISM: Homo sapiens
US-10-276-774-552

Query Match 24.7%; Score 740; DB 7; Length 14302;

Best Local Similarity 55.5%; Pred. No. 3.9e-212; Mismatches 1210; Indels 96; Gaps 7;

Matches 1632; Conservative 0; Mismatches 1210; Indels 96; Gaps 7;

Qy 70 CAATGATGCCGACGCTAGAGACGATCTTAGCGGAGTGACCAATTGCTGAGTCAAGC 129
Db 9737 CCAACATTTCCGCTTTTGAGAGAACTCATGAGAAAGATCGTGAATTAGCCGATCCGCG 9796
Qy 130 AAGACGTACACGAGGCGCGCATATCATGATGTGTGCTGCTTTACTCTGTTCTTAT 189
Db 9797 ATTGCGTCACTCAATATGCAATGTCATGTGAAGTCAATCTGCCATCTTTGACAGTAC 9856
Qy 190 TTGCGGTGTGTGCGGACAGGCGCTGATATATGTTATCTCCTACTCGGCGAAACACGTA 249
Db 9857 ATGTCTGTTGTGGAGATGACCTGAGAACATTCAGAACGCGCGAGATGTGCTGC 9916
Qy 250 ACAATGTATACAGCGGAAACATGAAACAGCTCTCAAGAAATGTTCTGAAGCTCATCAA 309
Db 9917 ACGCCCTGAACTCAGAGACATGAAACACTTCTTAGGGAACATTTGAATAATCATATAT 9976
Qy 310 AAGAACATCGGCAATGAGAACGCGCGTGTGATGACCCGATCGCACTTACACGAGCAG 369
Db 9977 AATACTTGGGATTTGATGAGGAGCTGTGATGAGAGGCTAGAGTGTTCCTCAGCCT 10036
Qy 370 ATCATCATCAACAGCTCCAGAGAACTGTGAGGAGATCTTCTCTCCGCTCGCTGAAGCT 429
Db 10037 ATTAATTAATTAAGTGAACCTCAGCTCTTGAATACTCATTTCTCCGTTAATGAGAAA 10096
Qy 430 GTTCCCAACGACGACCAATATGTTTCATTAAGAGAGAGCTTGAAGGCGGTTTATTAAG 489

Db 10097 CTCAAGAAAAAGGACCTACCGTGTGTCTGAGAGAACCACTGAAAAGCTGA----- 10149
Qy 490 TCGTCAACAGACGACATCCAGAGTAGAGTCTGATTAACAAGAGACTGCGACCTGCTG 549
Db 10150 --GGCCAGGGGGGACATGTGAGAGCAGAACTCTTCACTCTGATGATTCACACACTG 10207
Qy 550 GTCAAGACATCTACTCTCTTCTACCGCTGCTCATGATACGTGACCTGCAAGAAC 609
Db 10208 GCGAGAGATCTCTATGCTTCTTACCTCTCTGATTTAGATTGTGACTATTAACAGGGCA 10267
Qy 610 CACTGCTCAGAGAACATATGTTCCAGAGCGGAAAGCTGTACCAACACGTGCGTGAATC 669
Db 10268 AAGTGGCTAAAGAGCGCTTAACCCAGAGCAAGAGAGCTCTTCCGATGTGTGAAAGTG 10327
Qy 670 TTCAACATCTGTGAGAGAGCGAGATCTTCTTGAAGAGAGAACAGAACTTCACTCTGCC 729
Db 10328 TTTATCTACTGTGAGAGTCCCATTAATTTCAAAAGAGAGCGAACTTCTGTGTACG 10387
Qy 730 AACGAAATGTATTAACATGTGTCTGATTAATGCCAACAGCAACAGAGAGTACAGAGTA 789
Db 10388 AATGAATCAACAAATATGTCTTCTTATTAATGATTAACAGTCAAGTCAAGATGTCAAGCA 10447
Qy 790 ACAATGTACTCTCTCAAGGTGTGAGAAAGAAAAGAGAGCCTGTATTAAGAAAGC 849
Db 10448 GCTGTTCTGATCAGAAAGAGAGAAATAGAGCGCAAGAGAGATCGGTATTTCA----- 10502
Qy 850 GACAAAGCAAGAGAGTCCAGAGCTCCATATGAGCTGTGAGAGGTGTTACCA 909
Db 10503 -----TGCAACCTCTGTGATGTAGAGCTCTGAAAGCGTTACTGCC 10546
Qy 910 GTTGGCTTAACTTATCTGCTGCGAGAGAACAGAACTGTGAGCAATGTGAAGACAG 969
Db 10547 ATTGGGTGAACATCTGTGCGCCGCGGAGCAAGAGCTCATGTCTGCGCCAAATATGA 10606
Qy 970 TTCTGAAGAAATGTGAGAAACAGATGTGACAAATTCGGAAGACCCAGCTGACACTT 10229
Db 10607 TTAGCCCTGAAGATCTGAGAGATGAAGTGAAGATTAATCCGACAGAAATTAATTA 10666
Qy 1030 CCAGTAAATTAAGATCCGCGAGAC-----GAAATGTCTTGCAACATTACTGTAT 1080
Db 10667 CAGGCAAGTTGAGAGATCTGTCTATTAATGAGCAATGCTCTTACAAAGACTTACCA 10726
Qy 1081 AGCAAGTTAGGTTGAGAGATGAGAGCAATTAATCTGTGAACCTGTGAATTAAGCC 1140
Db 10727 AACAGACTGATGATCCTGATTCAGATCCAGAGAGACGATGAAGAGATGATGATAGCA 10786
Qy 1141 AAGATTATGATGATCCGTCGAGAGAACTGCTGATGATTAAGTCTTTGCGATTG 1200
Db 10787 AATGTCTTTTCACTTTGAACAGAACTTAACGTGTGAGTCCAGACATTAAGTCTG--- 10842
Qy 1201 CATATGATGACCAATCCCAACAAATGATGAACGCTGACCGGTGCTGTGCTGATA 1260
Db 10843 --TCTGTGGAACATCTCAGAGATCTAAAGAGCTGATGAGCAATTAATCTATGCTAG 10900
Qy 1261 CAAGCAAGCGCGCTGATCGCTGCTTCCGAAACCTTCACTACATTTCTGCTCCGAGA 1320
Db 10901 CAGAGAGAAAGGCTGTGTGACCTGCTTCCGATGAGCGCCCTTAATTAATCTGCCAAG 10936
Qy 1321 CATGAGCGTGAACATCTTGCCTCGACGATACGAGCTCTGTGTGAAGAGAGAAC 1380
Db 10961 CATGGGCTGCAATCTCTTCTTCAAGGATATGAAGATCTTGATTAAG----- 11011
Qy 1381 ATTGAGCAAGAGATGATGATGAAGATTTTACTCAATCAATTCGAAGACGAGACTGAG 1440
Db 11012 ACAGAGAACATTACTTGAAGATTAATGATGAAGATTAAGCAAACTGAGGAGCTGA 11071
Qy 1441 AAGATGACTGTGTGAGAGAGTGAAGAGCTGACCCCTCAGCGAGCTGTCAACACC 1500
Db 11072 CCTCAGAGAAAGATGAGAGGACATTAAGAGATTTATCTCTACATCAGCTGATCTTCTG 11131
Qy 1501 TTCTGTGCGGTGCAATGATGAGAGGTCCGAGCTTTGACAGAGATCTCTATACATG 1560
Db 11132 TTTAGTCGAGAGCTTTTAACAGAGAAAT---GCAAACTGAGAGAAAGATTTTATATATG 11188

Oy	1561	TCTTACGCACAATCATTAGCGAAGTCCTGGTGGAAGAABAAAGGAGCAAGAGCGGGTTGGCGAG	1620
Db	11189	GCTTATGACAGATATTATTAATGCAAAAGATTGTCTATGATGAGAAAGATACATGATGGTAGAAG	11248
Oy	1621	GAAGAGGAAGGGGGGTGAGAGAACGAGGCTTGAAAGACGAAGGCCAGAGCCAGTATACAGAA	1680
Db	11249	GAAGTAGAAG-----AGTTTTGAAGAA	11269
Oy	1661	CAGAATAATGAGAAACAAGAAAGCTCTTATTCACCAAGACGGGGCTGGCGGACCGTGGCGTT	1740
Db	11270	AAGAAATGAAAAAGCAAAGCTTCTATACAGAGACCAGACTCCACATGCTGGCGGG	11329
Oy	1741	GCCGAATATGATGTGTGTGTGACATCTCCGCGTCAAAAGGCGTCGGCCACGAGATGTGTATG	1800
Db	11330	GCTGAGATGGTGCTACAGACAAATCATGTCGACGAGAAAGTGAACCTGGACCAANTGGTAGCA	11389
Oy	1801	AAGACTTTACAGCTCTCGTATTAGTATATCTGAAGGGGGCGGCAATATTTATATACATGGGT	1860
Db	11390	GCTACTCTGAAACCTGGAAATGGCTATTTTAAATGGTGGGAACCCACAGATACGCGAGAA	11449
Oy	1861	ATGTTGAACCACTTGAAAGAACAAGAAAGACGTGGGGCTCTTTACGTCCATATGCGCGGCTTC	1920
Db	11450	ATGCTTGAATCTACTCAAGAGAAAAGAAATGTGGGCTTTCTTACAGAGCTGGCGGGCTTG	11509
Oy	1921	ATGAACTTCCTGGCTCCGTGCTCGATCTTTGACGCCCTTCGAGAGAAACAAGGCTGAAGT	1980
Db	11510	ATGCAATCATATGATGTGCTCTTGAACCTAAATGCAATTTGAGCGCAAAACCAAGCTGAAGGT	11569
Oy	1981	CTGGGCGGTGGTCTGGAAGGTGGCGGGGAGAAABAACAATGATACACGCCAGTATCAC	2040
Db	11570	CTTGGGAATGGTGAACAGAGAAAGATCAAGAGAAAAGTTCTGAGAGCATATAGATTAC	11629
Oy	2041	TGCGCACTCTTCAGGTTCAATTCAGCTCACTGTGAAGGACACAACCTGGACTGGCAGAAC	2100
Db	11630	TGTGACCTCTTCGGAATTCCTGCAACATATCTGTGAGGGAACAACTCAATTTTACAGAT	11689
Oy	2101	TACCTGCGAACTCAGGCGCGGTAAACAGACAACGTGACGTGTCACTTGCAACCGTCCAC	2160
Db	11690	TATCTGGAACCTCAGACTGCAATTAATACACGTCAACATATTTATTCACCTGTAGAC	11749
Oy	2161	TACCTGCGGGCGTGCAGAGTGCATATAGGACCTTCACTGGGCACTACTCAAGCAAGGA	2220
Db	11750	TACCTACTGAGAGTTCAAGGAATCAATTAAGTACCTTTATTTGGTATTACTCTGGGAAAGAT	11809
Oy	2221	CTGATGCAACCCGGCGGCAAGCAACTTCTCAAGGCCATTTGGCGTGGCTTCCAGATA	2280
Db	11810	GTTATTTGATGAACAAGAGAACAGGAATTTCTCCAAGCTATCCAGTGGCAAAACAATGC	11869
Oy	2281	TTTCAACACCTCACTGAAGTCAATACAGGGAACCTTTATACGCAAAATACAGAGGCTTGGCT	2340
Db	11870	TTTAAACCTCTTAAGAGTATATATTCAGGGGCTCTTGCACTGGGAATTAACAAGATTGGCA	11929
Oy	2341	CACCTCAAGTTTGTGGAGCGCTGTCCGGTGTGTTCTGTCTCTATTTCTCCCACTGAGGAC	2400
Db	11930	CACAGCAGGGCTGTGGAGTGTCTGTGGTGGGCTTTCTTCAATGTGTTGCCAATGACAAATG	11989
Oy	2401	AAGTTTGTGAAAGCACTGTGTGCGCAGGTGGAACCTGCTGAAGAACTCTCAATCTGCAAG	2460
Db	11990	AAGCTGTGCGCAGGAATTCAGTCAAAATTTGAACTTTAAAGAAATTAATGTGATCTGCAAG	12049
Oy	2461	GACATGATCCCAATGATGTGTGCATATGCTTGAAGAAATGTTTAAATGGTACAAATCGGC	2520
Db	12050	GATATGTGTGATCATATTTGTCTGTCTCAATGTTGAAGAGTATATTTTATTAATGAACGATGGC	12109
Oy	2521	AAGCAATATGTGGAACAACCTAGTATGGGCTCTCAACGTGGAACCTGATCTTGAATAC	2580
Db	12110	AAACAGATGTGGATATAGCTTTGGAAATCTTCCAAACAAGTGAAGATATCTCAAAATTT	12169
Oy	2581	TTTGCACATGTTCCATCAAGCTGAAGGACCTGAACCTCAAGGCCAGCTTCCAGAGAAATGAT	2640
Db	12170	TTTGAACATGTTCTTAAACCTTAAAGAAATTTGACGTGCTGTGATCTTTTAAAGAAATATGAC	12229

QY	2641	GCCAAATACGACGGCTGGGTGTCGCCAAGGACTTCAAGGAGAAATGGAAACAACGAAG	2700
Db	12230	CCCGATGGCAAGGAGTCAITTCGAAAGGAGACTTCCAAAGCGATGGAGAGCCATNAG	12285
QY	2701	AGTATACTCCCGCAAGAAATCGAGTTCTTCTCTAGCTTGTGCGAGACGAACGACGCGC	2760
Db	12280	CACATCACGCAATCGAAGAACGGAATTTCTTTGTCTTGTGCGAGACGATGGAATGAA	12344
QY	2761	AAGTTAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCTGCGCAAGAGATCGGTTT	2820
Db	12350	ACCCTCGACTACGAAGAGTTGTCGCAACGGTTCCACGAACCTGCGAAGGACATCGGCTTC	12409
QY	2821	AACTTGGCCGTTTACTGACTTAATTGTCTGAACATATGCGGACGACCTTAGATTGGCA	2880
Db	12410	AACGTCCGCGCTTCTTGACAAACCTCTTGAGACATGCGCCCAACGATACCCGACTTTCAG	12468
QY	2881	CGTTTCTTGAGAGACGAGGTTAGTCTGGAATCTTGGAACCAATTCCTGCGGCCGTATC	2940
Db	12470	ACTTTTCTGGAATTTAGACAGAGCGTCTGGAATTAATTTCCAGCCCTTTCGCGCCGCAATC	12529
QY	2941	GAGATCAATGGGCGGCTCCAGCGCATCGAGCGTGTCTAACTTCGAGATCAAGAGTGTATA	2998
Db	12530	GAAATCATGGAAAGCCGCAACGCACTCGAGAGGGTCTAATTTTGAATCATGTAATCTCA	12587

```

RESULT 15
US-10-887-553A-490
: Sequence 490. Application US/10887553A
: Publication NO. US20050085436A1
: GENERAL INFORMATION:
: APPLICANT: Garza, Dan
: APPLICANT: Li, Hao
: TITLE OF INVENTION: Method to treat condit
: TITLE OF INVENTION: with insulin signal1
: FILE REFERENCE: 4-33362
: CURRENT APPLICATION NUMBER: US/10/887,553A
: CURRENT FILING DATE: 2004-07-08
: PRIOR APPLICATION NUMBER: 60/485,883
: PRIOR FILING DATE: 2003-08-07
: NUMBER OF SEQ ID NOS: 1208
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 490
: LENGTH: 15731
: TYPE: DNA
: ORGANISM: human
US-10-887-553A-490

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Query Match 24.7%; Score 740; DB 9; Length 15731;

Best Local Similarity 55.5%; Pred. No. 4.1e-212;
Matches 1632; Conservative 0; Mismatches 1210; Indels 96; Gaps 7

Oy	70	CAATGATGCGAAGCTAGAGACATCTTAGGGAGGTGACCAATCTGTGAGTCAGAC	129
Db	9737	CCAAACATTCCTGCTTTGGAGAACTCATGGAAGAAATGTGTGAATTAGCCAGTCCGGC	9796
Oy	130	AAGAAGTACACGAGGCGCCGACATATCATCATGTGTGCTGCTCTTACTCTGTCTTAT	189
Db	9797	ATTGCTACACTCAATATGCCATATGCATGGAAGTATCTGCCCAGCTTTTGACATCAC	9856
Oy	190	TTTGCGCTTCTGTGTGGGCACAGGGGCGTGAATATGTTATCTCTCATCTGTGGGAAACACGTA	249
Db	9857	ATGTCTCGTTGTGTGGAGCATGGAACCTGTGAAACATCCAGAACGGGCGCAGATGTGCTGC	9916
Oy	250	ACAATGGTAAACAGCGGAACATGAAACAGCTCCTCAAGATGTTCTGAAGCTCATCAA	309
Db	9917	ACAGCCTGAATCTCAAGACACATGAACAACATCTTAGGGAACATATGAAAATCATATAT	9976
Oy	310	AAGAACATCGGCATAGAACCGCGCCGTGATGACCCGCATCGCACTTACACGACGACG	369
Db	9977	AATTAATCTTGGGATTTATGAGGGAGCGCTGATGGAAGGCTGACATGTTTCCAGCGCT	10036
Oy	370	ATCATCATCAACGCTCCAGGAATCTGTGAGGAATCTTCTCTGCGCTCGCTGAAGCT	429

Db 10037 ATAAATTAATTAAGTAAACCTCAGCTCTGTAATACTCAATTTCTGCGCTTAATGAGAA 10096
Qy 430 GTTGCAGAACGCGAGCAATATGTTCCATAAGAGAGAGCTTGAGGGGGTTTATTAAG 489
Db 10097 CTCAAGAAAAGGCGAGCTACGGGTGTGTGAGAGAGACCACTGAAAGCTCA----- 10149
Qy 490 TCGTCAAGAGAGAGCAATCCAGAGTGAAGTCAAGATACAGAAAGCTGCGAGCTGCTG 549
Db 10150 --GGCAGGGGGGAGATGTGGAGGAGAACTCTCATCTAGATGAGTTTCAACACTG 10207
Qy 550 GTCAAGAGATTAATCTCTTCTTACCGCTGCTCATCAAGTACGTGACCTGAGAGAAC 609
Db 10208 GCGAAGATCTCTATGCTCTTACCTCTCTTGAATTAATGTTGTGACATTAACAGGGCA 10267
Qy 610 CACTGCTCAGGAGCAATGTTCCAGAGCGGAGAGCTGTACAAACAGTGGCTGAATTC 669
Db 10268 AAGTGGCTAAAGAGCTTAACCGAAGAGAGAGAGCTTCCGAGTGGTGTGAGTTG 10337
Qy 670 TTCAACATCTGTGCGAAGAGCGAGTACTTCTTGAAGAGAGAACAGAACTTCACTCTGCG 729
Db 10338 TTTATCTATGCTGTGAGAGTCCCATATTTCAAAAGAGAGAGCAAACTTGTGTACAG 10387
Qy 730 AACGAATTTGATTAATGCTGTGCTGATTAATGCAACAGCAAGAAAGTGAACAGACTA 789
Db 10388 AATGAATCAACAAATATGCTTCTCTTATTAATGATACCAAGTCAAAAGTGTCAAAGCA 10447
Qy 790 ACAGATGTAATCTCTCAAGTGTGTGAAGAAAGAAAGAGCAACGCTGATGAAGAGCG 849
Db 10448 GTGTTTCTGATCAGAGAAAGAGAAATGAAGCCGAAAGAGAGATGGTATTC----- 10502
Qy 850 GACAAAGACAGAGAGATCCAGAGCTCCCTTAATGATGATGCTGTGTAAGAGTGTATACA 909
Db 10503 -----TGAGACCTCTCTGATTTGATGAGCAGCTGAAGGGTTACTGCGC 10546
Qy 910 GTTGGCTTTAACTTATGCTGCGAGAGAAAGAACTGTGTGACAGATTTTAAAGACAG 969
Db 10547 ATTTGGTTGAACATCTGTGCCCCCTGGGAGCAGAGCTCATTTGCTGGCCAAATGCA 10606
Qy 970 TTCTGAAAGAAATGTCAAGAACAGATGTGAGAAATTCGAGAACCCAGCTGACACTT 1029
Db 10607 TTATGCTGAAAGATCTGAGGATGAAGTCAAGATTAATTCGAGCAAGATTAATTA 10666
Qy 1030 CCAGATAAATATGATCCGCGAGAC-----GAAATGTCTTGGCAACATTAATCTGTAT 1080
Db 10667 CAGGCAAGTTGAGAGATCTGCTATTAATGAGCAATGTGCTTTACAAAGACTTACCA 10726
Qy 1081 AGCAATTTAGTTTCAAGAGTAAAGCAATTAATCTGTGAAATCTGTGAAATTAAGCC 1140
Db 10727 AACAGGACTGATGATACCTCAGATCCAGAGAGAGAGCTGAAGAGTATGATATGCA 10786
Qy 1141 AAGATTTATGATTAACGCTGAGAGAAATCGCTATGAGTAAAGTCTTTCCGATTTG 1200
Db 10787 AATGTCTTTTTCATCTTGAAACAGAAATCTTAAACGTGTGGTGAAGACATTAACG--- 10842
Qy 1201 CATATGATCGACCATCCCAACAAATGAGTAAAGCTGTACCGGTGGTGTGCTGATA 1260
Db 10843 --TCTGTGAGACATCTCTCAGAGATCTAAAGAGCTGTATGAGCAATTAATCTGTAG 10900
Qy 1261 CAAGCGAAGCGGCGGTGATCGCTGTCCGACAACTTCAATTTCTGTCCGAGA 1320
Db 10901 CAGAGAAAGAGGGCTGTGTAGCTGTCTCCGATGGCCCCCTTATTAATATCTGCAAGG 10960
Qy 1331 CATGAGGCTGTAAATCTTGTGCTGTGCACTACAGAGCTGTGTGGAAGAGAGAAC 1380
Db 10961 CATCGGCTGTCAATCTTTCTTCAAGGATTAAGAAAGTCTTGAATTTGA----- 11011
Qy 1381 ATTGACAAGAGTATGATAGAGATCTTCAATCAATTCGAAGACGAGAGCTGAG 1440
Db 11012 ACAGAAAGAACTTACTTTGAAGATTAACGATAGAGATTTAGCAAACTGTGGGCTGAA 11071
Qy 1441 AAGAGTGAAGTGTGAGAGAGAGTGAAGACCTGACCCCTTCAAGAGCTGTGACCAAC 1500
Db 11072 CCTCCAGAAAGATGAAGGCACTAAAGAGTTGATCTCTTCACTCAGCTGATCTCTGCTG 11131

Qy 1501 TTCTGCGCGGTGCAATGATGAGAGGTCCGCGCTTTGCAAGAGATCTCTATACATG 1560
Db 11132 TTTATGTGAGACAGCTTTAAGAGAAAT---GCAACCTGAGAGAAAGATTTTATATATG 11188
Qy 1561 TCTTAAGCAACATCATTAAGCAAGTCTGTGAGAGAGAGAGAGAGAGGGGCTGGAG 1620
Db 11189 GCTATGAGATATTAATGAGCAAGAGTTGTATGATGAGAGATGACGATGTGAAGAG 11248
Qy 1621 GAAGAGAGAGGGGGTGAAGAGAGAGCTGAAGAGCAAGGCAAGGCAATTAACGAA 1680
Db 11249 GAAGTGAAG-----AGTTTGAAGAA 11269
Qy 1681 CAAGAAATGAGAAACAAAGCTCTTATTCACAGAGCGGCTGCGAGACCGTGGGTT 1740
Db 11270 AAAGAAATGAGAAAGCAAAAGCTTCTATACAGAGAGCCGACCTCAAGATCTGTGGCG 11329
Qy 1741 GCGGAATGTGTGTGCTGACATCTCGCGTCCAAAGGCTGCGCAGAGAGTGTATG 1800
Db 11330 GCTGAGATGTGTCTAACAGACATGATGCCAGAAAGGTGAATCTGACCAATGTGTAGCA 11389
Qy 1801 AAGATTTAAGCTCGGTATTAATGATCTGAGGGGCGCAATATTAATTAAGATGAGT 1860
Db 11390 GCTACTGAAACTTGAATGTCTATTTAAATGTGTGAATCTCCACAGTACAGAGAA 11449
Qy 1861 ATGTTGAACCACTTGAAGAGCAAGAAAGAGCTGGGCTCTTACGTCATCGCGGCTC 1920
Db 11450 ATGCTGATCTACCTCAAGAGAGAAAGATGTGGCTCTTTCAAGAGCTGTGGCGCTG 11509
Qy 1921 ATGAATCTCTGCTCGGTCTGATCTTGACGCTTCCAGAGAGAACCAAGAGCTGAAGT 1980
Db 11510 ATGAGTATGATGATGCTCTTGAACCTTAATGCAATTTGAGCGCAAAAGCTGAAGT 11569
Qy 1981 CTGGGCGTGGGTCTGGAAGAGTGGCGGAGAGAGAAAGCATGACAGCCGAGTTCAAC 2040
Db 11570 CTGGAGATGTGACAGAGAGAGATCAGAGAGAAAGGTTCTGACAGAGATGATGATC 11629
Qy 2041 TGCGCACTCTTCAAGTTCAATCACTCACTGTAAGGACAACTTGAAGCTGCGAGAAC 2100
Db 11630 TGTACCTCTTCCATCTCTGCACTACTCTGTGAGGAGCAACCTCAAGATTTCAAGAT 11689
Qy 2101 TACTTGCAACTCAGGCGGCTTAACAGACAAACAGTGAAGTGTGATCTGACCGTGCAC 2160
Db 11690 TATCTGAAGACTCAGACTGAGATTAATTAACCTGTCAACATTAATTAATCACTGTAGAC 11749
Qy 2161 TACTGTCTGCGGCTGCAAGATCCATCACTGATCTTACTGTGCACTTCAAGAGAGAA 2220
Db 11750 TACTTACTGAAGTTCAGGAATCAATTAAGTGAATTTGATTTGATCTGTGGAAGAT 11809
Qy 2221 CTGATCGACCGGCGGCGAAGCGAACTTTCAGAGGCAATTTGGCGTGTCCCAAGTA 2280
Db 11810 GTTATTTATGAACAAAGACAAAGCAAGATTTCTCCAAAGCTATTCAGATGTGCAAAAGCTC 11869
Qy 2281 TTCAACACCTCACTGAAGTATTAACAGGACCTTGTATGAGAAATCAAGAGCTTGTGCT 2340
Db 11870 TTTAACTCTTACAGAGTAAATTAATCAGGCTCTTGTGCACTGGGAATCAACAGTTGCA 11929
Qy 2341 CACTCAGGTTGTGAGAGCTGTGTGAGTTTCTGTCTTCTTCTTCTTCTTCTTCTTCTTCT 2400
Db 11930 CACAGCAGGCTGTGAGAGTGTGTGTGCTGTCTTCTTCAATGTGTGTGCTTCAATCAAGT 11989
Qy 2401 AAGTTGTGAAGCACTGTGCGAGGTGAGCTGTGAGAGAGAACTCTCAATCTTCAAGAG 2460
Db 11990 AAGCTGTGAGAAATTCAGATCAAGTAAATGAGCTATTAAGAAATTAATGAGATCTGCAAG 12049
Qy 2461 GACATGATCCCATGATGCTGTGATGCTTGAAGAAATGTGTAAATGATGATCAATCGGC 2520
Db 12050 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 12109
Qy 2521 AAGCAATGTGTGAGACACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580
Db 12110 AAAAGATGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 12169

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Qy 2581 TTCGACATGTTCTCAAGCTGAAGGACCTGCACGCGCCAGCTTCCAGAGATTGAT 2640
    |||||
Db 12170 TTGACATGTTCTTAAACTTAAGGATTGACGTCTGATACTTTTAAAGAAATATGAC 12229
    |||||
Qy 2641 GCCAATAACGACGGCTGGGTGCTGCCAAGGACTTCAAGAGAAATGAAACAAGAG 2700
    |||||
Db 12230 CCGATGGCAAGGGAGTCATTTCCAGAGGACTTCCAAAGCGATGAGAGCCATAG 12289
    |||||
Qy 2701 AGTTATACTCCCGAAGAAATCGAGTTCTCTAGCTTGTGCGAGACGAAACGACGCGC 2760
    |||||
Db 12290 CACTACACGAGTCAGAAACGAAATTTCTTTGTCTGTGCGAGACGATGAGAAATGAA 12349
    |||||
Qy 2761 AAGTTAGCTACATCGGTTTCTGCGACCTTTCCAGAGCCTGCCAAGAGATCGGTTT 2820
    |||||
Db 12350 ACCCTCGACTACGAAAGATTCTGTCAAACGCTTCCAGAACTGCGAAGACATCGGCTTC 12409
    |||||
Qy 2821 AACTTGGCCGTTACTGACTTACTGTCTGAACATATGCCGAAAGAGCTAGATTGCA 2880
    |||||
Db 12410 AACGTGCGCTCTTCTGACAAACCTCTGTAGGACATGCCAACGATACCAGCTTCAG 12469
    |||||
Qy 2881 CGTTTCTGAGACGGCAGGTTCACTGCTCTGAACCTTGAACATTCCTGGCCGTATC 2940
    |||||
Db 12470 ACTTTTCTGAAATTAGCAGAGAGGCTCTGAATTATTTCCAGCCCTTCTGGGCGGATC 12529
    |||||
Qy 2941 GAGATCATGGCGGCTCCAAGCGCATGAGCGTGTCTACTTCGAGATCAGAGTCTTA 2998
    |||||
Db 12530 GAAATCATGGGAGAGCGCCAAACGATCGAGAGGGTCTATTTTGAATCATGAGTCCA 12587
    |||||
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Search completed: April 14, 2006, 22:12:51
Job time : 2311 secs

XX The present invention describes an isolated nucleotide fragment (I) comprising: (a) a nucleic acid sequence encoding a ryanodine receptor having an amino acid sequence identity of at least 80% when compared to a polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8, 128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO. 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant construct comprising (I) operably linked to at least one regulatory sequence; (2) a transformed host cell comprising the recombinant construct; (3) a method to isolate (I) encoding ryanodine receptors and related polypeptides; (4) an isolated polypeptide having ryanodine receptor activity; (5) a method for evaluating at least one compound for its ability to modulate calcium homeostasis; (6) a method for evaluating at least one compound which modulates ryanodine receptor activity; (7) an isolated nucleic acid fragment encoding an insect ion channel comprising at least two fully defined polypeptide sequences selected from SEQ ID NO. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56, 120-126; (8) a method for identifying a nucleic acid sequence encoding an insect ion channel; (9) a method for expressing an isolated nucleic acid fragment encoding a toxic insect ion channel; and (10) recombinant construct comprising in the 5' to 3' direction a promoter operably linked to an isolated nucleic acid fragment encoding a toxic insect ion channel. The isolated nucleotide fragment (I) encoding a ryanodine receptor is useful for the isolation of other pest ryanodine receptors and developing of screens to identify insecticidally active compounds. The nucleic acid fragments are useful as pesticides, fragments of protein for antibody production, fragments of protein for determination of the structure of insecticide binding sites and in the identification of insecticides that disrupt the calcium balance in cells through other messengers that interact with the receptor calcium release mechanism. The present sequence is used in the exemplification of the present invention.

50 Sequence 15387 BP; 4065 A; 3845 C; 4182 G; 3295 T; 0 U; 0 Other;

Query Match 100.0%; Score 3001; DB 12; Length 15387;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGTTCTCTGCTGTAAGAGATCGCTGACCAATCTTTGGAAGCCCAAGACATATGAG 60
Db 10000 CAGTTCTCTGCTGTAAGAGATCGCTGACCAATCTTTGGAAGCCCAAGACATATGAG 10059
QY 61 AAAATGGAACAATGATCGACCGCTAGAGACGATCTTAGCGAGGTGACCAATTCGTG 120
Db 10060 AAAATGGAACAATGATCGACCGCTAGAGACGATCTTAGCGAGGTGACCAATTCGTG 10119
QY 121 GAGTCAGACAGATGATGACAGAGAGCGCGCATATCATGATGTGTGCTGCTTTACTC 180
Db 10120 GAGTCAGACAGATGATGACAGAGAGCGCGCATATCATGATGTGTGCTGCTTTACTC 10179
QY 181 TGTCTTATTTGCGGTTCTGGTGGGACAGAGGAGCCTGATATGTTACTCTACTGAGCGGA 240
Db 10180 TGTCTTATTTGCGGTTCTGGTGGGACAGAGGAGCCTGATATGTTACTCTACTGAGCGGA 10239
QY 241 AACCAAGTAAACATGTTAAGACGCGAACAACACAGCTCTCAAGAAATGTTCTGAAAG 300
Db 10240 AACCAAGTAAACATGTTAAGACGCGAACAACACAGCTCTCAAGAAATGTTCTGAAAG 10299
QY 301 CTCAATCAAAAAGAAATGCGAATGAGAAAGCGCGCTGATGACCCGATGCCACCTTAC 360
Db 10300 CTCAATCAAAAAGAAATGCGAATGAGAAAGCGCGCTGATGACCCGATGCCACCTTAC 10359
QY 361 ACGAGAGCATCATCATCAACAGGCTCGAGGAACGTCGAGAGGATTCCTTCTGCGCGTGC 420
Db 10360 ACGAGAGCATCATCATCAACAGGCTCGAGGAACGTCGAGAGGATTCCTTCTGCGCGTGC 10419
QY 421 GCTGAACGTTGTCGAAACGACGCGAACAATATGTTCCATAGAGAGAGCTTGAAGGAGG 480
Db 10420 GCTGAACGTTGTCGAAACGACGCGAACAATATGTTCCATAGAGAGAGCTTGAAGGAGG 10479
QY 481 TTTATTAAGTGTCAACAGACGACATCCAGGTGAGTCTCAATACAAAGAAAGCTGG 540
|||||

Db 10480 TTTATTAAGTGTCAACAGACGACATCCAGGTGAGTCTCAATACAAAGAAAGCTGG 10539
QY 541 CAGTGTGTCAGAGACATCTACTCTTACCCGCTGCTCATCAATAGTCGACCTG 600
Db 10540 CAGTGTGTCAGAGACATCTACTCTTACCCGCTGCTCATCAATAGTCGACCTG 10539
QY 601 CAGAGAAACACTGGCTCAGGAACAATGTTCCAGAGCGGAAAGCTGTACACACGTCG 660
Db 10600 CAGAGAAACACTGGCTCAGGAACAATGTTCCAGAGCGGAAAGCTGTACACACGTCG 10659
QY 661 GCTGAATCTTCAACATCTGCTCGAAGAGCAGTACTTCTTGAAGAGAAACAGAACTTC 720
Db 10660 GCTGAATCTTCAACATCTGCTCGAAGAGCAGTACTTCTTGAAGAGAAACAGAACTTC 10719
QY 721 ATCTCTGCAACGAATTTGATATACATGGTGTGTTATGCAACGCAACAAGAAAGTG 780
Db 10720 ATCTCTGCAACGAATTTGATATACATGGTGTGTTATGCAACGCAACAAGAAAGTG 10779
QY 781 ACAGCATTAACAGATGTTACTCTTCAAGGTGTGAAAAGAAAAGAAAGACACCGTAT 840
Db 10780 ACAGCATTAACAGATGTTACTCTTCAAGGTGTGAAAAGAAAAGAAAGACACCGTAT 10839
QY 841 AAGAAAGCGGACAAAGACAGAGAGTCCAGACCTTAAATGATAGCTTGTCTAAGAG 900
Db 10840 AAGAAAGCGGACAAAGACAGAGAGTCCAGACCTTAAATGATAGCTTGTCTAAGAG 10899
QY 901 TTGTTACAGTTGGCTTAACTTATTCGCTGGCAGAGAACAAAGACTGGTCAGCATTTG 960
Db 10900 TTGTTACAGTTGGCTTAACTTATTCGCTGGCAGAGAACAAAGACTGGTCAGCATTTG 10959
QY 961 AAAGACAGTTCTGAAAGAAATGTCAAGAACAGATGTGGCAATTCGCAAGACCCAG 1020
Db 10960 AAAGACAGTTCTGAAAGAAATGTCAAGAACAGATGTGGCAATTCGCAAGACCCAG 11019
QY 1021 CTGACACTTCAGATTAATTAATGATCCGCGACAGACGAATATGCTTGGCAACATTAATGAT 1080
Db 11020 CTGACACTTCAGATTAATTAATGATCCGCGACAGACGAATATGCTTGGCAACATTAATGAT 11079
QY 1081 AGCAAGTTAGGTTGGAAGATTAAGAGCAATTAATCTGTGAAACTGTGAAATTAAGGCC 1140
Db 11080 AGCAAGTTAGGTTGGAAGATTAAGAGCAATTAATCTGTGAAACTGTGAAATTAAGGCC 11139
QY 1141 AAGATTAATGATGATACCGTTCGAGAGATGCTGTGATAGTAAAGTCTTTGCGATTG 1200
Db 11140 AAGATTAATGATGATACCGTTCGAGAGATGCTGTGATAGTAAAGTCTTTGCGATTG 11199
QY 1201 CATATGATGACCATTCGCCCAACAAATGATTAAGAAAGCTGTACCGGTGCTGTGATTA 1260
Db 11200 CATATGATGACCATTCGCCCAACAAATGATTAAGAAAGCTGTGCTGTGATTA 11259
QY 1261 CAACGCAAGGCGCGCATTCGCTGCTGCGAACAACTTCACTACATTCCTGCGAGAG 1320
Db 11260 CAACGCAAGGCGCGCATTCGCTGCTGCGAACAACTTCACTACATTCCTGCGAGAG 11319
QY 1321 CATGAGCGGTGTAACATCTTTCGCTCGACGTACTACAGCTCTGTTGGAAGAGAGAAC 1380
Db 11320 CATGAGCGGTGTAACATCTTTCGCTCGACGTACTACAGCTCTGTTGGAAGAGAGAAC 11379
QY 1381 ATTGGAACAAGATTAATGATTAAGAAATCTTAATCAATTTCAAGACGCAAGCTGAG 1440
Db 11380 ATTGGAACAAGATTAATGATTAAGAAATCTTAATCAATTTCAAGACGCAAGCTGAG 11439
QY 1441 AAGAGTACGTTGGTGGAGAGAGGTAAGACCTGACCCCTCAACGCAAGCTGTGTACACAC 1500
Db 11440 AAGAGTACGTTGGTGGAGAGAGGTAAGACCTGACCCCTCAACGCAAGCTGTGTACACAC 11499
QY 1501 TTCTGTGCGGTGCGATGACTGAGAGGTCCGCGCTTTTGAAGAGAGATTCCTTAATCATG 1560
Db 11500 TTCTGTGCGGTGCGATGACTGAGAGGTCCGCGCTTTTGAAGAGAGATTCCTTAATCATG 11559
QY 1561 TCTTAAGCAACATCATAGCGAAAGTCTGTGAGAGAGAGAGAGAGAGAGGAGTGGGAG 1620
Db 11560 TCTTAAGCAACATCATAGCGAAAGTCTGTGAGAGAGAGAGAGAGAGAGGAGTGGGAG 11619
|||||

Oy	1621	GAAGAGGAAGAGGGGTGGAGAAAGGAGGCTGAAGACGAAGGAGCCAGTATACAGAA	1680
Db	11620	GAAGAGGAAGAGGGGTGGAGAAAGGAGGCTGAAGACGAAGGAGCCAGTATACAGAA	11679
Oy	1681	CAAGAAATGAGAAACAAGAAAGCTCTATTCCAACAAAGCGCGGTGGAGCCGTGGGGTT	1740
Db	11680	CAAGAAATGAGAAACAAGAAAGCTCTATTCCAACAAAGCGCGGTGGAGCCGTGGGGTT	11739
Oy	1741	GCCGAAAATGATGTTGCTGCACATCTCCGCGTCCAAAGGCTCGCCAGCGAATGATCATG	1800
Db	11740	GCCGAAAATGATGTTGCTGCACATCTCCGCGTCCAAAGGCTCGCCAGCGAATGATCATG	11799
Oy	1801	AAGACTTTAAGCTCCGGTATTACTATATCTGAAGGGGGGGAATATGATATACAGATGGAT	1860
Db	11800	AAGACTTTAAGCTCCGGTATTACTATATCTGAAGGGGGGGAATATGATATACAGATGGAT	11859
Oy	1861	ATGTTGAACAACCTTGAAAGAACAAGAAAGAGTGGGCTTCTTTACGTCACATCCGCGGCTTC	1920
Db	11860	ATGTTGAACAACCTTGAAAGAACAAGAAAGAGTGGGCTTCTTTACGTCACATCCGCGGCTTC	11919
Oy	1921	ATGAACCTCTGCTCCGTGCTCGATCTTGAAGCCTTCGAAGAGACAACAAAGCTGAAGAT	1980
Db	11920	ATGAACCTCTGCTCCGTGCTCGATCTTGAAGCCTTCGAAGAGACAACAAAGCTGAAGAT	11979
Oy	1981	CTGGGCGTGGGTCTGGAAGGTGGGGCGGAGAGAAACAATGACATGACCGCCGATTCACC	2040
Db	11980	CTGGGCGTGGGTCTGGAAGGTGGGGCGGAGAGAAACAATGACATGACCGCCGATTCACC	12039
Oy	2041	TGCGCACTCTTCAAGSTTCAATTCAAGCTCAACCTGGAAGGACAACAATTTGACCTGGACAGAC	2100
Db	12040	TGCGCACTCTTCAAGSTTCAATTCAAGCTCAACCTGGAAGGACAACAATTTGACCTGGACAGAC	12099
Oy	2101	TACCTGCGAACTCAGGCGCGGTAAACAACAACAAGTACAGTGGTCACTGCAACCGTGCAC	2160
Db	12100	TACCTGCGAACTCAGGCGCGGTAAACAACAACAAGTACAGTGGTCACTGCAACCGTGCAC	12159
Oy	2161	TACCTGTGCGGGCTGCAAGAGTCATCATGAACTTCTAATGSCACTAATCAAGACAAGAA	2220
Db	12160	TACCTGTGCGGGCTGCAAGAGTCATCATGAACTTCTAATGSCACTAATCAAGACAAGAA	12219
Oy	2221	CTGATTCGAACCCGCGCGGCAAGGGAATTCTTCAAGGCAATTGGCGTGGCTTCCAAAGTA	2280
Db	12220	CTGATTCGAACCCGCGCGGCAAGGGAATTCTTCAAGGCAATTGGCGTGGCTTCCAAAGTA	12279
Oy	2281	TTCAACAACCCCTCACTGAAGTCAATACAGAGAACCTTGTACAGAGAGCTTTGGCT	2340
Db	12280	TTCAACAACCCCTCACTGAAGTCAATACAGAGAACCTTGTACAGAGAGCTTTGGCT	12339
Oy	2341	CACCTCAAGTGTGGGAGCGCTGTCCGTGTGTTCTGTCTCTAATCTCCACAATGCAGAC	2400
Db	12340	CACCTCAAGTGTGTGGAGCGCTGTCCGTGTGTTCTGTCTCTAATCTCCACAATGCAGAC	12399
Oy	2401	AAATTGTGAAAGCACTGCTGCAGGTGGAACCTGCTGAAGGAATCTCTAATCTGCAGAAAG	2460
Db	12400	AAATTGTGAAAGCACTGCTGCAGGTGGAACCTGCTGAAGGAATCTCTAATCTGCAGAAAG	12459
Oy	2461	GACATGATCCCAATGATGCTGTCCATATGTTGAAGGAAGAAATGTTATATGATCAATCCGAG	2520
Db	12460	GACATGATCCCAATGATGCTGTCCATATGTTGAAGGAAGAAATGTTATATGATCAATCCGAG	12519
Oy	2521	AAGCAAAATGATGAGACACATAGTAGATCCGAGCTCCACATGAGAACCTGATCTGAATAC	2580
Db	12520	AAGCAAAATGATGAGACACATAGTAGATCCGAGCTCCACATGAGAACCTGATCTGAATAC	12579
Oy	2581	TTTCGACATGTTCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGCTTCCAGAGATTTGAT	2640
Db	12580	TTTCGACATGTTCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGCTTCCAGAGATTTGAT	12639
Oy	2641	GCCAAATACAGACGGCTGGGTGCTGSCCAAGAACTTCAAGGAAGAAATGAAACAACAAGAG	2700
Db	12640	GCCAAATACAGACGGCTGGGTGCTGSCCAAGAACTTCAAGGAAGAAATGAAACAACAAGAG	12699

QY	2701	AGTATAC	CCCCAAGAAAT	CGAGTTC	CTCCT	AGCTTG	CTGC	GAGACGAAC	CA	CGACGC	2760	
Db	12700	AGTATAC <th>CTCCGAGAAAT</th> <th>CGAGTTC</th> <th>CTCCT</th> <th>AGCTTG</th> <th>CTGC</th> <th>GAGACGAAC</th> <th>CA</th> <th>CGACGC</th> <td>12755</td>	CTCCGAGAAAT	CGAGTTC	CTCCT	AGCTTG	CTGC	GAGACGAAC	CA	CGACGC	12755	
QY	2761	AACTTAG <th>ACTACAT</th> <th>TCGGTTC</th> <th>CTGCGA</th> <th>CCGTTTC</th> <th>CCACGAG</th> <th>CGCTGCA</th> <th>AGAGAT</th> <th>CGGGTTT</th> <td>2820</td>	ACTACAT	TCGGTTC	CTGCGA	CCGTTTC	CCACGAG	CGCTGCA	AGAGAT	CGGGTTT	2820	
Db	12760	AACTTAG <th>ACTACAT</th> <th>TCGGTTC</th> <th>CTGCGA</th> <th>CCGTTTC</th> <th>CCACGAG</th> <th>CGCTGCA</th> <th>AGAGAT</th> <th>CGGGTTT</th> <td>12811</td>	ACTACAT	TCGGTTC	CTGCGA	CCGTTTC	CCACGAG	CGCTGCA	AGAGAT	CGGGTTT	12811	
QY	2821	AACTTGG <th>CCCGTGT</th> <th>TACTGAC</th> <th>TAACTT</th> <th>GTCTGAA</th> <th>CATATG</th> <th>CCGAA</th> <th>CGAGCCT</th> <th>TAGTTGGCA</th> <td>2880</td>	CCCGTGT	TACTGAC	TAACTT	GTCTGAA	CATATG	CCGAA	CGAGCCT	TAGTTGGCA	2880	
Db	12820	AACTTGG <th>CCCGTGT</th> <th>TACTGAC</th> <th>TAACTT</th> <th>GTCTGAA</th> <th>CATATG</th> <th>CCGAA</th> <th>CGAGCCT</th> <th>TAGTTGGCA</th> <td>12871</td>	CCCGTGT	TACTGAC	TAACTT	GTCTGAA	CATATG	CCGAA	CGAGCCT	TAGTTGGCA	12871	
QY	2881	CGTTT <th>CCTGAGAG</th> <th>CGG</th> <th>CAGGTT</th> <th>CAGT</th> <th>CTCTGAA</th> <th>CTAATT</th> <th>CGAAC</th> <th>CAATTCCT</th> <th>CGGGCCGATC</th> <td>2940</td>	CCTGAGAG	CGG	CAGGTT	CAGT	CTCTGAA	CTAATT	CGAAC	CAATTCCT	CGGGCCGATC	2940
Db	12880	CGTTT <th>CCTGAGAG</th> <th>CGG</th> <th>CAGGTT</th> <th>CAGT</th> <th>CTCTGAA</th> <th>CTAATT</th> <th>CGAAC</th> <th>CAATTCCT</th> <th>CGGGCCGATC</th> <td>12931</td>	CCTGAGAG	CGG	CAGGTT	CAGT	CTCTGAA	CTAATT	CGAAC	CAATTCCT	CGGGCCGATC	12931
QY	2941	GAGATCA <th>TGGGCGG</th> <th>CGCTCA</th> <th>AGCGCAT</th> <th>GAGCGGT</th> <th>CTACT</th> <th>TCGAGAT</th> <th>CAAGAGT</th> <th>CTAAT</th> <td>3000</td>	TGGGCGG	CGCTCA	AGCGCAT	GAGCGGT	CTACT	TCGAGAT	CAAGAGT	CTAAT	3000	
Db	12940	GAGATCA <th>TGGGCGG</th> <th>CGCTCA</th> <th>AGCGCAT</th> <th>GAGCGGT</th> <th>CTACT</th> <th>TCGAGAT</th> <th>CAAGAGT</th> <th>CTAAT</th> <td>12991</td>	TGGGCGG	CGCTCA	AGCGCAT	GAGCGGT	CTACT	TCGAGAT	CAAGAGT	CTAAT	12991	
QY	3001	A	3001	A	3001							
Db	13000	A	13000									

RESULT 2
ADM68901
ID ADM68901 standard; DNA; 15303 BP

DT 17-JUN-2004 (first entry)

KW ryanodine receptor; insect ion channel; insecticide; pesticide; calcium balance disruption; receptor calcium release mechanism; gene; ds

OS Heliothis virescens.

Key	Location/Qualifiers
FH	1. .15303
PT	/*tag= a
FT	/product= "ryanodine receptor"
FT	

PN WO2004027042-A2

PF 23-SEP-2003; 2003WO-US029834.

PR 23-SEP-2002; 2002US-0412795P.
PR 18-NOV-2002; 2002US-0427324P.

PA (DUPO) DU PONT DE NEMOURS & CO E I.

PI Caspar T, Cordova D, Gutteridge S, Rauh JJ, Smith RM, Wu L;

PI Tao Y;

XX
DB WBT, 2004-205411/27

DR P-PSDB; ADM68902.

New isolated nucleot

PT for isolating other
PT identify insecticide

Identically Insecticide

AA
PS

Claim 6; SEQ ID NO 1

[illegible]

CC The present invention

CC comprising: (a) a m

CC having an amino acid

CC polypeptide selected
CC 128 130 144 or 148

CC 128, 130, 144, OF 1

The present invention describes an isolated nucleotide fragment (1) comprising: (a) a nucleic acid sequence encoding a ryanodine receptor having an amino acid sequence identity of at least 80% when compared to a polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8, 128, 130, 144, or 146; or (b) the complement of (a). (1) comprises a

CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO. 1, 3, 5, 7, 9, 127, 129, or 145). Also described: (1) a recombinant construct comprising (1) operably linked to at least one regulatory sequence; (2) a transformed host cell comprising the recombinant construct; (3) a method to isolate (1) encoding ryanodine receptors and related polypeptides; (4) an isolated polypeptide having ryanodine receptor activity; (5) a method for evaluating at least one compound for its ability to modulate calcium homeostasis; (6) a method for evaluating at least one compound which modulates ryanodine receptor activity; (7) an isolated nucleic acid fragment encoding an insect ion channel comprising at least two fully defined polypeptide sequences selected from SEQ ID NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56, 120-126; (8) a method for identifying a nucleic acid sequence encoding an insect ion channel; (9) a method for expressing an isolated nucleic acid fragment encoding a toxic insect ion channel; and (10) recombinant construct comprising in the 5' to 3' direction a promoter operably linked to an isolated nucleic acid fragment encoding a toxic insect ion channel. The isolated nucleotide fragment (1) encoding a ryanodine receptor is useful for the isolation of other pest ryanodine receptors and developing of screens to identify insecticidally active compounds. The nucleic acid fragments are useful as pesticides, fragments of protein for antibody production, fragments of protein for determination of the structure of insecticide binding sites and in the identification of insecticides that disrupt the calcium balance in cells through other messengers that interact with the receptor calcium release mechanism. The present sequence is used in the exemplification of the present invention.

Sequence 15303 BP; 4036 A; 3822 C; 4161 G; 3284 T; 0 U; 0 Other;

Query Match 99.8%; Score 2996.2; DB 12; Length 15303;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2998; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGTCTCTCTGCTGAACAGATCGTGCATCTTTGGAAGCCCAAGACATTAATGACG 60
DB 9916 CAGTCTCTCTGCTGAACAGATCGTGCATCTTTGGAAGCCCAAGACATTAATGACG 9975
QY 61 AAAATGGAACAAATGCAATGCGGACGCTAGAGACATTTTAAAGGATGAGCAATTCGTG 120
DB 9976 AAAATGGAACAAATGCAATGCGGACGCTAGAGACATTTTAAAGGATGAGCAATTCGTG 10035
QY 121 GAGTGAAGCAACGTAACAGAGCGCGCATATCATGATGTGTGCTTATCTC 180
DB 10036 GAGTGAAGCAACGTAACAGAGCGCGCATATCATGATGTGTGCTTATCTC 10095
QY 181 TGTCTTAATTTGCGCTTCTGTGTGACAGAGGCGCTGATATGTTACTCTTACGCGGA 240
DB 10096 TGTCTTAATTTGCGCTTCTGTGTGACAGAGGCGCTGATATGTTACTCTTACGCGGA 10155
QY 241 AAACACGTAAACATGATGTAACAGCGGAACATGAACAGCTCTCAAGATTTCTGAAG 300
DB 10156 AAACACGTAAACATGATGTAACAGCGGAACATGAACAGCTCTCAAGATTTCTGAAG 10215
QY 301 CTGATCAAAAAAAGAAATGCGGCAATGAGAACGCGCGGTGATGACCCGCTATGCCACCTAC 360
DB 10216 CTGATCAAAAAAAGAAATGCGGCAATGAGAACGCGCGGTGATGACCCGCTATGCCACCTAC 10275
QY 361 ACGCAGCAGATCATCATCAACAGCTCCGAGGAAGCTGTAGAGGATTTCTTCTGCGCTC 420
DB 10276 ACGCAGCAGATCATCATCAACAGCTCCGAGGAAGCTGTAGAGGATTTCTTCTGCGCTC 10335
QY 421 GCTGAACGTTTCCGAAACGACGCAATATGTTCAATAGAGAGAGAGCTTGAAGGAG 480
DB 10336 GCTGAACGTTTCCGAAACGACGCAATATGTTCAATAGAGAGAGAGCTTGAAGGAG 10395
QY 481 TTTATTAATAGTCTCAACAGACGACATCTCCAGGTAGATCTCAATACAAAGAACTGG 540
DB 10396 TTTATTAATAGTCTCAACAGACGACATCTCCAGGTAGATCTCAATACAAAGAACTGG 10455
QY 541 CAGCTGCTGTGAGAGACATCTACTCTTCAACCGCGCTCATCAAGATAGCTGACCTG 600
DB 10456 CAGCTGCTGTGAGAGACATCTACTCTTCAACCGCGCTCATCAAGATAGCTGACCTG 10515

QY 601 CAGAGAAACCACTGGCTCAGGAACAATGTTCCAGAGCGGAAAGACTGTATCAACACCTG 660
DB 10516 CAGAGAAACCACTGGCTCAGGAACAATGTTCCAGAGCGGAAAGACTGTATCAACACCTG 10575
QY 661 GCTGAATCTTCAACATGTGTGAGAGAGCCAGTACTTCTTGAAGAGAACAGACTTC 720
DB 10576 GCTGAATCTTCAACATGTGTGAGAGAGCCAGTACTTCTTGAAGAGAACAGACTTC 10635
QY 721 ATCTGCGCAACGAATTTGATTAACATGCTGCTGAATTAATGCAACCAAGAGAGT 780
DB 10636 ATCTGCGCAACGAATTTGATTAACATGCTGCTGAATTAATGCAACCAAGAGAGT 10695
QY 781 ACGACATGAACATGATGATCTCTCAAGTGTGAGAGAGAGAGAGAGAGAGAGAGT 840
DB 10696 ACGACATGAACATGATGATCTCTCAAGTGTGAGAGAGAGAGAGAGAGAGAGAGT 10755
QY 841 AAGAAACGCAACAAAGACAGAGAGTCCAGAGCTCCTTAATGATGCTTGTGAAGAG 900
DB 10756 AAGAAACGCAACAAAGACAGAGAGTCCAGAGCTCCTTAATGATGCTTGTGAAGAG 10815
QY 901 TTGTTACAGATTGGCTTAACTTATTCCTGCTGACAGAGACAAAGCTGTGACGATTT 960
DB 10816 TTGTTACAGATTGGCTTAACTTATTCCTGCTGACAGAGACAAAGCTGTGACGATTT 10875
QY 961 AAAGCAGGTTCTGAAGAAATGTCAGAACATGTTGGCAGAAATTCGCAAGCCAG 1020
DB 10876 AAAGCAGGTTCTGAAGAAATGTCAGAACATGTTGGCAGAAATTCGCAAGCCAG 10935
QY 1021 CTGACACTTCAGATTAATTAATGATCCGCGACAGAGAAATGCTTGGCAACATTAATT 1080
DB 10936 CTGACACTTCAGATTAATTAATGATCCGCGACAGAGAAATGCTTGGCAACATTAATT 10995
QY 1081 AGCAAGTTAGGTTCCAGAGAGTAAGACAAATTAATCTGTGAAATCTGTGAAATTAAGGCC 1140
DB 10996 AGCAAGTTAGGTTCCAGAGAGTAAGACAAATTAATCTGTGAAATCTGTGAAATTAAGGCC 11055
QY 1141 AAGATTATTAATGATACCGTGAAGAAATCGTGTATGAGTAAGTAAGTCTTTCCGATTG 1200
DB 11056 AAGATTATTAATGATACCGTGAAGAAATCGTGTATGAGTAAGTAAGTCTTTCCGATTG 11115
QY 1201 CATATGATGACCAATCCGCAACAAATGATGAAGAGCGTACCGGTGTGTGATTA 1260
DB 11116 CATATGATGACCAATCCGCAACAAATGATGAAGAGCGTACCGGTGTGTGATTA 11175
QY 1261 CAACGCAACGCGCGCGTATGCTGCTTCCGACAACTTCACTCAATCTCTGCGAGGA 1320
DB 11176 CAACGCAACGCGCGCGTATGCTGCTTCCGACAACTTCACTCAATCTCTGCGAGGA 11235
QY 1321 CATGAGCGGTGTAACATCTTGGCTGCAAGTATGAGAGCTGTGTGAGAGAGAGAAC 1380
DB 11236 CATGAGCGGTGTAACATCTTGGCTGCAAGTATGAGAGCTGTGTGAGAGAGAGAAC 11295
QY 1381 APTGGAAGAAAGTAATGATGAAGATCTTAATCAATATTCGAAGAGCGAGAGCTGAAG 1440
DB 11296 APTGGAAGAAAGTAATGATGAAGATCTTAATCAATATTCGAAGAGCGAGAGCTGAAG 11355
QY 1441 AAGAGTACGTTGTGAGAGAGAGTGAAGAGCTGACCCCTCAACGACGCTGTCAACAC 1500
DB 11356 AAGAGTACGTTGTGAGAGAGAGTGAAGAGCTGACCCCTCAACGACGCTGTCAACAC 11415
QY 1501 TTTCTGCGGCTGCCATGACTGAAGAGTCCGCGCGCTTTGACAGAGAGATCTCTATACATG 1560
DB 11416 TTTCTGCGGCTGCCATGACTGAAGAGTCCGCGCGCTTTGACAGAGAGATCTCTATACATG 11475
QY 1561 TCTTAACGACATCAATAGCGAAGTCTCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 1620
DB 11476 TCTTAACGACATCAATAGCGAAGTCTCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 11535
QY 1621 GAAAG 1680
DB 11536 GAAAG 11595
QY 1681 CAAGAAATGAG 1740

Db 11596 CAGAGAAATGAGAAACAAAGCTCTATTCCAGCAAGGCGGCTGGCGGAGCTGGGGTT 11655
 Qy 1741 GCCGAATAGTGTCTGTGCACTTCGCCGTCCAAAGGCTGCGCAGAGATGGTCAATG 1800
 Db 11656 GCCGAAATAGTGTGTCTGCACTTCGCCGTCCAAAGGCTGCGCAGAGATGGTCAATG 11715
 Qy 1801 AAGACTTACAGCTGCTGTATTAATGATACAGAGGGGCGCAATATGATATACAGATGGT 1860
 Db 11716 AAGACTTACAGCTGCTGTATTAATGATACAGAGGGGCGCAATATGATATACAGATGGT 11775
 Qy 1861 ATGTGAACCACTTGAAGAACAAAGAAAGAGCTGGGCTTTCTTACCTCCATCGCCGCTC 1920
 Db 11776 ATGTGAACCACTTGAAGAACAAAGAAAGAGCTGGGCTTTCTTACCTCCATCGCCGCTC 11835
 Qy 1921 ATGAATCTCTGCTCCGTGCTGATTTGAAGCTTTGAGAGGACCAAGGCTGAAGGT 1980
 Db 11836 ATGAATCTCTGCTCCGTGCTGATTTGAAGCTTTGAGAGGACCAAGGCTGAAGGT 11895
 Qy 1981 CTGGGCGTGGGTCTGGAAGGTTCGGCGGAGAGAAACATGACAGCGCGAGTTCAAC 2040
 Db 11896 CTGGGCGTGGGTCTGGAAGGTTCGGCGGAGAGAAACATGACAGCGCGAGTTCAAC 11955
 Qy 2041 TGGGCACTCTTCAAGGTTCACTTCAAGCTCACTGTGAAGACCAACTTGGACTGGCAAG 2100
 Db 11956 TGGGCACTCTTCAAGGTTCACTTCAAGCTCACTGTGAAGACCAACTTGGACTGGCAAG 12015
 Qy 2101 TACCTGCAACTCAGGCGGCTGAACAGAACAGTGAACAGTGTCACTGCAACCTTCCAG 2160
 Db 12016 TACCTGCAACTCAGGCGGCTGAACAGAACAGTGAACAGTGTCACTGCAACCTTCCAG 12075
 Qy 2161 TACCTGCTGGCGCTGCAAGAGTCCCATCAGTGAACCTTCACTGCACTCACTCAAGCAAGAA 2220
 Db 12076 TACCTGCTGGCGCTGCAAGAGTCCCATCAGTGAACCTTCACTGCACTCACTCAAGCAAGAA 12135
 Qy 2221 CTGATGCAACCCGCGCGGCAAGACGAACTTCTTCAAGGCACTTGGCGTTCCTCCAGTA 2280
 Db 12136 CTGATGCAACCCGCGCGGCAAGACGAACTTCTTCAAGGCACTTGGCGTTCCTCCAGTA 12195
 Qy 2281 TTCAACACCTTCACTGAAGTCAATACAGAGGACCTTGTACGAGAAATCAAGAGCTTTGGCT 2340
 Db 12196 TTCAACACCTTCACTGAAGTCAATACAGAGGACCTTGTACGAGAAATCAAGAGCTTTGGCT 12255
 Qy 2341 CACTCAGAGTTGTGGGACGCTGTGGTGTTCCTGTTCTTATTCCTCCACATGAGAGAC 2400
 Db 12256 CACTCAGAGTTGTGGGACGCTGTGGTGTTCCTGTTCTTATTCCTCCACATGAGAGAC 12315
 Qy 2401 AAGTGTGGAAGCACTCGTGGAGGTGACCTGTGAAGAACTCTCAATCTGCAAGAG 2460
 Db 12316 AAGTGTGGAAGCACTCGTGGAGGTGACCTGTGAAGAACTCTCAATCTGCAAGAG 12375
 Qy 2461 GACATGATCCCATGATGCTGTCAATGCTTGAAGAAATGTTTAAATGTTAACTTCGCGC 2520
 Db 12376 GACATGATCCCATGATGCTGTCAATGCTTGAAGAAATGTTTAAATGTTAACTTCGCGC 12435
 Qy 2521 AAGCAATGTTGGAACACACTAATGAATGGCTTCCAAAGTGAATCTGTAATTC 2580
 Db 12436 AAGCAATGTTGGAACACACTAATGAATGGCTTCCAAAGTGAATCTGTAATTC 12495
 Qy 2581 TTGCAATGTTCTCAAGCTGAAGGACCTGACCTCAGGCGCAGCTTCCAGAGATTGAT 2640
 Db 12496 TTGCAATGTTCTCAAGCTGAAGGACCTGACCTCAGGCGCAGCTTCCAGAGATTGAT 12555
 Qy 2641 GCCAATTAACGACGCTGCTGTGCTCCAGAGACTTCAAGAGAAATGGAACAACAGAG 2700
 Db 12556 GCCAATTAACGACGCTGCTGTGCTCCAGAGACTTCAAGAGAAATGGAACAACAGAG 12615
 Qy 2701 AATTATATCTCCGAAAGAAATCGAGTTCTCTTACCTGCTGCGAGACCAACAGAGCGC 2760
 Db 12616 AATTATATCTCCGAAAGAAATCGAGTTCTCTTACCTGCTGCGAGACCAACAGAGCGC 12675
 Qy 2761 AAGTTAGATTACATGGTTTCTGCGACGCTTCCAGAGCTGCGCAAGAGATCGGGTTT 2820

Db 12676 AAGTTAGATTACATGGTTTCTGCGACCGTTTCCAGAGAGCTGCCAAGAGATCGGGTTT 12735
 Qy 2821 AACTTGGCGGNTTACTGACTAATGTTGTAACATATATGCGGAAAGAGCTAGATTGGCA 2880
 Db 12736 AACTTGGCGGNTTACTGACTAATGTTGTAACATATATGCGGAAAGAGCTAGATTGGCA 12795
 Qy 2881 CGTTTCTGAGAGACGCGAGGTTCAAGTCTGAACTTCACTTGAACCAATTCCTGGCGGATC 2940
 Db 12796 CGTTTCTGAGAGACGCGAGGTTCAAGTCTGAACTTCACTTGAACCAATTCCTGGCGGATC 12855
 Qy 2941 GAGATCATGGCGGCTCCAGCGCATGAGCGTGTCTAATCTTGAATATAGAGATCTAAT 3000
 Db 12856 GAGATCATGGCGGCTCCAGCGCATGAGCGTGTCTAATCTTGAATATAGAGATCTAAT 12915
 Qy 3001 A 3001
 Db 12916 A 12916

RESULT 3
 ADM68757
 ID ADM68757 standard; DNA; 15679 BP.
 XX
 AC ADM68757;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Heliothis virescens ryanodine receptor encoding DNA SEQ ID NO:1.
 XX
 KW ryanodine receptor; insect ion channel; insecticide; pesticide;
 KW calcium balance disruption; receptor calcium release mechanism; gene; ds.
 XX
 OS Heliothis virescens.
 XX
 FH Key Location/Qualifiers
 FT CDS 251..15679
 FT /tag= a
 FT /product= "ryanodine receptor"
 XX
 FN W02004027042-A2.
 XX
 PD 01-APR-2004.
 XX
 PF 23-SEP-2003; 2003WO-US029834.
 XX
 PR 23-SEP-2002; 2002US-0412795P.
 PR 18-NOV-2002; 2002US-0427324P.
 XX
 PA (DUPO) DU PONT DE MEMOURS & CO E I.
 XX
 PI Caspar T, Cordova D, Gutteridge S, Raub J, Smith RM, Wu L;
 PI Tao Y;
 DR P-PsDB; ADM68758.
 XX
 PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
 PT for isolating other pest ryanodine receptors and in developing screens to
 PT identify insecticidally active compounds.
 XX
 PS Claim 6; SEQ ID NO 1; 687bp; English.
 XX
 CC The present invention describes an isolated nucleotide fragment (1)
 CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
 CC having an amino acid sequence identity of at least 80% when compared to a
 CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
 CC 128, 130, 144, or 146; or (b) the complement of (a). (1) comprises a
 CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
 CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
 CC construct comprising (1) operably linked to at least one regulatory
 CC sequence; (2) a transformed host cell comprising the recombinant
 CC construct; (3) a method to isolate (1) encoding ryanodine receptors and
 CC related polypeptides; (4) an isolated polypeptide having ryanodine

QY 1786 AGCGAGATGTCATGAGAGCTTTACAGCTCGGTATTAAGTATCTAGAGGCGCGCAATAT 1845
 DB 12077 AGCGAGATGTCATGAGAGCTTTACAGCTCGGTATTAAGTATCTAGAGGCGCGCAATAT 12316
 QY 1846 GATATACAGATGGGTATGTTGACCACTTTAAAGACAGAAAGAGCTGGCTTTTACG 1905
 DB 12137 GATATACAGATGGGTATGTTGACCACTTTAAAGACAGAAAGAGCTGGCTTTTACG 12196
 QY 1906 TCCATCGCGCGCTCATGAACTCGCTCGGTCTGAACTGATCTTGAAGCCTTGAGAGAAC 1965
 DB 12137 TCCATCGCGCGCTCATGAACTCGCTCGGTCTGAACTGATCTTGAAGCCTTGAGAGAAC 12256
 QY 1966 ACCAAGCTGAAGGTCTGCGCGCTGAGTCTGAAAGGTGCGCGGAGAGAAAGAACATGCA 2025
 DB 12257 ACCAAGCTGAAGGTCTGCGCGCTGAGTCTGAAAGGTGCGCGGAGAGAAAGAACATGCA 12316
 QY 2026 GACGCGAGTTCACTCGCGCACTTTCAAGTTCACTTCAAGCTCACTGTGAGAGACAAAC 2085
 DB 12317 GACGCGAGTTCACTCGCGCACTTTCAAGTTCACTTCAAGCTCACTGTGAGAGACAAAC 12376
 QY 2086 TTGACCTGGCAAGTCTACCTGGAATCTAGCGCGGTAAACAGAACAGTGAACGTGATC 2145
 DB 12377 TTGACCTGGCAAGTCTACCTGGAATCTAGCGCGGTAAACAGAACAGTGAACGTGATC 12436
 QY 2146 ATCTGACCGTGCATCTACCTGCGGCTGAGAGTCAATCATGGAATTTCTACTGCGAC 2205
 DB 12437 ATCTGACCGTGCATCTACCTGCGGCTGAGAGTCAATCATGGAATTTCTACTGCGAC 12496
 QY 2206 TACTCAAGCAAGAACTGATGACCCGCGCGGCAAGGCAATTTCTCAAGGCAATTTGCG 2265
 DB 12497 TACTCAAGCAAGAACTGATGACCCGCGCGGCAAGGCAATTTCTCAAGGCAATTTGCG 12556
 QY 2266 GTGGCTTCCCAAGTATTTCAACCCCTCACTGAAGTCAACAGAGACTTTGACAGAAAT 2325
 DB 12557 GTGGCTTCCCAAGTATTTCAACCCCTCACTGAAGTCAACAGAGACTTTGACAGAAAT 12616
 QY 2326 CAGCAGGCTTTGGCTCACTCCAGTGTGAGAGCGCTGCGGCTTCTGTTCTTATTC 2385
 DB 12617 CAGCAGGCTTTGGCTCACTCCAGTGTGAGAGCGCTGCGGCTTCTGTTCTTATTC 12676
 QY 2386 TCCCAATGACAGAGCAAGTGTGAGAGCACTGTCGAGGTGAGCTTCTGAAGAACTC 2445
 DB 12677 TCCCAATGACAGAGCAAGTGTGAGAGCACTGTCGAGGTGAGCTTCTGAAGAACTC 12736
 QY 2446 CTCAATCTGCAGAGAGCAATGATCCCAATGATGCTGCTGATGAGAAATTTGTT 2505
 DB 12737 CTCAATCTGCAGAGAGCAATGATCCCAATGATGCTGCTGATGAGAAATTTGTT 12796
 QY 2506 AATGTACAAATCGGAGCAAAATGTTGAGCACTAGTAAATGAGGCTCCCAAGTGA 2565
 DB 12797 AATGTACAAATCGGAGCAAAATGTTGAGCACTAGTAAATGAGGCTCCCAAGTGA 12856
 QY 2566 CTGATCTGAAATTACTTGCACATGTTCTCAAGCTGAAGAGCACTGACCGCCAGC 2625
 DB 12857 CTGATCTGAAATTACTTGCACATGTTCTCAAGCTGAAGAGCACTGACCGCCAGC 12916
 QY 2626 TTCCGAGAGTATGATCCCAATACAGCGGCTGGTCTGCGCAAGAGCTTCAAGAGAAA 2685
 DB 12917 TTCCGAGAGTATGATCCCAATACAGCGGCTGGTCTGCGCAAGAGCTTCAAGAGAAA 12976
 QY 2686 ATGGAACCAAGAGAGTATATCTGCGGAAGAAATCGATCTCTGCTGCTGCGAG 2745
 DB 12977 ATGGAACCAAGAGAGTATATCTGCGGAAGAAATCGATCTCTGCTGCTGCGAG 13036
 QY 2746 ACAGACCAAGAGAGTATGATCCCAATACAGCGGCTGGTCTGCGCAAGAGCTTCC 2805
 DB 13037 ACAGACCAAGAGAGTATGATCCCAATACAGCGGCTGGTCTGCGCAAGAGCTTCC 13096
 QY 2806 AAGGAGATCGGTTTAACTTGGCGGTGTTACTGACTAACTTGTCTGAACATATGCGAAC 2865
 DB 13097 AAGGAGATCGGTTTAACTTGGCGGTGTTACTGACTAACTTGTCTGAACATATGCGAAC 13156

QY 2866 GAGCCTAGATTGCAAGCTTCTGAGAGACGCGAGTTCACTGTAAGTCTTGAACCA 2925
 DB 13157 GAGCCTAGATTGCAAGCTTCTGAGAGACGCGAGTTCACTGTAAGTCTTGAACCA 13216
 QY 2926 TTCTGGGCGGTATCGAGATGATGAGCGGCTTCAAGGCAATCGAGCGTCTACTGAG 2985
 DB 13217 TTCTGGGCGGTATCGAGATGATGAGCGGCTTCAAGGCAATCGAGCGTCTACTGAG 13276
 QY 2986 ATCAAGAGTCTAATA 3001
 DB 13277 ATCAAGAGTCTAATA 13292

RESULT 4
 ADM6885
 ID ADM6885 standard; DNA; 15405 BP.
 XX
 AC ADM6885;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Heliothis virescens ryanodine receptor encoding DNA SEQ ID NO:129.
 XX
 KW ryanodine receptor; insect ion channel; insecticide; pesticide;
 KW calcium balance disruption; receptor calcium release mechanism; gene; ds.
 OS Heliothis virescens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..15405
 FT /*tag= a
 FT /product= "ryanodine receptor"
 XX
 PN WO2004027042-A2.
 PD 01-APR-2004.
 XX
 PF 23-SEP-2003; 2003WO-US029834.
 XX
 PR 23-SEP-2002; 2002US-0412795P.
 PR 18-NOV-2002; 2002US-0427324P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Caspar T, Cordova D, Gutteridge S, Rauh JJ, Smith RM, Wu L;
 PI Tao Y;
 XX
 DR WPI; 2004-295411/27.
 DR P-PSDB; ADM68895.
 XX
 PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
 PT for isolating other pest ryanodine receptors and in developing screens to
 PT identify insecticidally active compounds.
 XX
 PS Claim 6; SEQ ID NO 129; 687bp; English.
 CC
 CC The present invention describes an isolated nucleotide fragment (1)
 CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
 CC having an amino acid sequence identity of at least 80% when compared to a
 CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
 CC 128, 130, 144, or 146; or (b) the complement of (a). (1) comprises a
 CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
 CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
 CC construct comprising (1) operably linked to at least one regulatory
 CC sequence; (2) a transformed host cell comprising the recombinant
 CC construct; (3) a method to isolate (1) encoding ryanodine receptors and
 CC related polypeptides; (4) an isolated polypeptide having ryanodine
 CC receptor activity; (5) a method for evaluating at least one compound for
 CC its ability to modulate calcium homeostasis; (6) a method for evaluating
 CC at least one compound which modulates ryanodine receptor activity; (7) an
 CC isolated nucleic acid fragment encoding an insect ion channel comprising
 CC at least two fully defined polypeptide sequences selected from SEQ ID
 CC NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,

CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an insect ion channel; (9) a method for expressing an isolated nucleic acid fragment encoding a toxic insect ion channel; and (10) recombinant construct comprising in the 5' to 3' direction a promoter operably linked to an isolated nucleic acid fragment encoding a toxic insect ion channel. CC The isolated nucleic acid fragment (II) encoding a ryanodine receptor is useful for the isolation of other pest ryanodine receptors and developing CC of screens to identify insecticidally active compounds. The nucleic acid CC fragments are useful as pesticides, fragments of protein for antibody CC production, fragments of protein for determination of the structure of CC insecticide binding sites and in the identification of insecticides that CC disrupt the calcium balance in cells through other messengers that CC interact with the receptor calcium release mechanism. The present CC sequence is used in the exemplification of the present invention.

Sequence 15405 BP; 4086 A; 3850 C; 4173 G; 3296 T; 0 U; 0 Other;

Query Match 94.8%; Score 2846.4; DB 12; Length 15405;

Beet Local Similarity 96.8%; Pred. No. 0;

Matches 2920; Conservative 0; Mismatches 81; Indels 15; Gaps 1;

QY 1 CAGTTCCTCTGCTGACAGATCGCTGACCATTTCTTGGAAAGCCCAAGATATATGAG 60
Db 10003 CAGTTCCTCTGCTGACAGATCGCTGACCATTTCTTGGAAAGCCCAAGATATATGAG 10062
QY 61 AAAATGAAACAATGATGATCCGACGCTGAGACGATCTTAAAGCGAGTGGACCAATTCGTG 120
Db 10063 AAAATGAAACAATGATGATCCGACGCTTAAAGCGAGTGGACCAATTCGTG 10122
QY 121 GAGTCAGCAAGACGTAGACAGAGGCGCGCATATCATCGATGAGTGTCTGCTTATCTC 180
Db 10123 GAGTCAGCAAGACGTAGACAGAGGCGCGCATATCATCGATGAGTGTCTGCTTATCTC 10182
QY 181 TGTTCCTATTTGCGCTTGTGTGTGGACAGAGGCGCTGATTAATGTTACTCTTACTGCGCA 240
Db 10183 TGTTCCTATTTGCGCTTGTGTGTGGACAGAGGCGCTGATTAATGTTACTCTTACTGCGCA 10242
QY 241 AACCACTGTAACAATGTAACAGCGGAACAATGAAACAAGCTCTCAAGAAATGTTCTGAAG 300
Db 10243 AACCACTGTAACAATGTAACAGCGGAACAATGAAACAAGCTCTCAAGAAATGTTCTGAAG 10302
QY 301 CTCATCAAAAAGAAATGCGGAATGAGAACCGCGGTGATGATCCCGCATGCCACCTTAC 360
Db 10303 CTCATCAAAAAGAAATGCGGAATGAGAACCGCGGTGATGATCCCGCATGCCACCTTAC 10362
QY 361 ACGGACGATCATCATCAAGAGCTCCGAGGAACCTGCTGAGGAAATCTTCTGCGCGCTC 420
Db 10363 ACGGACGATCATCATCAAGAGCTCCGAGGAGTTGCTGAGGAAATCTTCTGCGCGCTC 10422
QY 421 GCTGAACTGTTCGCAACCGACGGAACAATATGTTCCATTAAGAGAGAGCTTGAAGGAG 480
Db 10423 GCTGAACTGTTCGCAACCGACGGAACAATATGTTCCATTAAGAGAGAGCTTGAAGGAG 10482
QY 481 TTTTATTAAGTGTGTAACAGAGACACATCCCAAGTAAGTCTCAGATTAAGAAAGACTGG 540
Db 10483 TTTTATTAAGTGTGTAACAGAGACACATCTCAAGTAAGTCAAGTAAGAAAGACTGG 10542
QY 541 CAGCTGTGTGTCAGAGACATCTACTCTTACCGCGTGTCACTCAAGTAAGTGAAGCTG 600
Db 10543 CAGCTGTGTGTCAGAGACATCTACTCTTACCGCGTGTCACTCAAGTAAGTGAAGCTG 10602
QY 601 CAGAGGAACAAGCTGCTGAGGAACAATGTTCCAGAGGCGGAAGAGCTGTACACACAGTG 660
Db 10603 CAGAGGAACAAGCTGCTGAGGAACAATGTTCCAGAGGCGGAAGAGCTGTACACACAGTG 10662
QY 661 GCTGAAATCTTCAACATCTGTGTCGAAGGCGCATCTTCTTGAAGAGAAACAGAACTTC 720
Db 10663 GCTGAAATCTTCAACATCTGTGTCGAAGGCGCATCTTCTTGAAGAGAAACAGAACTTC 10722
QY 721 ATCTGTGCAAGAAATGATTAACATGAGTGTGATTAATGCAACAGCAACAAGAAAGTG 780
Db 10723 ATCTGTGCAAGAAATGATTAACATGAGTGTGATTAATGCAACAGCAACAAGAAAGTG 10782

QY 781 ACACAGTAAACAGATGTAATCTCTCAAGTGTGTGAAAGAAAGAAAGAACACCTGTAT 840
Db 10783 ACACAGTAAACAGATGTAATCTCTCAAGTGTGTGAAAGAAAGAAAGAACACCTGTAT 10842
QY 841 AAGAAAGCGCAAGAAAGCAAGGAAGTCCAGCGCTTAAATGTAAGTGTGTGTAAGAG 900
Db 10843 AAGAAAGCGCAAGAAAGCAAGGAAGTCCAGCGCTTAAATGTAAGTGTGTGTAAGAG 10902
QY 901 TTTTACAGTGTGCTTAACTTAATGCTGTGCAAGAACAAAGAACTGTGACATTTGT 960
Db 10903 TTTTACAGTGTGCTTAACTTAATGCTGTGCAAGAACAAAGAACTGTGACATTTGT 10962
QY 961 AAGACAGTGTCTG-----AAGAAATGTCAAGCAAGATGTGCAAGAA 1005
Db 10963 AAGACAGTGTCTGAGATGAGGACCTCAAGAAATGTCAAGCAAGATGTGCAAGAA 11022
QY 1006 TTGCGGAAGACCAAGCTGACATCTTCCAGATTAATATATCCGCAAGCAAAATGTTGG 1065
Db 11023 TTGCGGAAGACCAAGCTGACATCTTCCAGATTAATATATCCGCAAGCAAAATGTTGG 11082
QY 1066 CAACATTACTTGTATACAGATTAAGTTCGAAGAGTAAGACAAATATATCTGTGAAGT 1125
Db 11083 CAACATTACTTGTATACAGATTAAGTTCGAAGAGTAAGACAAATATATCTGTGAAGT 11142
QY 1126 GCTGAAATTAAGCCAAAGATTAATGATGATACCGTGAAGAAATCGTGTATGATTA 1185
Db 11143 GCTGAAATTAAGCCAAAGATTAATGATGATACCGTGAAGAAATCGTGTATGATTA 11202
QY 1186 GTGCTTTTGGATTTGCAATATGATGACATATCCCAACAATATGATGAAGATGTGACCG 1245
Db 11203 GTGCTTTTGGATTTGCAATATGATGACATATCCCAACAATATGATGAAGATGTGACCG 11262
QY 1246 TCGGTGTGTGATATACCAACCAAGCGCGGTGATGATGCTGTCTTCCGACAACTTCA 1305
Db 11263 TCGGTGTGTGATATACCAACCAAGCGCGGTGATGATGCTGTCTTCCGACAACTTCA 11322
QY 1306 CATTTCTGTCCGAGACATCGAGCGTGTATCATCTTGTGCTGACAGTACATGAGCTGTG 1365
Db 11323 CATTTCTGTCCGAGACATCGAGCGTGTATCATCTTGTGCTGACAGTACATGAGCTGTG 11382
QY 1366 TTGGAAGAGGAACAATTTGGAACAAGATTAATGTAAGATCTTCAATCATTCGAA 1425
Db 11383 TTGGAAGAGGAACAATTTGGAACAAGATTAATGTAAGATCTTCAATCATTCGAA 11442
QY 1426 GACGACAGCTGGAAGAAAGATGACGTGTGGAAGAAAGTGAAGAGCTGACCCCTGACG 1485
Db 11443 GACGACAGCTGGAAGAAAGATGACGTGTGGAAGAAAGTGAAGAGCTGACCCCTGACG 11502
QY 1486 CAGCTGTGCAACCTTCTGTGCGGTGCCATGATGAGAGTCCGCGCTTTGCAAGAG 1545
Db 11503 CAGCTGTGCAACCTTCTGTGCGGTGCCATGATGAGAGTCCGCGCTTTGCAAGAG 11562
QY 1546 GATTCCTTAACATGTCTTACGCAACATCATAGCGAAGTCCCTGTGGAAGAAAGAGAA 1605
Db 11563 GATTCCTTAACATGTCTTACGCAACATCATAGCGAAGTCCCTGTGGAAGAAAGAGAA 11622
QY 1606 GAAAGGGGTGGGAGGAAGAGAAAGGGGTGGAAGAGAGCTGAAAGCAAGGCA 1665
Db 11623 GAAAGGGGTGGGAGGAAGAGAAAGGGGTGGAAGAGAGCTGAAAGCAAGGCA 11682
QY 1666 GCCAGTATACAGAACAAAGATTAAGAAACAAAGCTCTTATTCACCAAGCGCGCTG 1725
Db 11683 GCCAGTATACAGAACAAAGATTAAGAAACAAAGCTCTTATTCACCAAGCGCGCTG 11742
QY 1726 GCGGACCGTGTGCTTCCGAAATGATGTGTGCTGCAATCTCCGCGTCCAAAGGCTGGCC 1785
Db 11743 GCGGACCGTGTGCTTCCGAAATGATGTGTGCTGCAATCTCCGCGTCCAAAGGCTGGCC 11802
QY 1786 AGCGAGTGTGATGAAGACTTATACAGCTCGGATTAATGATTAAGTGAAGGCGCAATAT 1845
Db 11803 AGCGAGTGTGATGAAGACTTATACAGCTCGGATTAATGATTAAGTGAAGGCGCAATAT 11862
QY 1846 GATATACAGATGAGTATGTTGAACAACCTGAAAGCAAGAAAGACGTGGGCTTTTACG 1905

Db 11863 GATATACAGATGGGTATGTGAACCACTTGAAGACAAGAAAGACGTGGATTTCTTCAAG 11922
Gy 1906 TTCCATCGCGCGGCTCATATGAATCCCTGCTCCGCTGCTCATCTTGAAGCCCTTGCAGAGAAC 1965
Db 11923 TTCCATCGCGCGGCTCATATGAATCCCTGCTCCGCTGCTCATCTTGAAGCCCTTGCAGAGAAC 11982
Gy 1966 ACCAAGGCTGAAGGTCTGGGCGTGGGCTGGAAGGTGCGCGGAGAGAGAAACATGCAAT 2025
Db 11983 ACCAAGGCTGAAGGTCTGGGCGTGGGCTGGAAGGTGCGCGGAGAGAGAAACATGCAAT 12042
Gy 2026 GACGCCGAGTTCACTCTGCGCACTCTTCAAGTTTCACTTCAAGCTCACTGTGAAGACACAAC 2085
Db 12043 GACGCCGAGTTCACTCTGCGCACTCTTCAAGTTTCACTTCAAGCTCACTGTGAAGACACAAC 12102
Gy 2086 TTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAAACAACAACAGTGAACCTGTCTC 2145
Db 12103 TTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAAACAACAACAGTGAACCTGTCTC 12162
Gy 2146 ATCTGACCGTGCATACCTGCGGCTGCGGCTGCGAGAGTGCATCATGAGACTTCTACTGGCAC 2205
Db 12163 ATCTGACCGTGCATACCTGCGGCTGCGGCTGCGAGAGTGCATCATGAGACTTCTACTGGCAC 12222
Gy 2206 TACTGACGAGAACTGATCGACCCGCGGCAAGCGAACTTCTTCAAGGCCATTGGC 2265
Db 12223 TACTGACGAGAACTGATCGACCCGCGGCAAGCGAACTTCTTCAAGGCCATTGGC 12282
Gy 2266 GTGGCTTCCCAAGTATTCAACACCTCTCACTGAAGTCAACAGGACCTTGTACGCAAAAT 2325
Db 12283 GTGGCTTCCCAAGTATTCAACACCTCTCACTGAAGTCAACAGGACCTTGTGTACTCAAAAC 12342
Gy 2326 CAGCAGGCTTTGGCTCACTCCAGGTGTGGAGCGCTGTCCGAGTTCCTGTCTCTATTC 2385
Db 12343 CAGCAGGCTTTGGCTCACTCCAGGTGTGGAGCGCTGTCCGAGTTCCTGTCTCTATTC 12402
Gy 2386 TCCCACTGCGAGCAAGTGTTCGAAAGCACTGTGCGAGGTGACCTGTGAAGAACTC 2445
Db 12403 TCCCACTGCGAGCAAGTGTTCGAAAGCACTGTGCGAGGTGACCTGTGAAGAACTC 12462
Gy 2446 CTCAATCTGCGAGAGCAATGATCCCATGATGCTGTCTCATGCTTGAAGAAATTTGTT 2505
Db 12463 CTCAATCTGCGAGAGCAATGATGCTGTCTCATGCTTGAAGAAATTTGTT 12522
Gy 2506 AATGATCAATGCGGAGAAATGATGAGCACTAGTAAATGCGGCTCCAGAGTGA 2565
Db 12523 AATGATCAATGCGGAGAAATGATGAGCACTAGTAAATGCGGCTCCAGAGTGA 12582
Gy 2566 CTGATCTGGAATATCTTGCACATGTTCTCAAGCTGAAGSACCTGACCTCCAGCGCCAGC 2625
Db 12583 CTGATCTGGAATATCTTGCACATGTTCTCAAGCTGAAGSACCTGACCTCCAGCGCCAGC 12642
Gy 2626 TTCCAGAGATTGATGCCAATACAGCGGTGGGTGCTGCCAGAGACTTCAAGAGAAA 2685
Db 12643 TTCCAGAGATTGATGCCAATACAGCGGTGGGTGCTGCCAGAGACTTCAAGAGAAA 12702
Gy 2686 ATGGAACAACAGAAAGTTATCTGCCAAGAAATCGAGTTCTCTAGCTTGTGCTGGAG 2745
Db 12703 ATGGAACAACAGAAAGTTATCTGCCAAGAAATCGAGTTCTCTAGCTTGTGCTGGAG 12762
Gy 2746 ACGAACACGACGCGAAGTTAGTACATCGGTTTCTGAGACCGTTTCCACGAGCCTCC 2805
Db 12763 ACGAACACGACGCGAAGTTAGTACATCGGTTTCTGAGACCGTTTCCACGAGCCTCC 12822
Gy 2806 AAGAGATCGGGTTTAACTTGGCGGTGTTACTGACTAATCTTGTGAACATATGCGGAAC 2865
Db 12823 AAGAGATCGGGTTTAACTTGGCGGTGTTACTGACTAATCTTGTGAACATATGCGGAAC 12882
Gy 2866 GAGCCTAATTTGGCAGCTTCTCTGAGACGCGAGTTCAAGTCTGAACACTTGCAGACA 2925
Db 12883 GAGCCTAATTTGGCAGCTTCTCTGAGACGCGAGTTCAAGTCTGAACACTTGCAGACA 12942
Gy 2926 TTCCTGGCGCTTATGAGATCAATGGGCGGCTCAAGCGCATGAGCGTGTACTTCCAG 2985

Db 12943 TTCCTGGCGCTTATGAGATCATGGCGGCTTAAAGCGCATGAGCGAGTCTACTTCGAG 13002
Gy 2986 ATCAAGAGTCTAATA 3001
Db 13003 ATCAAGAGTCTAATA 13018
RESULT 5
ID ADM68899 standard; DNA; 15429 BP.
XX
AC ADM68899;
XX
DT 17-JUN-2004 (first entry)
XX
DE Heliothis virescens ryanodine receptor encoding DNA SEQ ID NO:143.
XX
KW ryanodine receptor; insect ion channel; insecticide; peaticide;
XX calcium balance disruption; receptor calcium release mechanism; gene; ds.
XX Heliothis virescens.
XX
FH Key Location/Qualifiers
FT CDS 1..15429
FT /tag= a
FT /product= "ryanodine receptor"
XX
PM WO200402742-A2.
XX
PD 01-APR-2004.
XX
PF 23-SEP-2003; 2003WO-US029834.
XX
PR 23-SEP-2002; 2002US-0412795P.
PR 18-NOV-2002; 2002US-0427324P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Caspar T, Cordova D, Gutteridge S, Rauh J, Smith RM, Wu L,
PI Tao Y,
XX
DR WPI; 2004-295411/27.
XX P-PSDB; ADM68900.
XX
PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT for isolating other pest ryanodine receptors and in developing screens to
PT identify insecticidally active compounds.
XX
PS Claim 6; SEQ ID NO 143; 687bp; English.
XX
CC The present invention describes an isolated nucleotide fragment (1)
CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (1) comprises a
CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC construct comprising (1) operably linked to at least one regulatory
CC sequence; (2) a transformed host cell comprising the recombinant
CC construct; (3) a method to isolate (1) encoding ryanodine receptors and
CC related polypeptides; (4) an isolated polypeptide having ryanodine
CC receptor activity; (5) a method for evaluating at least one compound for
CC its ability to modulate calcium homeostasis; (6) a method for evaluating
CC at least one compound which modulates ryanodine receptor activity; (7) an
CC isolated nucleic acid fragment encoding an insect ion channel comprising
CC at least two fully defined polypeptide sequences selected from SEQ ID
CC NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC insect ion channel; (9) a method for expressing an isolated nucleic acid
CC fragment encoding a toxic insect ion channel; and (10) recombinant
CC construct comprising in the 5' to 3' direction a promoter operably linked
CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC The isolated nucleotide fragment (1) encoding a ryanodine receptor is

CC useful for the isolation of other pest ryanodine receptors and developing
CC of screens to identify insecticidally active compounds. The nucleic acid
CC fragments are useful as pesticides, fragments of protein for antibody
CC production, fragments of protein for determination of the structure of
CC insecticide binding sites and in the identification of insecticides that
CC disrupt the calcium balance in cells through other messengers that
CC interact with the receptor calcium release mechanism. The present
CC sequence is used in the exemplification of the present invention.

XX Sequence 15429 BP; 4084 A; 3856 C; 4190 G; 3299 T; 0 U; 0 Other;

Query Match 94.8%; Score 2844.8; DB 12; Length 15429;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2319; Conservative 0; Mismatches 82; Indels 15; Gaps 1;

QY 1 CAGTTCCTCTGCTGAAGAGATCGCTGACATCTCTTGGAAAGCCCAAGACATTAATGAG 60
DB 10027 CAGTTCCTCTGCTGAAGAGATCGCTGACATCTCTTGGAAAGCCCAAGACATTAATGAG 10086
QY 61 AAAATGGAACAATGCATGCCGCGCTTGAAGACATCTTGAAGCGAGTGGACCAATTCGTG 120
DB 10087 AAAATGGAACAATGCATGCCGCGCTTGAAGACATCTTGAAGCGAGTGGACCAATTCGTG 10146
QY 121 GAGTCAGACAAGACGTAGACAGAGCGCGCATATCATCGATGTGAGTGTCTCTTACTC 180
DB 10147 GAGTCAGACAAGACGTAGACAGAGCGCGCATATCATCGATGTGAGTGTCTCTTACTC 10206
QY 181 TGTTCCTATTTGCCGTTCTGTGGGACAGAGGGCCGTGAATGTACTCTACTGGCGGA 240
DB 10207 TGTTCCTATTTGCCGTTCTGTGGGACAGAGGGCCGTGAATGTACTCTACTGGCGGA 10266
QY 241 AACCACTGAACAATGTGAACAGCGGAACAATGAACGACTCTCAAGAAATGTTCTGAAG 300
DB 10267 AACCACTGAACAATGTGAACAGCGGAACAATGAACGACTCTCAAGAAATGTTCTGAAG 10326
QY 301 CTCATCAAAAAGAACATGCGCAATGAGAACGCGCGTGTGATGACCCGATGCGCACTTAC 360
DB 10327 CTCATCAAAAAGAACATGCGCAATGAGAACGCGCGTGTGATGACCCGATGCGCACTTAC 10386
QY 361 ACGGAGCAGATCATCATCAACAGCTCCGAGGAACCTGTAGGGAAATTCCTCTCCGCTC 420
DB 10387 ACGGAGCAGATCATCATCAACAGCTCCGAGGAATTCCTGTAGGGAAATTCCTCTCCGCTC 10446
QY 421 GCTGAACGTGTTCGCAAAACGCAACGCAATATGTTCCATTAAGAGAGAGCTTGAAGGGG 480
DB 10447 GCTGAACGTGTTCGCAAAACGCAACGCAATATGTTCCATTAAGAGAGAGCTTGAAGGGG 10506
QY 481 TTTATTAAGTGTCAACAGAGACATCCCAAGTGAAGTCTCAGATTAACAAGAACTGG 540
DB 10507 TTTATTAAGTGTCAACAGAGACATCCCAAGTGAAGTCTCAGATTAACAAGAACTGG 10566
QY 541 CAGCTGCTGTCAAGAGACATCTACTCTTACCCTGCTCATCAAGATAGTGAACCTG 600
DB 10567 CAGCTGCTGTCAAGAGACATCTACTCTTACCCTGCTCATCAAGATAGTGAACCTG 10626
QY 601 CAGAGGAACAACGCTGCTGAGGAACAATGTTCCAGAGCGGGAAGACTGTACAACACCTG 660
DB 10627 CAGAGGAACAACGCTGCTGAGGAACAATGTTCCAGAGCGGGAAGACTGTACAACACCTG 10686
QY 661 GCTGAATCTTCAACATCTGTGCGAAGAGCCAGATCTTCTTGAAGAGAGAACTTC 720
DB 10687 GCTGAATCTTCAACATCTGTGCGAAGAGCCAGATCTTCTTGAAGAGAGAACTTC 10746
QY 721 ATCTCTGCAACGAATGATTAACATGAGTGTGATTAATGCAACAGCAACAAGAGAGT 780
DB 10747 ATCTCTGCAACGAATGATTAACATGAGTGTGATTAATGCAACAGCAACAAGAGAGT 10806
QY 781 ACAGCAGTAACAGATGTGTAATCTCAAGAGTGTGAAAGAAAGAAAGAACACCTGAT 840
DB 10807 ACAGCAGTAACAGATGTGTAATCTCAAGAGTGTGAAAGAAAGAAAGAACACCTGAT 10866
QY 841 AAGAAAGCGCAACAAGACAGAGAGTCCAGCGTCTTAATGTGATGTTGTGAAGAG 900

DB 10867 AAGAAAGCGCAACAAGACAGAGAGTCCAAAGCTCCCTAATGTGATGTTGTGAAGAG 10926
QY 901 TTGTTACAGATGGCTTAACTTAATGTGCTGGCAGAGAACAGATGTGACATTTG 960
DB 10927 TTGTTACAGATGGCTTAACTTAATGTGCTGGCAGAGAACAGATGTGACATTTG 10986
QY 961 AAGACAGGTTCTG-----AAGAAATGTCAAGAACAGATGTGCAAGAA 1005
DB 10987 AAGACAGGTTCTGAAAGGTAGGAGCCCTCAAGAAATGTCAAGAACAGATGTGCAAGAA 11046
QY 1006 TTGCGAAGAGCCGAGCTGACATCTCCAGATTAATGATCCGAGAGCGAAATGTCTGG 1065
DB 11047 TTGCGAAGAGCCGAGCTGACATCTCCAGATTAATGATCCGAGAGCGAAATGTCTGG 11106
QY 1066 CAACATTACTGTATAGCAAGTTAGTTCCAGAGGTAAAGCAATATATCTGTGAAC 1125
DB 11107 CAACATTACTGTATAGCAAGTTAGTTCCAGAGGTAAAGCAATATATCTGTGAAC 11166
QY 1126 GCTGAATAATAGCGCAAGATTAATGATGATACCGTCAAGAAATCGTGTGATGA 1185
DB 11167 GCTGAATAATAGCGCAAGATTAATGATGATACCGTCAAGAAATCGTGTGATGA 11226
QY 1186 GTGCTTTTGGATTGCAATGATCGACATCCCAACAAATGATGAAGAAACGTGACCG 1245
DB 11227 GTGCTTTTGGATTGCAATGATCGACATCCCAACAAATGATGAAGAAACGTGACCG 11286
QY 1246 TCGGTGTGTGATTAACAACGCAAGCGCGCGTCAATCGCTTCGCAACAACTTCACTA 1305
DB 11287 TCGGTGTGTGATTAACAACGCAAGCGCGCGTCAATCGCTTCGCAACAACTTCACTA 11346
QY 1306 CATTCCTGCGAGACATCGAGCGTGTACATCTTGTGCTGCAAGTACATGAGCTGTG 1365
DB 11347 CATTCCTGCGAGACATCGAGCGTGTACATCTTGTGCTGCAAGTACATGAGCTGTG 11406
QY 1366 TTGGAAGAGAGAAACATTTGACAAAGATTAATGATGAAGAACTTACTCAATTCGAA 1425
DB 11407 TTGGAAGAGAGAAACATTTGACAAAGATTAATGATGAAGAACTTACTCAATTCGAA 11466
QY 1426 GACGAGAGCTGAAGAAAGTGAAGTGTGAGAGAAAGTGAAGAGCTGACCCCTCAAG 1485
DB 11467 GACGAGAGCTGAAGAAAGTGAAGTGTGAGAGAAAGTGAAGAGCTGACCCCTCAAG 11526
QY 1486 CAGCTGTCAACAATCTGTGCGGCTGCGATGATGAGAGTCCGCGCTTTGCAAGAG 1545
DB 11527 CAGCTGTCAACAATCTGTGCGGCTGCGATGATGAGAGTCCGCGCTTTGCAAGAG 11586
QY 1546 GATTCCTTAATCAATGTCTTAACGCAACATCATGCGAAGTCTGTGAGAAAGAGAA 1605
DB 11587 GATTCCTTAATCAATGTCTTAACGCAACATCATGCGAAGTCTGTGAGAAAGAGAA 11646
QY 1606 GAAGGGGTGTGGAGAGAAAGAGGGGTGAGAAAGAGAGCTGAAGAGCGACAG 1665
DB 11647 GAAGGGGTGTGGAGAGAAAGAGGGGTGAGAAAGAGAGCTGAAGAGCGACAG 11706
QY 1666 GCCAGTATACAGAACAGAAATGAGAAACAAAGCTCCTAATTCACCAAGCGGCTG 1725
DB 11707 GCCAGTATACAGAACAGAAATGAGAAACAAAGCTCCTAATTCACCAAGCGGCTG 11766
QY 1726 GCGGACCGGTGGTTCGCAAAATGTGTGCTGCAACATCTCCGCTGCAAAAGCCCTG 1785
DB 11767 GCGGACCGGTGGTTCGCAAAATGTGTGCTGCAACATCTCCGCTGCAAAAGCCCTG 11826
QY 1786 AGGAGATGTCAATGAAGACTTTACAGCTCGGTATAGTATACTGAGGGCGGCAATAT 1845
DB 11827 AGGAGATGTCAATGAAGACTTTACAGCTCGGTATAGTATACTGAGGGCGGCAATAT 11886
QY 1846 GATATACAGATGTGATGTTGAACAACCTTGAAGAACAAGAAAGACGTGGGCTTCTTAC 1905
DB 11887 GATATACAGATGTGATGTTGAACAACCTTGAAGAACAAGAAAGACGTGGGATTTCTTCA 11946
QY 1906 TCCATGCGCGGCTCATGAATCTGCTCCGCTGCTGATCTTGAAGCTTCCGAGAGAA 1965
DB 11947 TCCATGCGCGGCTCATGAATCTGCTCCGCTGCTGATCTTGAAGCTTCCGAGAGAA 12006

QY 301 CTGATCAAAAAGACATCGCGAATGAGACCGCGCTGTGATGACCCGCACTGCA 360
Db 10222 ATGATCAAGAAAGACATTTGGCAACGATTAACGCCCTTGTGATGACTCGCATTTGCCCTAT 10281
QY 361 ACGAGCAGATCATCATCAACAGCTCCGAGGAACGTGCTGAGGAAATTCCTTCTGTCCGCTC 420
Db 10282 ACGCAGCAGATTTATCATCAATACGTGGAGAGCTGCTCAAGAACCCGTTCTTGCCTGTG 10341
QY 421 GCTGACGTGTTCGCAACCGACCGACCAATATGTTCCATAAGAGAGAGCTTGAGGGGG 480
Db 10342 GCGAGCCGGGTGAAGAACCGCACTGAGAACATGCTGCAACAAGAGAGACAGATGAGAGA 10401
QY 481 TTTATTAAGTGTCAACAGAGCAACATCCAGGTAGGTCTCAGATACAGAAAGCTGG 540
Db 10402 TTTCATCAAGTGGGCCACGAGCACTTCGAGGTGAGAGCCAGCTCAGAGAGACTGG 10461
QY 541 CAGCTGCTGTCAAGAGATCTACTCTTCAACCGGCTGCTCATCAAGTACGTGACCTG 600
Db 10462 AATCTGTAAGTGCAGAGCATATATCTGTTCTATCCCTGCTCATCAAGTACGTGATCTG 10521
QY 601 CAGAGAACCACTGGCTCAGGACCAATGTTCCAGAGCGGAGAGCTTACCAACAGTG 660
Db 10522 CAGGAAACCACTGGCTGAGAGCAACATCCGAGGCGGAGAGCTTACCAACATGTG 10581
QY 661 GCTGAAATCTTCAACATCTGTGTCAGAGCCAGTACTTTTGAAAGAGAACAGACTTC 720
Db 10582 GCAGAGATCTTCAATATATGTGCTTAAAGCCAGTACTTCTTAAAGAGAGCAAACTTC 10641
QY 721 ATCTGTGCAACGAAATTGATTAACATGGTGTGATTAAGCCACAGCAACAAAGAGTGTG 780
Db 10642 ATCTGTGCAATGATATGATGACAACTGGCTTGTATGATCCCACTGCAACAGAGAGTGTG 10701
QY 781 ACAGCAGTAAAGATGTACTCTCAAGTGTG---TGAAAGAAAGAAAGAACACCGT 837
Db 10702 GCCATCTCGAAGGTGCTCTGCTGTGGTGGCAAGTAAAGAAAGAAAGAAACAG 10761
QY 838 GATTAAGAAACCGCAACAAAGCAAGAGATCCAGGCTCCCTTAATGTGATGCTTGTGAG 897
Db 10762 GACAAAGAACCGCAACAGAGCAAGAGAGTGCAGGCTGATGTGTGGCTGCTGAAA 10821
QY 898 AGGTGTTAACAGTGTGGCTTAACCTATTCGCTGCAAGAGAACAAAGATCTGTGACAGAT 957
Db 10822 CGCTCTTACCCGTGTGACTAATCTGTTCCGGGTGCAAGAGAACCTGTGTGAGAC 10881
QY 958 TGTAAAGCAGATTCCTGAAGAAATGTCAAGACAAAGATGTGAGATTTGCGCAAGAC 1017
Db 10882 TGCAGAGATCGGTACTGAAGAGATGCCCCAGTACATGTGATCGATTCGCCCGCAAC 10941
QY 1018 CAGCTGACATTCAGATTAATATGATCCGCGACAGCAAAATGTCTTGGCAACATTACTTG 1077
Db 10942 CAGCTGACCTGCGCGATTAATGTGACCCGTGCGACGAGATGTCTGGCAACATTACTTG 11001
QY 1078 TATAGCAAGTAAAGTTGCA-----AGATTAAGCAATTAAT 1116
Db 11002 TACTCAAAAGCTGGCGAAGACGAGAGAACCGGTGACGAACAGCGCTGAGAAAGCCCAAT 11061
QY 1117 GTGAAAACGTGCTGAATAAGGCAAGATTAATGATGATACCTGTCAGAGAAATGTGCTG 1176
Db 11062 GTTAACTTCAACGAGAGAGGCAAGAAACCAAGAGACAGTGTGATGTGCTGCGC 11121
QY 1177 ATGAGTAAAGTCTTTTCGATGTGCAATGATGACCAATGCCCAAAATGATGAGAAC 1236
Db 11122 ATGACCAAGTCTTGTGTTGGCTGCAATGATGACCAATCCCAACAGCAGAGCAAAAT 11181
QY 1237 GTGTAACGGGTGCTGTGCTGATTAACAAGCAAGCGCGCTGATCGCTGTTCCGCAAA 1296
Db 11182 GTCTACAGAGAGCGTGTGTGATCAATCAAGAAAGCGTGTGTAATGCAATGCTTCCGTAG 11241
QY 1297 ACTTCACTACATTCCTGCGCAGACATCGAGCGTGTAACTTCCTGCTGCACTGACTAC 1356
Db 11242 ACATGCTGCTGATCTTCTACCAAGACATGGGCTGTGCAAACTTCCTGCAAGATCTTAC 11301
QY 1357 GAGCTCTGTGTGAAGAGAGAACATTTGACAAAGAAATATGATGAAGATCTTACTCA 1416
Db 11302 GAGCAGTGTGTGACAGAGAGAGAACTGTGGGCAAGAGGTATGTGCAAGATCTGACCAAG 11361
QY 1417 TCATTCGAAGCGCAGAGCTGAAGAAAGTGAAGTGTGAGAGAAAGGTGAGAACCTGAC 1476
Db 11362 ACGTTCAAGAGATCTCGAAATCCAGAGAGAGGCGAGAGACGACAGACCCGAT 11421
QY 1477 CCCCTCAACGAGCTGTGACCAACTTCTGTCTGCGGTGCCATGACTGAGAGTCCGCGCT 1536
Db 11422 CCGGTAAACCAACGTGTTACACTTCTGCGGGCGGCATGACGAACCAAGCGGTGCC 11481
QY 1537 TTGCAAGAGATCTCTATATCATGTCTTACGACACTCAATAGCAAACTCTGTGAGAA 1596
Db 11482 CTCACAGAGATCTGCTCTACATGTCTTATGCCAGATCCGCGCAAGTCCACGGGCAAG 11541
QY 1597 GAAGAGAAAGAGGGGTGGGGAGAAAGAAAGGGGTGAGAAAGAGAGGCTGAGAC 1656
Db 11542 GAGAGAGAGAGAGGGCGGACAGAGAAAGCGGTGAGGGTGG-----CGAAGAG 11589
QY 1657 GAAGCAGAGCCAGTATACAGAAACAAGAAATGAGAAACAAAGCTCTTATTCACCAA 1716
Db 11590 GCGAAGGACACAGCATCCATGAACAAGATGAGAGAGAGAGAGCTCTTCCATCAG 11649
QY 1717 GCGGCGTGGCGGAGCGGTGGGTTCGCAAAATGAGTGTGCTGACATCTCCGCTCAA 1776
Db 11650 GCAGCTCTTCAATCTGTGCGTGGCCGAATAGTGTGTTGCAATTCGCTCCCAA 11709
QY 1777 GGCCTGCGCAGAGATGTGATGAAGACTTTCAGCTGGTATTTGATACAGAGGGG 1836
Db 11710 GGTATACCTTCGAGATGATGATGACACACTCAATTCGCGCATTCGCCATTTTGGCGGCG 11769
QY 1837 GGCATATTTGATTAACAGATGGTATGTTGAAACACTTGAAGAACAAAGAAAGACGTGGC 1896
Db 11770 GGCACATGACATCCAAATGGGCATGTGTAACACTGAAAGAAAGAAAGACGTGGC 11829
QY 1897 TTTCTTACGTCAATCGCGGCTCAATGAATCTCTGCTCGGTCTGATCTTGAACCTTC 1956
Db 11830 TTTCTTACCTTCATCGCGGACATGATGAATCTCTGCAATGTATCTGACCTGAGCGCTTT 11889
QY 1957 GAGAGAAACCAAGGCTGAAGGTGTGGGCGTGGAGTGTGGAAGTGTGGCGGAGAGAG 2016
Db 11890 GAGCGAAACCAAGAGCAGAGGATCTTGTGTGTAGGTTCCAAAGCCCGCGGCGAGAG 11949
QY 2017 AACATGATGACCGCGAGTCACTGTGCGCACTTTCAGTTCACTCACTGACCTGAGAA 2076
Db 11950 AACATGACGACCGGAGTTCACCTGTGGCTTTCGCGTTCACAGCTGACCTGGAG 12009
QY 2077 GACACAACTTGAATGCGCAAACTACCTGCGAACTCAAGCGGCTAACAGACAGACGTG 2136
Db 12010 GGCACAACTTGAATGCGCAAACTATTTGAGAGACCCAGCGGCTAACACACCAACCGTG 12069
QY 2137 AAGTGTGATCTGCAACCGTGCATACCTGTGCGGTGCGAGAGTCCATCATGGAATTC 2196
Db 12070 AAGTGTGATCTGTACTGTGATGATTTTGTCTGTGCAAGATTCATCATGGAATTC 12129
QY 2197 TACTGCACTTCAAGCAAGAACTGATGACCCGCGCGCAAGGCACTTCTTCAAG 2256
Db 12130 TACTGCACTTCAAGCAAGAAAGATCATGATCCGCTGAGAAAGGCACTTCTTCAAG 12189
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Db 12190 GCCATGGAAGTGTGCTGACCAAGATTTTAAACCTCTCACTGAATCATACAGGAGTGTG 12249
QY 2317 ACGAGAAATCAGAGGCTTGTGCTCACTCAGGTTGAGGAGCTGTCCGTTGTTCTG 2376
Db 12250 ACCCTCAATAGCAGAGGCTTGTGCACTCGAGGTTGTGAGATCAATGTTGTGCTTCTC 12309
QY 2377 TTCTTATTTCTCCCAATGACAGCAAGTGTGTGAGCACTGTGCAAGGTGAGACTGCTG 2436
Db 12310 TTCTGTGTTTCCCAATGACAGCAAGTGTGTAAAGCACTCCAGCAAGTGTGATCTGCTC 12369
QY 2437 AAGAACTCTCAATCTGCAAGAAAGACATGATCCCAATGATGTGCTGCTTGAAGAA 2496

Db 10288 ACGCAGCAGATTATCATCAATACGTGAGAGCTGCTCAAGAACTCCCTTTCGCGCTG 10347
Qy 421 GCTGAACGTGTTGCGAAACGCAACGCAATATGTTCCATTAAGAGAGAGCTTGAAGGCG 480
Db 10348 GCGAGCCGGGTGAAGAGCGCACTGAGAAATGCTGCAACAGAGAGACAGCATGAGAGA 10407
Qy 481 TTTATTAATGCTGTCACAGACGACATCCAGGTAAAGTCTCAGATCAAGAAAGCTG 540
Db 10408 TTCAATCAAGTCGGCCACGAGACACTTCGCGAGGTGAGACCAGCTCAGAGAGACTGG 10467
Qy 541 CAGCTGCTGTCAGAGACATCTACCTTCAACCCGCTGCTCACTCAATAGTGAAGCTG 600
Db 10468 AATCTGCTAGTGCAGAGACATATCTGTTTATCCCTGCTCATCAAGTACGTGATCTG 10527
Qy 601 CAGAGAAACCACTGGCTCAGAGAACATGTTCCAGAGCGGAGAGCTGTACAAACACG 660
Db 10528 CAGCGAAACCACTGGCTGAGAGACATACCGAGGCGGAGAGCTTACACACATGTG 10587
Qy 661 GCTGAATCTTCAACATCTGCTCGAAGACCAAGTACTTCTTGAGAGAGAACAGACTTC 720
Db 10588 GCAGAGATCTTCAATATATGTGCTTAAGCCAGTACTTCTTAAGAGAGAACAGAACTTC 10647
Qy 721 ATCTCTGCCAAGAAATGATTAACATGCTGCTGATTAAGCCAGACAGAACAGAAAGTG 780
Db 10648 ATCTCTGCCAATGAGATGAGAACATGGCTTTGATCATGCAACTGCAACAGAGAGTGC 10707
Qy 781 ACACAGATPAACAGATGTAATCTCTCAAGTGG---TGAAGAAAGAAAGAAAGCAACCTG 837
Db 10708 GCCATCTCGAAGAGGTCTCTGCTGTGAGTGGCAAGATTAAGAGAGAGAAAGAAACAG 10767
Qy 838 GATAAGAAACGCGAACAAAGACAGAGAGTCCAAAGCTCCATATGTAAGTCTGTGAG 897
Db 10768 GACAAAGAACCGCAACAGAGACAGAGAGTGCAGGCCAGTCTAATGTGTGCTGCTGAAA 10827
Qy 898 AGGTGTTTACCAATTTGGCTTTAATCTATTCGCTGCGAAGAAACAGAACTGTGTGACAT 957
Db 10828 CGCTCTCAACCGTTGACATGAATCTGTTCCGGGTGCGAGAGACAGAACTGTGTGACAG 10887
Qy 958 TGTAAAGACAGGTTCTGTAAGAAATGTCAGAAACAGATGTGGGAGAAATTCGCGAAGAC 10947
Db 10888 TGCAGAGATCGGTACTGAAAGAAATGCCAGATGCAATGTGATGAGTTGCCCGCAAC 10947
Qy 1018 CAGCTGACATTCAGATTAATATGATCCGCGACAGCAAGATGTCTTGGCAACATTAATCTG 1077
Db 10948 CAGCTGACCTGCGGATPAAGTGAACCGCTGCGACGAGATGCTGTGGCAACATTAATCTG 11007
Qy 1078 TATAGCAAGTTAAGTTGCA-----AGATTAAGCAATTAATCT 1116
Db 11008 TACTCAAAAGCTGGSCAAGACGAGAGAACCGGTGACGAAACAGCGCTGAGAGAGCCAAAT 11067
Qy 1117 GTGGAACCTGCTGAATAATPAAGCCAAAGATTATGATGATACCGTCGAGAGAAATGTCGCT 1176
Db 11068 GTTAATCTCAACGAGAGAGGGAAGAAACCAAGAGACAGTGTGATGCTGTGCGC 11127
Qy 1177 ATGAATAAGTCTTTTCGATTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1236
Db 11128 ATGACCAAGGTTCTGTTGGCTGCTGACATGATGATGATGATGATGATGATGATGAT 11187
Qy 1237 GTGTAACCGGTGCTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1296
Db 11188 GTTCAACAGAGAGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 11247
Qy 1297 ACTTCACTACATCTCTGCGCAGACATGAGCGTGTAAATCTTTCGCTGCGACATGATGAT 1356
Db 11248 ACATCTGCTGATTTCTTACCAAGACATGTGGCTGTGCAACATCTTTCGCAACATGATGAT 11307
Qy 1357 GAGCTGTGTTGAGAGAGAGACATGAGCAAGAGATGATGATGATGATGATGATGATGATGAT 1416
Db 11308 GAGCAGTGTGTGAGAGAGAGAGAGAGTGGGCAAGAGGTGATGATGATGATGATGATGATGAT 11367
Qy 1417 TCATTTCAAGACGAGAGCTGAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1476

Db 11368 ACGTTGAGAGATCTCCGAGAAATCCAGAGAGAGGCGAGAGACGACAGCAACCCGAT 11427
Qy 1477 CCCCTCAGCAGAGCTGTGACCAACCTTCTGTGCGGCTGCCATGACTGAGAGGTCCGCGCT 1536
Db 11428 CCGCTTAACCAACGTGTACCACTTTCTGTGCGGCGGCCCATGACGAAACGACGCGGTGCC 11487
Qy 1537 TTGCAAGAGATCTCTTAATCATGTCTTACGCAACATCATATAGCAAGTCTGTGAGAA 1596
Db 11488 CTCACAGAGATCTGCTTACATGTCTTATGCCAGATGCCGCAAGTCCACGCGCAAG 11547
Qy 1597 GAAGAGAGAGAGGCGGTGGGAG 1656
Db 11548 GAGAGAGAGAGAGGCGCGACAG 11595
Qy 1657 GAAGCAGACAGCAGATATACAGAACAGAAATGAGAGAAAGAAAGCTCTTAATTCACAA 1716
Db 11596 GCGAAGGCAACAGACATCCATGAAACAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 11655
Qy 1717 GCGCGCTGGCGAGACGTTGGGAGTTGCCAAATGATGTTGCTGCAATCTCCGCTCAAA 1776
Db 11656 GCACGTCTTCAATCTGGCGCTTGGCCGAATGATGCTGTGCACTTTCCGCTCCAA 11715
Qy 1777 GCGCTGCCAGCAGATGTCATGAAGACTTTCACGCTGGTATTAATTAATGAGAGGCG 1836
Db 11716 GGTATACCTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 11775
Qy 1837 GGCATATTTGATATACAGATGGGTATGTTGAACCACTTGAAGAACAGAAAGAGAGAGAG 1896
Db 11776 GGCATATTCACATTCCAATAGGCGATGCTGACACCTTGAAGAAAGAGAGAGAGAGAGAG 11835
Qy 1897 TTTCTTAATGTCATGCGCGGCTTCAATGAACTCTGCTCGGTCTGATCTTGAAGCTTC 1956
Db 11836 TTTCTTAATCTCAATCGCGGACATGATGAACTCTGCAATGATGATGATGATGATGATGAT 11895
Qy 1957 GAGAGAAACACAAAGCTGAAGGTGCGGAGTGGGTGAGAGAGAGAGAGAGAGAGAGAGAG 2016
Db 11896 GAGGAAACACAAAG 11955
Qy 2017 AACATGATACAGCCCGAGTTCACTGCGCACTCTTCAAGTTCACTTCACTCACTGAA 2076
Db 11956 AACATGACAGACCGAGAGTTCACTGTGCGCTGTTCGATTCAGCTGACCTGAGAG 12015
Qy 2077 GAAACAACTTGAATGAGCAAACTATCTGCGAATCTGAGCCGAGTAAACAGCAACAGT 2136
Db 12016 GGCACAACTTGAATGAGCAAACTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 12075
Qy 2137 AAGTGTGATCTGCAACCGTCACTAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2196
Db 12076 AAGTGTGATCTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 12135
Qy 2197 TACTGCACTACCAAGCAAGAACTGATGACCCGCGCGCAAGCACTTCTTCAAG 2256
Db 12136 TACTGCACTACCAAGCAAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 12195
Qy 2257 GCCATTGGCGTGTCTTCCAGATTAATCAACCTTCACTGAATCATACAGAGAGAGAGAG 2316
Db 12196 GCCATGCAAGTGTGCTGCAAGATTAATCAACCTTCACTGAATCATACAGAGAGAGAG 12255
Qy 2317 AGCAGAAATGAGAGAGGTTTGGCTCACTCAGGTTGAGAGAGAGAGAGAGAGAGAGAGAG 2376
Db 12256 ACCCTCAATAGAGAGGCTTGGCACTGAGGTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 12315
Qy 2377 TTCTTAATCTCCACATGAGAGCAAGTTGTGCAAGCACTCTGCGAGAGTGAAGTCTG 2436
Db 12316 TTCTTAATCTCCACATGAGAGCAAGTTGTGCAAGCACTCTGCGAGAGTGAAGTGTGCTC 12375
Qy 2437 AAGAACTCTCAATCTGCAAGAGACATGATCCCATGATGCTGTCCATGCTTGAAGAG 2496
Db 12376 AAGAACTCTCAATCTGCAAGAGACATGATCCCATGATGCTTTCATGCTGGAAGAG 12435
Qy 2497 AATGTTGTAATGATCAATCTGCAAGCAAAATGATGAGCACTAATGAGAAATGCGCTCC 2556
Db 12436 AATGTTGTAATGATCAATCTGCAAGCAAGATGATGAGCACTGATGAGATGCTGCAAGC 12495

QY 2557 AACGTGGAAGTATCTGAAATACCTGACATGTTCTCAGCTGAAAGACCTGACTCC 2616
DB 12496 AATGTGAGCTGATCTTAACTTGAACATGTTCTCAGAGCTCGCCGACCTTATGAA 12555
QY 2617 AGCCGCACTTCCAGAGATGATGCAATTAACAGCGCTGGTCTGCTGCCAGACTTC 2676
DB 12556 TCGCCAGCTTCCAGAGATGATGCAATTAACAGCGCTGGTCTGCTGCCAGACTTC 12615
QY 2677 AAGAGAAATGGAACACAGAAAGTATATCTCCCAAGAAATCGAGTTCTCTAGCT 2736
DB 12616 AAGGAAAGATGAGGACATCCAGAAATCAACACCGAAGAAATGATTTCTTTGGCC 12675
QY 2737 TGCTGCGAGCAAGCAACGAGCAAGTTAGTACATACGTTTCTGCGACCGTTTCCAC 2796
DB 12676 TGCTGCGAGCAAGCAACGAGCAAGTTAGTACATACGTTTCTGCGACCGTTTCCAC 12735
QY 2797 GAGCTGCGAGCAAGATCGGTTTAACTTGGCCGTTTACTGACTAACTTGTGAAAT 2856
DB 12736 GAAACATCAAGAGATGATGTTTCACTGCTGCTGCTGACCAACCTCAGGAAAC 12795
QY 2857 ATGCCAAACGAGCTTAACTTGGCCGTTTACTGACTAACTTGTGAAAT 2916
DB 12796 ATGCCAAACGAGCTTAACTTGGCCGTTTACTGACTAACTTGTGAAAT 12855
QY 2917 TTGCAACATCTCTGCGCCGATGAGATCAATGAGCGGCTCAGAGCGATGAGCGTGC 2976
DB 12856 TTGCAACATCTCTGCGCCGATGAGATCAATGAGCGGCTCAGAGCGATGAGCGTGC 12915
QY 2977 TACTTCGAGATCAAGAGTCTAATA 3001
DB 12916 TACTTCGAGATCAAGAGTCTAATA 12940

RESULT 8
ADM68763
ID ADM68763 standard; DNA; 15413 BP.

AC ADM68763;

DT 17-JUN-2004 (first entry)

DE *Pterodroma melodia* ryanodine receptor encoding DNA SEQ ID NO:7.

KM ryanodine receptor; insect ion channel; insecticide; pesticide;
KW calcium balance disruption; receptor calcium release mechanism; gene; ds.

OS unidentified.

FT Key Location/Qualifiers
FT CDS 17..15400
FT /tag= a
FT /product= "ryanodine receptor"

XX MO2004027042-A2.

XX 01-APR-2004.

XX 23-SEP-2003; 2003WO-US029834.

XX 23-SEP-2002; 2002US-0412795P.

XX 18-NOV-2002; 2002US-0427324P.

XX (DUPO) DU PONT DE NEMOURS & CO B I.

XX Caspar T, Cordova D, Gutierrez S, Rauh JJ, Smith RM, Wu L;

XX WPI; 2004-295411/27.

XX DR P-PSDB; ADM68764.

PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
for isolating other pest ryanodine receptors and in developing screens to

PT identify insecticidally active compounds.

XX Claim 6; SEQ ID NO 7; 687bp; English.

CC The present invention describes an isolated nucleotide fragment (1)
CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (1) comprises a
CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC construct comprising (1) operably linked to at least one regulatory
CC sequence; (2) a transformed host cell comprising the recombinant
CC construct; (3) a method to isolate (1) encoding ryanodine receptors and
CC related polypeptides; (4) an isolated polypeptide having ryanodine
CC receptor activity; (5) a method for evaluating at least one compound for
CC its ability to modulate calcium homeostasis; (6) a method for evaluating
CC at least one compound which modulates ryanodine receptor activity; (7) an
CC isolated nucleic acid fragment encoding an insect ion channel comprising
CC at least two fully defined polypeptide sequences selected from SEQ ID
CC NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC insect ion channel; (9) a method for expressing an isolated nucleic acid
CC fragment encoding a toxic insect ion channel; and (10) recombinant
CC construct comprising in the 5' to 3' direction a promoter operably linked
CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC The isolated nucleotide fragment (1) encoding a ryanodine receptor is
CC useful for the isolation of other pest ryanodine receptors and developing
CC of screens to identify insecticidally active compounds. The nucleic acid
CC fragments are useful as pesticides, fragments of protein for antibody
CC production, fragments of protein for determination of the structure of
CC insecticide binding sites and in the identification of insecticides that
CC disrupt the calcium balance in cells through other messengers that
CC interact with the receptor calcium release mechanism. The present
CC sequence is used in the exemplification of the present invention.
CC XX

SQ Sequence 15413 BP; 4666 A; 2966 C; 3619 G; 4160 T; 0 U; 2 Other;

Query Match 52.6%; Score 1578.6; DB 12; Length 15413;

Best Local Similarity 71.2%; Pred. No. 0; Mismatches 829; Indels 36; Gaps 3;

Matches 2142; Conservative 0; Mismatches 829; Indels 36; Gaps 3;

QY 1 CAGTTCTCTGCTGCAAGAGATGCTGACATCTTTGGAAGCCCAAGACATATATGAC 60
DB 10013 CAATTCCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 10072
QY 61 AAAATGGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
DB 10073 GAAATGGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 10132
QY 121 GAGTCAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 10133 GAGTCAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 10192
QY 181 TGTCTTATTTGCGGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 10193 TGTCTTATTTGCGGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 10252
QY 241 AACCAAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 10253 AATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 10312
QY 301 CTATCAAAAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 10313 ATGATTAAGAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 10372
QY 361 AAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 10373 AAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 10432
QY 421 GCTGAGAGTGTTCGCAAGCGACGACATATGTTCCATTAAGAGAGAGAGAGAGAGAGAG 480
DB 10433 GCTGAGAGTGTTCGCAAGCGACGACATATGTTCCATTAAGAGAGAGAGAGAGAGAGAG 10492

QY	481	TTTATTTAAAGTGGTCAACAGACGACACATCCAGGTAAAGTCTCAGATACAAAGAGCTG	540
Db	10493	TTCAATAAATCGGCTCTGATGACACTTCTCAGATTGAACGGCAAAATTCAAGAAAGATTG	10552
QY	541	CAGCGTGGTGCAGAGACATCTACTCCCTCTCAACCGGTGCTCAATCAAGTACGTCGACTG	600
Db	10553	CAACTTCTTGAGAGATATCTACTCATTTCTATCTACTCTCATCAAGTACGTTGACTTG	10612
QY	601	CAGAGAAACACTGGCTCAGAGACAAATGTTCCAGCGGGAAGAGCTGTCAACCACTG	660
Db	10613	CAAGAGAAATCATTTGGTTGAGAAATATATATTTCTGAACTGAAAGCTTTATATCATGTA	10672
QY	661	GCTGAATCTTCAACATCTGGTCCAGAGCCAGTACTTCTTGAAGAGAAACGAATCTTC	720
Db	10673	GCAGAAATCTTCAATATCTTGGTCCAGAGCTCAATATTTCTCAAGAAAGAACGAATCTTC	10732
QY	721	ATCTCTGCCAACGAATTTGATTAACATGGTGTGATTATGCCAACAGCACAGAGAGTGTG	780
Db	10733	ATTTCCGGGAATGAAATTTGATTAATTTGGTTCTCATATGCCACGGCTACTAGAGAAAT	10792
QY	781	ACAGCAGTAACAGA-----TGTAATCTCTCAAGGTGTGAAAGAAAGAAAGAAC	834
Db	10793	GCCGTATGACATGACAGTGTCTCTCCCTCGAGGCGCGCTTGAAGAAAGAAAGAAAC	10852
QY	835	CGTATTAAGAAACGCGACAAAGACAAAGAAAGTCCAAACCGTCCCTAATGTGAGCTGTCTG	894
Db	10853	AGAGAGAAAGAAAGGAGCAAGAGCAAAAGAGCTTCAACGCACTTAATGGTTGGTCTTG	10912
QY	895	AAGAGTTGTTACCAAGTTGGCTTAACTATTTGGTGTGGCAGAGAACAAAGACTGGTCAG	954
Db	10913	AAGAGCGCTCTCTGTTGTTGAATCTTTGCTGGAGAGAAACAAAGACTGGTCTAG	10972
QY	955	CATGTATAAGACAGGTTCCGTGAAGAAATGTCCGAACAAAGATGTGCAGATTTCCGCAAG	1014
Db	10973	CATTGCAAAGACAGATTTCTGAGAAATTCGAAGACTATGAATAGTGAATTTGCTAAG	11032
QY	1015	ACCGACGTGACACTTCCAGATTAATAATAGATCCGCGACAGCAAAATGTCTTGGCAACTTAC	1074
Db	11033	ATTCAATTGACCTTCTCCGCAAACTAGATCCAGGTGATGAGATGTCTGTGGCAGCACTAT	11092
QY	1075	TTGTATAGCAAGTTAGTTGCAGAGATGAAGCAATATTAATCTGTGAAACTGTCTGAAT	1134
Db	11093	CTGTATTCACCTCTGGCGACATGAAGAAAGAAATC-----ACCGAAGAGGCG	11137
QY	1135	AAGGCAAGATTAATTGATGATACCGTGCAGAGAAATGTGCTATGATGATAATGTCTTTTC	1194
Db	11138	AAACCTGACAGATCGATGATGGGTGTGTGAACAGGATTTGTGCCATGCTTAAATCTCTGTC	11197
QY	1195	GGATTGCAATGATCGACCAATCCCAACAATATAGTAAGAAGTGAACGTTACCGGTGGGTG	1254
Db	11198	GGTCTGCATATGATTTGACCAACCTCAGCTGCAAGAGCCAGTTATGTGTGGTGTGTT	11257
QY	1255	TCGATTAACGCAAGCGCGCGCTCATCTGCTCTTCCGAACATTCACATCAATCTCTG	1314
Db	11258	TCAACCCAAAGTAAACAGACAGTCAATGCTTTGTTTACAGACAGTATCACTAACGCTTTA	11317
QY	1315	CCGAGACATCGAGGCTGTAACTTCTGCTGCAAGTACTAGAGCTCTGTGTTGAAGAG	1374
Db	11318	CCAAAGCATTAAGTATCAACATATTTGTCTAAGTCTGATTTACAGCTGTGGCTGCTGA	11377
QY	1375	GAGAACTTTGGACAAGAGTATGATGATGAGATCTTATCTCAATCAATGGAAGACGCAAG	1434
Db	11378	GAGAAATGTTGACCCGAGGTTTGTGATTTGAAGACCTCAACGATCAATTTGAAGATCTGA	11437
QY	1435	CTGAAGAAAGTGAAGTGTGAGAGAGAGTGAAGACCTGACCCCTCAACGAGCTGTCT	1494
Db	11438	CTCAAGAAACAGATGAAAGATGAATGAAGGGAATCGAGATCCGCTGACACAGCTTGTG	11497
QY	1495	ACCACTTTCTGTGCGCGGTCCATGACTGAGAGGTCCGGCGCTTTGACAGAGGATCTCTA	1554
Db	11498	ACCACTTTCTGCAGAGAGCAATGACTGAGCGAAAGCGCGCTCCAGGAAACCTCTCTC	11557

QY	1555	TACATGCTTTACGCACACATCTATGCGCAAGTCTCTGTGGAGAAAGAAAGAAAGGGGGT	1614
Db	11558	TACATGCTCTATGCTGTGAGATCGCTGCCAAATCTTGTGGCCAAAGAAAGAAAGAGGTGGT	11611
QY	1615	GGGGAGGAAGAAAGGGGGTGGAGAGCAGAGCTTGAAACGAAGCCAGACGATATTA	1674
Db	11618	GATGAAGAGGAAGAGAGAAAGAGAGAAACAGG-----GTGCTTCAAAT	11667
QY	1675	CACGAAACAAGAAATGAGAAACAAAGCTCTATTTCCACCAGCGGGCTGGCGGACCGT	1734
Db	11663	CACGAAACAAGAAATGAGAAAGCAGAGCTGCTCTTCCATCAATCAAGATCGGCTAATAGA	11722
QY	1735	GGGGTGGCCGAATATGTGTGTCTGTGCACATCTCCGCGTCCAAAGGCTGCCAGCGAGTG	1794
Db	11723	GGCGGGCAGAGATGATGTGTTATTGTCCATTTCCGCTTGCATATGTGTTCCAAGTGAATAG	11782
QY	1795	GTCAATGAAGATTTTACAGCTCCGATATTAAGTATCTGAGGGGGCGGCAATATGATATACAG	1854
Db	11793	GTGAGAAAGACGCTTCAACTTGGATATTCGATTTCTTGAGAGTGGCAACATGATATTCGAA	11842
QY	1855	ATGGGTATGTGAAACAACCTTGAAAGACAAAGAAAGCGTGGGCTTCTTTACGTCCATCGCC	1914
Db	11843	ATGGGAATGCGATATCACTTAAGAAAGAAAGAAAGATGTGGATTTTTCATCTATACGCT	11902
QY	1915	GGCCTCATGAACTCTGCTCCGTGCTGCATCTTGAAGCTTCGAGAGAAACACAGGCT	1974
Db	11903	GGATTAATGAATCTCTCAGATGTACTGATTTTGAAGCATTTTGAAGCGCAATACGAAGGCA	11962
QY	1975	GAAAGTCCGGGCGGTGGGTCTGGAAGGTGGCGGGGAGAAAGAACATGATACAGCCGAG	2034
Db	11963	GAGGCTTGGGCGTGGGATCGAATGGCGAGCTGTGGAGAAAGAACAGACAGCGTGAAG	12022
QY	2035	TTCACTTGGCACTCTTCAAGTTCATTTCACTAGCTCACTGTGAAAGGACACAATTTGACTGG	2094
Db	12023	TTGACCTGCACATTTGTTCAATTTCAATTTCAATGTACATGTGAAGGTCACAATCTTGATAG	12082
QY	2095	CAGAACTACCTGCGAACTCAGGCCGGGTAAACAGCAACAAGTAAAGTGTGATCTTGACCC	2154
Db	12083	CAGAAATTAATTTGAGAACTCAAGCAGAGAAACACTAACACGTGAACGTTGTCAATATGTAAC	12142
QY	2155	GTGCACTACCTGCTGGCGGTCTGCGAGAGTCACTATATGGAATTTCTACTGTGCACTACTCAAG	2214
Db	12143	GTAAATTAATCTTCTGAGACTCAACGGAATCAATCATAGAACCTTTTATTGGCAATTAATTCGAGC	12202
QY	2215	AAGGACTGATTCGACCCGCGCGGCAAGGGAATTTCTTCAAGGCCATTTGGCGGCTTCC	2274
Db	12203	AAAGAAATTTGATTTGATCCAGCAGAGAAAGCCAAATTTTAAAGCTATAGGAATTTGCTAGT	12262
QY	2275	CAAGTATTTCAACACCTCTCATCTGAAGTCATACAGGACCTTGTATCGCAGATCAGACGCT	2334
Db	12263	CAGGTTTTTCAACAATTTGTCTGAGTTATTTCAAGGATGCTTGTATCTCAGAAACAGGAAGCT	12322
QY	2335	TTGGCTCACTCCAGGTTGTGGAGCGCTGTCCGGTGTTCCTGTTCTTATTTCTCCACATG	2394
Db	12323	TTGGCTCAATTCCAAATTTGTGGGACGCTGTCCGGTGTTCCTATTTTATTTCTCTCATATG	12382
QY	2395	CAGGACAAAGTTGTGGAAGCACTGTGCGAGGTGGAACCTGCTGAAGGAATCCTCAATCTG	2454
Db	12383	CAGATATAGCTATTCAAAGCAATTAAGTCAAGTGCAGCTTCTCAAGGAATCTCTAATCTTA	12442
QY	2455	CAGAGACATATGATCCCATATGATGCTGTCCATGCTTGAAGAAATGTTGTTAATGTACA	2514
Db	12443	CAGAAAGACATATGATCAACATGATGTTATCTATGCTTGAAGAAAGTTGTATATATGTACT	12502
QY	2515	ATCGGCAAGCAATGTGTGACACACTATGTAGAATGGGCTCCAAAGTGAACGTATCTTG	2574
Db	12503	ATTGGAAAGACAGATGTGTATCTTTGTTGATCTGCTTCAAAATGTTGAATGTTATCTG	12562
QY	2575	AAATATCTTGACATGTTCTTCAAGCTGAAGGACCTGAACCTCAAGGCGCACTTCCAGAG	2634
Db	12563	AAATATTTGATATGTTCTTGAAACTTAAAGCAATGACTGAAGCACCTTAGCTCTTTGAA	12622
QY	2635	ATTGAATGCCAATATACAGCGCTGGGTGCTGCCCAAGACTTCAAGAGAAATATGAAACA	2694

DB 12623 ATGATCCGATACGATGTTGGCTTACCCAAAGATTCAAGAAATGGAACAA 12682
QY 2695 CAGAGAGTTATATCTCCGAAAGAAATGAGTCTCTCAGTCTCTCGAGACGACAC 2754
DB 12683 CAAAGAGCTATATCAACAGAAAGAAATGAGTCTCTCAGTCTCTCGAGACGACAC 12742
QY 2755 GACGCAAGTTAGACTACATCGGTTTCTGACACCGTTTCCAGACCTGCAAGAGATC 2814
DB 12743 GATGAAAGGTTGATTTACATGCTTGGTTGACAGATTCATGAACTTCCAAAGAAATC 12802
QY 2815 GGGTTAACTTGGCCGTTTACTGACTAACTTGTCTGAACATATGCCGAAGACCTAGA 2874
DB 12803 GGTTCACCTGCTGATTTATTAACAACCTATCTGAGCAGATGCCGAATGAGCCGACG 12862
QY 2875 TTGGCAGTTTCTCTGAGACGCGGCTTCACTCTGAACTACTTCCAACTTCTGCGC 2934
DB 12863 TTGGCTGATTTTGGAAATGACGAGGAGTGTACTTAATTAATTGAACTTCTTGGGA 12922
QY 2935 CGTATCGAGATCATGGGCGCTCCAGGCGCATCGAGCGTGTCTACTTCCAGATCAAGAG 2994
DB 12923 CGATTGAATTTATGGCAGCAGATTAACGTATAGAAAGTGTATTTTGAATTAAGAG 12982
QY 2995 TCTAATA 3001
DB 12983 TCAATA 12989

RESULT 9
ADM68761
ID ADM68761 standard; DNA; 15315 BP.

XX
AC ADM68761;
XX
DT 17-JUN-2004 (first entry)
XX
DE Periplaneta americana ryanodine receptor encoding DNA SEQ ID NO:5.
XX
KW ryanodine receptor; insect ion channel; insecticide; pesticide;
KW calcium balance disruption; receptor calcium release mechanism; gene; ds.
XX
OS Periplaneta americana.
XX
FT Key Location/Qualifiers
FT CDS 1..15315
FT /*tag= a
FT /product= "ryanodine receptor"

XX
PN WO2004027042-A2.
XX
PD 01-APR-2004.
XX
PF 23-SEP-2003; 2003WO-US029834.
XX
PR 23-SEP-2002; 2002US-0412795P.
XX
PR 18-NOV-2002; 2002US-0427324P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Caspar T, Cordova D, Guteridge S, Rauh JJ, Smith RM, Wu L,
PI Teo Y;
XX
DR WPI, 2004-295411/27.
XX
DR P-PSDB; ADM68762.
XX
PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT for isolating other pest ryanodine receptors and in developing screens to
PT identify insecticidally active compounds.
XX
PS Claim 6; SEQ ID NO 5; 687bp; English.
XX
CC The present invention describes an isolated nucleotide fragment (1)
CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor

CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (1) comprises a
CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC construct comprising (1) operably linked to at least one regulatory
CC sequence; (2) a transformed host cell comprising the recombinant
CC construct; (3) a method to isolate (1) encoding ryanodine receptors and
CC related polypeptides; (4) an isolated polypeptide having ryanodine
CC receptor activity; (5) a method for evaluating at least one compound for
CC its ability to modulate calcium homeostasis; (6) a method for evaluating
CC at least one compound which modulates ryanodine receptor activity; (7) an
CC isolated nucleic acid fragment encoding an insect ion channel comprising
CC at least two fully defined polypeptide sequences selected from SEQ ID
CC NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56.
CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC insect ion channel; (9) a method for expressing an isolated nucleic acid
CC fragment encoding a toxic insect ion channel; and (10) recombinant
CC construct comprising in the 5' to 3' direction a promoter operably linked
CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC The isolated nucleotide fragment (1) encoding a ryanodine receptor is
CC useful for the isolation of other pest ryanodine receptors and developing
CC of screens to identify insecticidally active compounds. The nucleic acid
CC fragments are useful as pesticides, fragments of protein for antibody
CC production, fragments of protein for determination of the structure of
CC insecticide binding sites and in the identification of insecticides that
CC disrupt the calcium balance in cells through other messengers that
CC interact with the receptor calcium release mechanism. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 15315 BP; 5206 A; 2494 C; 3141 G; 4474 T; 0 U; 0 Other;

Query Match 49.6%; Score 1489.6; DB 12; Length 15315;
Best Local Similarity 69.3%; Pred. No. 0;
Matches 2083; Conservative 0; Mismatches 894; Indels 27; Gaps 3;

QY 1 CAGTTCCTTGTGTCGACAGATCGTACCATCTTGTGAGAGCCCAAGACATATATGAC 60
DB 9967 CAAATTTCCGTTCTTAAATGATTTCTGACAGTTCAATGGAAGCTCAGATATATATCT 10026
QY 61 AAAATGGAACATGATCGGACGCTGAGACATCTTAAAGCGAGGTGACCAATTTGCTG 120
DB 10027 AGAATGGAAGCACTAGTACCTCTAAGAACTGTATTAATGAAGTTGACCAATTTGCT 10086
QY 121 GAGTCGACAGACGATCAACAGAGAGCGCCCATATATCATGATGATGTCCTTATCTC 180
DB 10087 GAATCAGAAAGAAACATATGCTGATGACCTCACAATTAATGATTTATTTTACCTTAT 10146
QY 181 TGTCTTAATTTGCGGTTCTGTGGGACAGGGGCTGATATATGTTACTCTTACTGCGGA 240
DB 10147 TGTTCATATCTTACCGTACGTGTGGGACAGAGGTCAGATTAATGTTGCTGACACAGGT 10206
QY 241 AACCACTTAAACATGTGTAACAGCGGAACATGAAACAGCTCTCAAGAAATGTTCTGAG 300
DB 10207 AATCATGTTAAATGATGACAGAGGAACATATGAATGCTATATTAAGAAATGTTTAAAG 10266
QY 301 CTGATCAAAAAGAACATGCGCATGAGAGCGCGCTGATGATGACCCGATCGCACTTAC 360
DB 10267 TTAATTAATAAATAATATGGAATGATTAAGCCCTTGAATGACCAAAATAGCAGCTTAT 10326
QY 361 ACGCAGAGATCATCATCAACAGTCCGAGGAATCTGCTGAGGATTCCTCTCGCGCTC 420
DB 10327 ACACACAAATTAATTAATTTCTTCAAGAAATTAATAAAGATTCATTTTACCACTT 10386
QY 421 GCTGAACGTGTGCAAAACGACGCAACATATGTTCTCATTAAGAGAGAGCTTGAAGGAG 480
DB 10387 GCAGAAAGAGTTAAATAAAGCTAAGAAACATTAATCAATAAAGATCATTAAGAAGA 10446
QY 481 TTTATTAAGTCGTCAACAGACACATCCCAAGTGAAGTCTGATATCAAGAAAGATGAG 540
DB 10447 TTTATTAATAATCTACTGATGATGATGCTCCAAATGACCAAAATTAAGAAAGATTTGG 10506
QY 541 CAGCTGCTGTCAGAGACATCTACTCTTACCCGCTGCTCATCAAGTACGTCGACCTG 600

Db 10507 CAATTGGTGTGTAAGGATATTATATGCTTTTATCTCCTCCATATAAATCGTGAATCTT 10566
Qy 601 CAGAGAAACCACTGGCTCAGAGAACATGTTCCAGAGCGGAGAGCTGTACAACACAGTG 660
Db 10567 CAGGCAATCACTGGCTACGTAATACATATCAATCAATGCTGAAGTTTATACATCAATC 10626
Qy 661 GCTGAATCTTCAACATCTGGTCCAGAGCCAGTACTTCTTGAAGAGAACAGACTTC 720
Db 10627 TCTGAAATATTTAACATTTGGTCCAAATCCCAATACTTTTACCTGAAGAACAAACTTT 10686
Qy 721 ATCTCTGCAACGAAATTGATATACATGCTGCTGTTATGCCAAGAGAACAAAGAGTG 780
Db 10687 ATATCTCAATGAAATTTGATTAACAGTACTTATATGCAACGCACTCCGAGATCG 10746
Qy 781 ACAGCACTTAAACAGTGTACTCTCAAGS--TGGTGGAAAGAAAGAAAGAACACCGT 837
Db 10747 GCTGTATATACGAAACTCTGTTAGAGGCTCATCTGGAAAGAAAGAAAGAAAGACAG 10806
Qy 838 GATTAAGAAACGCGCAAAAGACAGAAATGCCAAGCGTCCCTAATGTAGCTTGTCTGAG 897
Db 10807 GATTAAGAAACGCGCAAAAGAAAGAAATTCAGACTTCATTAATGTAGGCTGTCTTAAA 10866
Qy 898 AGTGTATACAGTTGGCTTAACTATATGCTGGCAGAGAACAAAGAACTGTGCACAT 957
Db 10867 CGATTACTGCGAGTTGGTTTAAATTTGTGCGGGAAGAGAACAAAGATTAGTTCAACAT 10926
Qy 958 TGTAAAGACAGGTCTCTGAAGAAATGTCAAGAACATGTGCGAGAAATTCGCGAAGACC 1017
Db 10927 TGCAGAGATAGATTTCTTAAABAAAATCCAGATTATGATGTGATACAAATTTGTCAAAAT 10986
Qy 1018 CAGCTGACCTTCCAGTAAATATGATCCGCGACAGCAAAATGTCTTGGCAACTTACTTG 1077
Db 10987 CAATTGCACTTAAACCGATTAATTAAGCCAGCTGACGAAATGTCTGGCAGCACTATTTA 11046
Qy 1078 TATAGCAAGTATAGTTGGAAGATTAAGCAATTAATCTGTGAAATCTGCTGAATAAG 1137
Db 11047 TACTCCAAGTTAAGAGCAAAA-----AAGAAATACTGAAATTTAA 11088
Qy 1138 GCCAAGATTAATGATGATACCGTGCAGAGAAATCGTGCCTATAGTAAAGTCTTTTCCGA 1197
Db 11089 CCACACAACTGCAAGAGATGAGCGGATAGAAATGTCCCTATGCTTAAGTTCTTTATAGA 11148
Qy 1198 TTGCATATGATGCAATCAATCCCAACAAATGATGAAGACGTGAACCGGTGGTGTGCG 1257
Db 11149 TTGCATATGATGATCACTCTCAGCTTCAAGCAAGGCGACTTAATCGATCTGTGTATCG 11208
Qy 1258 ATTAACAAGCAAGCGCGCTCATCGCTGCTCCGAAACCTTCACTACATTTCTGCGCG 1317
Db 11209 ACGCAAGTAAAGAGCGCGTAAATGCTGTTTCCGAACCTTCACTCAACGCTTGTGACC 11268
Qy 1318 AGACATGAGCGGTGATACATCTTCCGCTCGACGTACTACAGAGCTGTGGTGAAGAGAG 1377
Db 11269 AGACACCGTGCAGTAATATATTCGTTCTGTTTTCGAACTTTGGCTTCAAGATAGA 11328
Qy 1378 AACATTTGACAAAGATTAATGATGAAGATCTTAATCAATCAATTCGAAGACGAGAGCTG 1437
Db 11329 AATATTGACAAAGATTAATGATGAAGATCTCAACAATCAATTTGAAGAGCGAACTT 11388
Qy 1438 AAGAAAGTGAACGTGTGAGAGAAAGTGAAGAGCTGACCCCTCAGCGAGCTGTCAAC 1497
Db 11389 AAAAAGCTGAACAAAGAAAGAAAGAAAGATGCAACCCATTAATCAAAATGGTTACA 11448
Qy 1498 ACCTTCTGTGCGGTGCTGATGAGAGGTCCGGGCTTTTGCAGAGAGATCTCTTAAC 1557
Db 11449 ACTTTCTGCGGAGAGCTATGATCTGAAGAAAGTGTCTTTTCAAGAGACCTCTTTTAC 11508
Qy 1558 ATGTCTTAACGCAACATATAGCGAAGTCTGTGAGAGAGAGAGAGAGAGAGGAGGTGAG 1617
Db 11509 ATGTCTTAATGCTGATATTTTGGCTAAGTCTGTGGGCGAAGAGAGAGAGAGAGAGAG 11562
Qy 1618 GAGAGAGAGAGAGGAGGTGAGAGAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1677

Db 11563 AATAACGAAGAGAGAGCTTCAATGCTTAACGAGATGAAGAGAGCGGTGCTTATTCAT 11622
Qy 1678 GAACAAAGAAATGAGAGAAACAAAAGCTCTTATTCACCAAGCGGCTGGCGGACCGTGGG 1737
Db 11623 GAGCAAGAAATGAGAGAAACAAAAGCTTTTGTTCACCAAGCTGATTTGGCTTAACCGTGGT 11682
Qy 1738 GTTCCGAAGATGTGTGCTGCAATCTCCGCGTCCAAAGGCTGCCAGCGAGATGCTC 1797
Db 11683 GTCCAGAAATGTGTTTATTAACATATCAGCTTGCAGAAAGTATACCAAGTGAATGCTT 11742
Qy 1798 ATGAAGCTTTACAGCTCCGATTAATGATTAATCTGAGGGGCGGCAATTTGATATACAGAT 1857
Db 11743 ATGAAGAGCTTTCAATTTGGAGATGCGAGTCTCCGATGTGTATTTAGATTCAAATG 11802
Qy 1858 GGTATGTGAACCACTTGAAGACAAAGAAAGAGTGGCTTCTTAAGTCCATCGCGCGC 1917
Db 11803 GGAATGTAAATCATTTTAAAGAAAGAAAGATTTGGAATTTTACTTCAGTTGCTGGT 11862
Qy 1918 CTGATGAATCTCTGCTCCGCTGCTCATCTTGAACGCTTGCAGAGAGAACACCAAGCTGAA 1977
Db 11863 TTATATGACTCATGACGCGTCTTGAATTTGAGCGCTTTGAGAGAAATCCAAAGCAGAA 11922
Qy 1978 GGTCTGGGCGTGGGCTGGAAGGTGCGGCGGAGAGAGAACTGATGACGCGAGTTTC 2037
Db 11923 GGTTTGAGAGTGAATCGAAGAGGTGCTGCTGTGAAGAAATATGCAATGATGAGAGTTTC 11982
Qy 2038 ACCTGGCACTCTTCAAGTTCATTCACTCACTGTGAAGACACAACTTGAACCTGGCAG 2097
Db 11983 AGGTATACCTATTTATGATTTATTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 12042
Qy 2098 AACTACCTGGCACTAAGCGCGGTAAACAGACAAAGTGAACGTGTCACTGACCGTTC 2157
Db 12043 AATTTGTTTAAAGAACCCAGCAAGAAATACCAACATGTAATGTTTCAATTTGTATACATG 12102
Qy 2158 GACTACCTGCGGCTGAGAGAGTGCATATGGAATTTCACTTCACTGCACTCAAGCAAG 2217
Db 12103 GATTAATTTACTTATGAGCTTCAAGAAATTAATGAGATTTTATTTGCAATTTTGAATTA 12162
Qy 2218 GAACGATGACACCGCGCGGCAAGGCAACTTCTCAAGGCAATTTGCGGTGCTTCCAA 2277
Db 12163 GAGTTAATGATGACACAGAGAAAGCAATTTCTTCAAGCAATGCGTGTCCGACGCA 12222
Qy 2278 GTATTCACACCTCTCATGTAATCATACAGGACCTTGAACGCAATACAGAGCTTGG 2337
Db 12223 GTGTTTAATACATTAATCCCAAGTAATCAAGGACCTATCAAAATCAACAGGCGCTTA 12282
Qy 2338 GCTCATCTGAGGTGTGGAGCGCTGCGGTGTTTCTGTCTTATCTCCCATGCGAG 2397
Db 12283 GCTCATCTGAGGTGTGGAGCGCTGTTGAGAGGCTTTTATTTATTTTCAACATGCA 12342
Qy 2398 GACAAATGTGCAAGCACTGTCAGAGTGAACCTGCTGAAGGAACTCCTCAATCTGCAG 2457
Db 12343 GATTAATTAATCGAAACATTTCTAGTGAAGATTAATTAAGAACTTTTGAATTTAACA 12402
Qy 2458 AAGGACATGATCCCATGATGCTGTGCTGATGCTTGAAGAAATGTTTATGATTAATC 2517
Db 12403 AAGATATATTAACGATGATGCTGATCAATGTGAAGGAAATGTTTATGATGAACAAT 12462
Qy 2518 GCGAAGCAATGATGAGACACATGATGAATGGGCTCCAAAGTGAACATGATCTCGAAA 2577
Db 12463 GGTAAACAAATGATGAGACCTAGTGAAGTGGGCTCAAAATGTGCAATGATTAATGA 12522
Qy 2578 TACTTGCATGTTCTCTCAAGCTGAAGACCTGACCTCAAGGCGCACTTCAAGAGATT 2637
Db 12523 TATTTTGAATGTTCTGTAATTTAAGATTTAAGAGTTTCAACAAAGCTTTTACGAAAT 12582
Qy 2638 GATGCCAATTAACAGCGCTGGGTGCTGCCAAGAACTTCAAGAGAAATGAAACAACG 2697
Db 12583 GACCCCAATTAAGATGTTGGGTATCATCCCAAGATTTTAAAGAAATGAAACAACAA 12642
Qy 2698 AAGATTTAATCTCCGAAGAAATCGAGTTCTCTAGCTTCTGCGAGACGAACGACGAC 2757
Db 12643 AAAAGTTAATCTGCGAGAGAAATGAAATTTATGTTAACAATGTTGTAATCTAATCAAT 12702

Qy	2758	GGCAAGTTAACAACAATCGGTTTCTGGACCGTTTCCAGAGCGTCGCAAGAGATCCGG	2817
Db	12703	GGAAAAATTGATTATTCATTGGCTTCACTGATCAATTCCAGAGCCATCTTAAGAAATTGCT	12762
Qy	2818	TTTAACTTGGCCGTTGTTACTGACTAACTGTCTGAACATATGCGGACGAGCTGATTTG	2877
Db	12763	TTTAACTTGGCCGTTATTTATTAACTAATCTATGCAACATATGCGCAATGAACTGATTA	12822
Qy	2878	GCACGTTTCTCGAGAGACGCGAGGTTCAAGTCCTGAACCTTTCGACACCATTTCTGGCCGT	2937
Db	12823	ACAAAGATTCTCTAGAAACAGCTAGCAGAGTCTTTTAACTATTTCCAACCGTTCTGGGTAA	12882
Qy	2938	ATCGAGATTCATGGGCGGCTCCAGACGATCGAGCGTGTCTACTTTCGAGATCAAGAGTCT	2997
Db	12883	ATTGAAATTTCTTGGAGGAAATGAAAGCTATGAAACGGGTGTACTTTGAAATTAAGAAATCA	12942
Qy	2998	ATAA 3001	
Db	12943	ATAA 12946	
RESULT 10			
ID	ADM68759	standard; DNA; 15845 BP.	
XX	ADM68759		
XX	ADM68759		
DT	17-JUN-2004	(first entry)	
XX			
DE	Myzus persicae ryanodine receptor encoding DNA SEQ ID NO:3.		
XX			
KW	ryanodine receptor; insect ion channel; insecticide; pesticide;		
XX	calcium balance disruption; receptor calcium release mechanism; gene; ds.		
XX			
OS	Myzus persicae.		
XX			
XX			
FT	Key	Location/Qualifiers	
FT	CDS	277..15582	
FT		/*tag= a	
FT		/product= "ryanodine receptor"	
XX			
PN	MO2004027042-A2.		
XX			
PD	01-APR-2004.		
XX			
XX	23-SEP-2003; 2003WO-US029834.		
XX			
PR	23-SEP-2002; 2002US-0412795P.		
PR	18-NOV-2002; 2002US-0427324P.		
XX			
PA	(DUPO) DU POINT DE MEMOURS & CO E I.		
XX			
PI	Caepar T, Cordova D, Gutierrez S, Rauh JJ, Smith RM, Wu L;		
PI	Tao Y;		
XX			
DR	MP1; 2004-295411/27.		
XX	P-BSDb; ADM68760.		
PT	New isolated nucleotide fragment encoding a ryanodine receptor, useful		
PT	for isolating other pest ryanodine receptors and in developing screens to		
PT	identify insecticidally active compounds.		
XX			
PS	Claim 6, SEQ ID NO 3; 687pp; English.		
XX			
CC	The present invention describes an isolated nucleotide fragment (I).		
CC	comprising: (a) a nucleic acid sequence encoding a ryanodine receptor		
CC	having an amino acid sequence identity of at least 80% when compared to a		
CC	polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,		
CC	128, 130, 144, or 146; or (b) the complement of (a). (i) comprises a		
CC	nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.		
CC	1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant		
CC	construct comprising (i) operably linked to at least one regulatory		

CC	sequence; (2) a transformed host cell comprising the recombinant
CC	construct; (3) a method to isolate (1) encoding ryanodine receptors and
CC	related polypeptides; (4) an isolated polypeptide having ryanodine
CC	receptor activity; (5) a method for evaluating at least one compound for
CC	its ability to modulate calcium homeostasis; (6) a method for evaluating
CC	at least one compound which modulates ryanodine receptor activity; (7) an
CC	isolated nucleic acid fragment encoding an insect ion channel comprising
CC	at least two fully defined polypeptide sequences selected from SEQ ID
CC	Nos. 63-119 provided that the polypeptide sequence is not SEQ ID NO. 56,
CC	120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC	insect ion channel; (9) a method for expressing an isolated nucleic acid
CC	fragment encoding a toxic insect ion channel; and (10) recombinant
CC	construct comprising in the 5' to 3' direction a promoter operably linked
CC	to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC	The isolated nucleotide fragment (1) encoding a ryanodine receptor is
CC	useful for the isolation of other pest ryanodine receptors and developing
CC	of screens to identify insecticidally active compounds. The nucleic acid
CC	fragments are useful as pesticides; fragments of protein for antibody
CC	production, fragments of protein for determination of the structure of
CC	insecticide binding sites and in the identification of insecticides that
CC	disrupt the calcium balance in cells through other messengers that
CC	interact with the receptor calcium release mechanism. The present
CC	sequence is used in the exemplification of the present invention.
XX	
SQ	Sequence 15845 BP; 5273 A; 2716 C; 3325 G; 4528 T; 0 U; 3 Other;
Query Match	48.5%; Score 1456; DB 12; Length 15845;
Best Local Similarity	68.6%; Pred. No. 0;
Matches 2062; Conservative	0; Mismatches 915; Indels 27; Gaps 3;
DY	1 CAGTTCCTTGCTGAAACAGATCGGTGAACATTCTTTGGAACCCCAAGACTAATGCAG 60
DB	10243 CAATATTCACCTTTCTTAATGATTCGCTCATAGTCAATGGAAAGCTCAAGATAATATGCA 103020
OY	61 AAATGGACAATGCANCGCCGACGCTAGAGAAGATCTTGGCGAGGTGACCATTGCG 120
DB	10303 AGAAGCAGAGAGCACTATGCCACTCTTGGAAACGGATTAAAGAAAGTTGATCAAGTTATNC 103652
OY	121 GAATCAGACAAAGACGTACACAGAGCGCGCCGATATCATGATGTGGTGCCTTTACTC 180
DB	10363 GAATCAGAAAAAACAATACACAGCGCACCATATCATATGATTATTTTGGCAATGTGG 104222
OY	181 TGTTCTTAATTTGCCGTTCTGTGTGGGCAAGGGGCTCGAATATGTTATCTCTATCTGCGCGA 240
DB	10423 TGTTCATATCTTACCGTATCTGTGTGGGCAAGGTCGATTAATGTGCTTAAACAAGGT 104821
OY	241 AACCAAGTAAACANTGGTAAACAGGGGAAACATGAACACAGCTCCTCAAGATGTTCTGAAG 300
DB	10483 AATCATATTCACATGTGTAATGTAACATATGAACGTGCTATGTAAAATTTTAAAAA 105452
OY	301 CTATCAAATAAGAACATTCGGCAATGAGAACGCGCCGTGATGACCCGCAATGCCACTAC 360
DB	10543 TTATATAAAAAAAAAATTTGGGAACGATTAATNGCTCTTGGATGACAAATATACACTTAT 106020
OY	361 ACGCAGACATCATCATCAACAGCTCCGAGAACTGCTGAGGATTCCTTCTGCGCGTCC 420
DB	10603 ACAACACAAATTAATTTATATCTTACAGAAATTTATTAAGAATCCATTTCTTACACTT 106621
OY	421 GCTGAACGTGTGGCAAAACGACGACCAATATGTTTCATPAAGAGAGAGCTTGAAGGGG 480
DB	10663 GCGGAACGAGTTAAAAAACCTACAGAAAGCTTGTACATTAAGAAAGAAATCGTTAAAGAGA 107222
OY	481 TTTATTAAGTCGTCAACAGACGACCATCCAGTAGAAGTCTCAAGTACAAAGAGACTGG 540
DB	10723 TTTATATAAATCATCTACTGACGATACATCCAAATGGAAGCCCAATATCAAGAAAGTTGG 107822
OY	541 CAGCTGCTGGTCAAGACATCTATCTCTTCTTACCCGCTGCTCATCAAGTACGTGACCTGG 600
DB	10783 CAATTAAGTGTGTAGGGAATATATATGCAATTTTATCCCACTCCATATAAAATCTGTGATCTT 108422
OY	601 CAGAGGAAACAACGTGGCTCAGGAAACAATGTTCCAGAGGGGAAAGAGCTGACAAACAACGCG 660
DB	10843 CAACGCAATCATCGTGTTACGTAAATGACATATCAAAATGCTGAAAGATTATATACATACGTA 109020

QY 661 GCTGAAATCTTCAACATCTGTCGAGAGCCAGTACTTTGAAAGAGAACAGACTTC 720
Db 10903 TCTGAAATATTTCAACATATGTCGCAAAATCTCAATACTTTTTCAGAGAAACAACAACTTT 10962
QY 721 ATCTCTCCCAACGAAATTTGATTAACATGTCGTGTTTATGCAACAGCAACAAAGAGTGC 780
Db 10963 ATTTCTCGAATGAAATTTGACACATATTAATTAATGCGCAACAGCTACCGAGATTCG 11022
QY 781 ACAGCACTTAAACAATGTAATCTCTCAAG--TGGTGAAGAAAGAAAGAACACCGT 837
Db 11023 GCTGTCAATTCAGAACTTCTGTTAGAGGATCAACAGAGAAAGAAAGAAACATATAG 11082
QY 838 GATTAAGAACGCGACAAAGACAGAAATCCAGCGTCCCTAATGTAAGCTTGTCTGAG 897
Db 11083 GATTAAGAAACGTGTTAAGAAAGAAATTCAGACATCATGATGTTGCTGTCTTAA 11142
QY 898 AGGTGTTTACAGTTGGCCCTTAACTTAATGCTGTGCGAGAAACAAAGAACTGTGCAGAT 957
Db 11143 CGATTATTTGCCAGTTGGTTTAAATTTGTTCGAGAGAAAGAGCAAGAAATTAATTCACAC 11202
QY 958 TGTAAAGACAGGTTCTGAAAGAAATGTCAGAAACAATGTGCGAGAAATTCGCAAGACC 1017
Db 11203 TGCAGAGATTAATCTTAAAGAAATCCAGACTATGACGTGATACATTTGTCAAAAT 11262
QY 1018 CAGCTGACCTTCAGATTAATTAATGATCCGCGACAGCAAAATGCTTGGCAACATTACTTG 1077
Db 11263 CAATTGCACTTACCTGCAAAATTTGACCAGCTGACGAAATGTCTGGCAACTATATTA 11322
QY 1078 TATAGCAAGTTAGTTGGAAGATTAAGCAATTAATCTGTGAAATGCTGAAATTAAG 1137
Db 11323 TACTCAAGCTTGAAGACAAA-----AAGGACTCTCTGAATTA 11364
QY 1138 GCCAAGATTAATTAATGATACCGTCGAGAGAAATCGCTATGAGTAAGTCTTTTCGA 1197
Db 11365 CTTCAACAATGTCAGAGGTTGGCGATAGAAATTTGTCTTAAGTTGCTTAATGA 11424
QY 1198 TTGCAATGATTCGACCAATCCCAACAAATGATTAAGAACTGTACCGGTGCTGTGTCG 1257
Db 11425 TTGCAATGATTTGATCTCAGCTTCAAGCAAGCGCAATTAATCATCATGTTGATTCG 11484
QY 1258 ATTCAGAGCAAGCGCGCTCATGCTGCTCCGAGAACTTCACATCAATCTCTGCGC 1317
Db 11485 ACGCAAGTAAGAGAGCGTAATTTGCTTTCCGAACCTTCACACGCTTTGACC 11544
QY 1318 AGACATGAGCGGTGTAATCTTCTGCTGCACTGACAGCTCTGTGTGAAGAGAG 1377
Db 11545 AGACATGAGCGGTGTAATTTTGTTCGTTTCGTTTACGAACTTTGGCTTCAAGATGA 11604
QY 1378 AACATTTGACAAAGTAATGATTAAGAAATCTTAATCAATCATTCGAAGCGCAGACTG 1437
Db 11605 AATTTGAGCAAGATGATGATGAAGATCTCACGAAATCGTTTGAAGAGCGAACTT 11664
QY 1438 AAGAAAGTACCGTGTGAGAGAAAGTGAAGAGCTTGAACCCCTCAGCGAGCTGTACC 1497
Db 11665 AAAAAAGTACAAAGAAAGAAAGAAAGTGAAGTGAAGTCACTTAATCAATGATGCTACT 11724
QY 1498 ACCTTCTGTGCGGGTGCATGACTGAGAGGTCCGGCCTTTGCGAGAGATTCCTTAAC 1557
Db 11725 ACCTTCTGTGCGGGTGCATGACTGAGAGAGTGTGCTTTACAGAGAGACCTCTTAAT 11784
QY 1558 ATGCTTACGCAACATCATAGCGAAGTCTGTGAGAGAAAGAAAGAGGGGGTGG 1617
Db 11785 ATGCTTATGCTGATATTTTAGCTTAATCTTTCGGGTGAAGAAAGAAAGGTAATTAAC 11844
QY 1618 GAGAAAGAGAGGGGGTGAAGAGCAGAGCTGAAGACAGAGCGCAGATTAATCAC 1677
Db 11845 GAAAGAAAGGTTCTACTGTTAAGGA-----GAAAGAAAGAGCGCGCTTCTATTCAC 11898
QY 1678 GAAACAAGAAATGAGAAACAAAGCTCTTAATTCACCAAGCGGGCTGTGCGAGCCGTGG 1737
Db 11899 GAAACAGAAATGAGAAACAAAGCTGTGTTTACCAAGCTGATTTGGCCAAACCGTGGT 11958

QY 1738 GTTCCGAAGATGATGTTGCTGCACATCTCCGCTCCAAAGGCTGCGCCAGCGATGTC 1797
Db 11959 GTGCAGAAATGATTAATGTTTACATATCATGACTTGCAGAAAGTAATACAGCGAAATGTT 12018
QY 1798 ATGAACATTTACAGCTCGGTATTAATTAATGATGAGGGGGCGCAATTAATGATTAACATG 1857
Db 12019 ATGAACATTTACATTTGGAATTCGAGTTCTACGTGTGTATTAATTAATTAATTAATG 12078
QY 1858 GGTATGTTGAACCACTTGAAGACAAAGAAAGAGTGGGCTTTTACGTTCATGCGCGCG 1917
Db 12079 GGTATGTTAAATCATTTAAAGAAAGAAAGATTTGGAATTTTACTCAGTTGCTGGT 12138
QY 1918 CTGATGAATCTCTGCTCGTCTGCATCTTGAAGCGCTTGAAGAGAAACCAAGGCTGA 1977
Db 12139 TTAAATGACTCGGCGAGCGCTTCGATTTGAGCGCTTTTGAAGAAATACCAAGCGGAG 12198
QY 1978 GGTGTGGGGTGGGTCTGGAAGGTGCGGGGAGAGAAACATGATGACGCGAGTTC 2037
Db 12199 GGTTAAGAGTGAATGAGATCGAAGGTGCTGTGTGAAGAAATATGCAAGATGCGAGTTC 12258
QY 2038 ACCTGCGCACTCTTCAGTTTCAATTCAGCTCACCTGTGAAGACACAACTTGAAGCTG 2097
Db 12259 AGGTATTAATTAATTAATGATTTATTCACCTTAATGATGAGCAATTAATTAAGATGCA 12318
QY 2098 AACTACCTGCGAATCAAGCGGCTTACAGCAACAGTGAACAGTGTCTATCTGACCGTC 2157
Db 12319 AATTAATTAAGACACAAAGAGAAATACACACATGTAATGTTTAAATTTGTATAGTG 12378
QY 2158 GACTACCTGCGGCTGCGAGAGATCATATGAACTTCTACTGCGCACTACTCAAGCAAG 2217
Db 12379 GATTAATTAATTAATGCTTACGAAATCTAATTAATGATTTTATTTGCAATTTTGAACCA 12438
QY 2218 GAACTGATGACCCCGCGCGCAAGCGAACTTCTTCAAGCGCAATTTGCGGTGCTTCCAA 2277
Db 12439 GAGCTAATTAAGACCAAGAGAAAGCAAAATTTCTCAAGCAATCGGTGAGCAACCTTA 12498
QY 2278 GATTTGAACCTCTCATGTAAGTCAATCAAGGACCTTGTACGAGAAATCAAGAGGCTTG 2337
Db 12499 GTTTTAAATACGTATCCGAAATTAATCAAGACCGTGTAACTCAAAATCAACAGGCTTC 12558
QY 2338 GCTCATCGAGGTTGGGAGCGCTGTGCGGTGCTCTGCTCTAATCTCCCATGACAG 2397
Db 12559 GCTCATCGAGTTGGGAGTGCCTGTGAGAGGTTTGTGTTTGTTCACATGACAA 12618
QY 2398 GACAAATGTCGAAGCACTGTGCAAGTGAACCTGCTGAAGAACTCTCAATCTGCA 2457
Db 12619 GATTAATTAATCAACATTTCTAGTGAAGATTAATTAAGAACTTTTAATTAATTAACA 12678
QY 2458 AAGCAATGATCCCATGATGCTGTCTCATGCTTGAAGAAATGTTGTTAATGATCAATC 2517
Db 12679 AAGATATGATTAAGATGATGCTGTCTCATGTTAAGAGGAAAGCTGTTAATGAAACAAT 12738
QY 2518 GGCAGCAATGATGAGCACTATGATGAATGGGCTCCAGCGTGAACATGATCTGAA 2577
Db 12739 GGTAAACAGATGTTGACATTAATGATGAGGCTCAAAATGTGCAAGTTGATTTGAA 12798
QY 2578 TACTTCAGATGTTCTCTCAAGCTGAAGACCTGACCTCCAGCGCCAGCTTCCAGAGAT 2637
Db 12799 TATTTGACATGTTCTGAAACCTTAAGATTAATTAATTAATTAATTAATTAATTAAT 12858
QY 2638 GATCCAAATTAAGACGCTGCTGCTGCTCCAGAGACTTCAAGAGAAATTAAGAAACAG 2697
Db 12859 GACCCCAATGATGATGTTGGGTGATCAATCCAAAGATTTTAAAGAAATTAAGAAACAA 12918
QY 2698 AAGAGTTATACCTCCGAGAAATTCAGATTCCTCTGATGCTGTGCGAGAGCAACAGAC 2757
Db 12919 AAAAGTTTACCTGCAAGAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 12978
QY 2758 GGCAGATTAGACTACGCTGCTTCTGCGACGCTTTCAGAGAGCTGCGCAAGAGATCGGG 2817
Db 12979 GGGAAATTAATGATTAATGCTTTCAGATCAATTCAGAGCGATCCAAAGAAATTTGGT 13038
QY 2818 TTAACTTGCGCGGTGTTACTGACTAATCTGTCTGAACATATGCGCAAGAGCTTAATG 2877

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Db      13039  TTCAATCTTGGCCGTTTGTGTACTAACCTATCAGAAACATGCCAATGAACCTAGAGTTA 13098
Oy      2878  GCAGGTTCTCGAGAGACGCGAGTTCACTCTGAACTACTCGAACATTCCTGGGCGCT 2937
Db      13099  ACGAGATTCTTAGAAACAGCTAGACAGTGTATTGAATTATTTCCAGCCATTCCTGGAGAA 13158
Oy      2938  ATCGAGATTCATGGCGGCTCCAGCGCATCGAGCGTGTCTACTTCGAGATCAAGAGCTT 2997
Db      13159  ATTGAATTTCTCGAGAGAACTTAACGCATAGAACCGGTGTACTTTGAATTAAGGATCA 13218
Oy      2998  AATA 3001
Db      13219  AACA 13222

RESULT 11
AAQ10613
ID  AAQ10613 standard; DNA; 15672 BP.
XX
AC  AAQ10613;
DT  26-APR-1991 (first entry)
DE  Rianodin receptor gene.
XX
KW  Rianodin receptor gene; calcium release modulator; tranquilliser;
   antagonist; ss.
XX
OS  Oryctolagus cuniculus.
XX
FH  Key
FT  GC_signal
   location/Qualifiers
   /tag= b
   /note= "feature unlabelled in specification"
FT  CAAAT_signal
   /tag= d
   /note= "feature unlabelled in specification"
FT  GC_signal
   /tag= c
   /note= "feature unlabelled in specification"
FT  misc_feature
   /tag= e
   /note= "feature unlabelled in specification"
FT  misc_feature
   /tag= f
   /note= "feature unlabelled in specification"
FT  CDS
   /tag= a
   /note= "feature unlabelled in specification"
   /product= "rianodin receptor"
FT  polyA_signal
   /tag= g
   /tag= 9

JP03011098-A.
XX
PD  18-JAN-1991.
XX
PP  07-JUN-1989; 89JP-00144569.
XX
PR  07-JUN-1989; 89JP-00144569.
XX
PA  (MITTU ) MITSUBISHI KASEI CORP.
XX
WP1; 1991-062003/09.
XX
DR  P-PSDB; AAR10834.
XX
PT  New rianodin receptor, genes encoding it and its prepn. - useful as
   calcium release modulator for tranquillisers and for assaying calcium
   antagonists.
XX
PS  Disclosure; Fig 1; 18pp; Japanese.
CC  RNA contg. poly(A) was prepared from rabbit skeletal muscle endoplasmic

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CC  reticulum. From the obtd. poly(A) mRNA, a cDNA bank corresp. to it was
CC  prepared by random primer method, oligo (dT) primer method, and primer
CC  extension method. A cDNA was obtained by screening with a DNA probe (see
CC  AAQ10614-15). By introducing the obtd. cDNA into an expression vector,
CC  vector pRRS7 was formed. The product is said to be involved in calcium
CC  release from sarcoplasmic reticulum which triggers constriction of
CC  skeletal muscle. Therefore, the receptor is useful as tranquilliser and
CC  assay series for screening of calcium antagonist
XX
SO  Sequence 15672 BP; 3139 A; 4909 C; 4955 G; 2669 T; 0 U; 0 Other;

Query Match      26.2%; Score 787.4; DB 2; Length 15672;
Best Local Similarity 56.8%; Pred. No. 4.5e-196;
Matches 1700; Conservative 0; Mismatches 1181; Indels 114; Gaps 9;

Oy      38  TCGAAGCCCAAGATATATGAGAAATGGAACAATGCAATGCCAGCTGAGACGATCT 97
Db      10131  TGGGGCTCCCAACAGGTGAGAGATGTCTGACATCCGCTGATCGCTCA 10190
Oy      98  TAGCGAGGTGAACCAATTCGTGAGTCAGACAAGACGTACAAAGAGCGCCGATATCA 157
Db      10191  TGGCAGACATCGGGGGCTGGCCGAGTCGGGGCCGCTACAGAGATCCGACGCTCA 10250
Oy      158  TCGATGTGTGCTGCTCTTATCTCTTATTTGCGGTTCTGTGGGCAACAGGAGCTGT 217
Db      10251  TCGAGATCAGCTGCCATGCTCTGACGTAACCTGCCGCTGGTGGAGACGCGGGCCCG 10310
Oy      218  ATATATTTACTTCTCACT-----GGCGAAACACGTAAACAATGTATCAACGGG 265
Db      10311  AGGGCCCCCTCCCGCCCTGCTGCGCGGCGCCCCCGCCCTGACAGGCTGTCACTCCG 10370
Oy      266  AACATGAACACAGCTCCTCAAGATGTTCTGAAGTCATCAAAAAGACATCGGCATG 325
Db      10371  ACCACCTCACTACTCTTGGGAAACATCTTGCCATCATTTGTCAACAACCTGGCATTTG 10430
Oy      326  AGAAGCGCGGTGATGACCGCATGCGCACTTACACGACGACAGATCATCAACAGCT 385
Db      10431  ACGAGGCACCTGAGTAAACGAGCTGTCTGTGTTGCGCCAGCCATGTCAGCGCGCGC 10490
Oy      386  CCGAGAACTGCTGAGGAGATTCCTTCTGCGCTGCTGTAACGTTTCGGAACAGCAGG 445
Db      10491  GGCCTGAGCTCTGTCATTCCTCACTTCCCACTCCACATCGGGCGGTGCGAAGGGGAG 10550
Oy      446  ACAATATGTTCCATTAAGAGAGAGCTTGAAGGGGATTATTAAGTCGTCAACAGACGA 505
Db      10551  GCAGGTGTGGCCGAGAGAGAGAGAGAGCTGGG-----CTGAGGCCAAGGCCAGG 10601
Oy      506  CATCCAGGTAGATCTCAAGATACAGAGAAGCTGGAGCTGTGTCAGAGACATCTACT 565
Db      10602  CCGAGAGGGGAGAGCTCTGTGTGGGACGAGTTCTGTGCTGTGCGGGACCTGTATCG 10661
Oy      566  CTTTCTACCGCTGCTCATAGTACGTGCAGCTGCGAGAGAACATCTGGCTCAGAAACA 625
Db      10662  CCTCTACCGCTGCTCATCGCTACGTGACAAACAAGGGCCACATGGCTGACGAGGC 10721
Oy      626  ATGTTCCAGAGCGGAGAGAGCTGTACAAACAGCTGGCTGAATCTTCAACATCGTGTGA 685
Db      10722  CCAAGCCCAACGCGAGAGAGTGTTCAGAGTGGGCGAGATTTCACTTACTGTGTCA 10781
Oy      686  AGAGCCAGTACTTCTTGAAGAGAGACAGAACTTCATCTGTGCCAAGAAATTGATTA 745
Db      10782  AGTCCCACTACTTCAACGCTGAGAGAGAACTTTGTGTGTCAAGAGATTCACAACA 10841
Oy      746  TGTGCTGATTTATGCCAACAAGAGAGTGTACAGACAGTACAGATGTACTCTCTC 805
Db      10842  TGTCTTCTGACGGCTGACAGCAAGAGCAAGTGTGCCAAGCGCGGAGACG-----CAC 10895
Oy      806  AAGGTGTGGAAGAAAGAAAGAGAGACCGGTGTATGAAGACGCAAGAACAGAGAG 865
Db      10896  AGTGGGCGCTCGACACAGAGACGACCAAGAGAGAGCGCGGGGAGACAGTACTCCG 10955
Oy      866  TCCAGGCTCCCTATAGTATGCTTGTGAGAGGTTGTATCAAGTTGGCTTAACTAT 925

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Db 10956 TGCAGCGTCACTGATCGTGGCCAGCTGGAAGAAAGTCTCCATTGGCTTGAACATGT 11015
Qy 926 TCCTGGGAGAGAACAGAACTGTGTGAGCAATTGTAAAGACAGGTTCTGTGAAGAAATGT 985
Db 11016 GTGGCCCAACCGACCAAGCACTCATCATGTGTGGCCAAAGACCGGCTGAGCCCTGAAAAGCA 11075
Qy 986 CAGAACAAAGATGTGGCAGAAATTTCCGGAAGACCCAGCTGACATTCACGATTAATTAATTC 1045
Db 11076 CAGACGAGAGAGTCCGGAAATTTCTGACAGAACATCTCACCTTCAGGAAAGGTCAGAG 11135
Qy 1046 CCGGAGACGAAATGTCTTGCAACATTTACTGTATAGCAATGTAGTTCCAGAGATTAAG 1105
Db 11136 GCTCCCGCTCCCTGCGCTGGAGATGGCGCTGTACG----- 11172
Qy 1106 GCAATATATACTGTGAAATCTGTGAAATTAAGGCCAAGATTTATGATATACCTGTGAGA 1165
Db 11173 -----GGGCTCCCGGCGCGAGAGAGACGCGACGACCCGGAGAAAATGTGGGCA 11225
Qy 1166 GAATCGTCGTATAGTAAAGTCTTTTCGATTTGCAATGTATGACCATTCGCAACAA 1225
Db 11226 GGGTCCAAAGATGTCAAGCGGTGTCTATCACTGTGAACAGACCGAGACCCCTTACAAAT 11285
Qy 1226 TGAATGAAGACGTGACCGGTGGGTGTGATTAACGCGACGCGCGGTATCGCT 1285
Db 11286 CCAAGAAAGCCGTGTGGCACAAGCTTTGTTCAGACAGCGCGCGAGCGGTGGCT 11345
Qy 1286 GCTTCGCACAAACTTCACTATCTCTGCCAGACATCGACGCTGTAACTTTCGCTC 1345
Db 11346 GCTTCGATGAGCGCCCTGTAAACCTGTCCACGACCGCGGCTGTAACTTTCGCT 11405
Qy 1346 GCACGTACTACAGCTCTGG---TTGGAAGAGGAACATTGGAACAAAGTAATGATAG 1402
Db 11406 AGAGCTCAAAAGCCGCTGTATCTGTACCGAAGATCAAGTTTGAAGACCGCATGTATAG 11465
Qy 1403 AAGATCTTACTCAATCACTTGTGAAGACGAGCTGAAGAAAGTGAAGTGGTGAAGAG 1462
Db 11466 ATGATCTT-----TCAAAAGCTGGAGAGCAGAGAGAGAGAGAGAGAGATGAGG 11516
Qy 1463 GTGAGAGAGCTGACCCCTCTCAACGAGCTGTGTCAACCATCTTCTGTCCGATGCACTG 1522
Db 11517 AGAAGAGCCAGACCCCTGTGACAGCGGTGTCTGTGACCTTCAAGCGGACCGCTGTAGCTG 11576
Qy 1523 AGAGGTCCGGGCTTTGCAAGAGATCCTGTATACATGTCTTACGCAACATCAATACGA 1582
Db 11577 AAAAGT---GCMAACTGACACAGGACTACCTGTATCAATGCAATATGCGAATCATGCGCA 11633
Qy 1583 AGTCTGTGAGAGAGAGAGAGAGAGGGGTGGGAGAGAGAGGGGTGGAGAG 1642
Db 11634 AGAGCTGCACCTGGAG 11693
Qy 1643 CAGAGGCTGAAGCAGAGGAGAGAGAGAGATATACAGAACAGAAATGAGAAACAAAGC 1702
Db 11694 TCTCTTTTGAAGAG-----AAGAGATGAGAGAGAGAGAGC 11729
Qy 1703 TCTTATTCACCAAGCGCGGTGGCGGACCGTGGGGTTGCCGAATGTGTGTGTGACAA 1762
Db 11730 TCTCTTACAGAGCTCAACGCTGTGACACGCGCGGGCGCGCGAGATGTCTGCAAGATGA 11789
Qy 1763 TCTCCGCTGCAAGAGGCTGCCAGAGAGATGTGCATGAGAGATTTTCACTGCTGATTTA 1822
Db 11790 TCAAGCGCTGTGAGAGAGAGAGAGAGAGTGCATGTGTCTTCACTTGAAGAGAGAGAG 11849
Qy 1823 GTAATCTGAGGGGCGGCAATATTGATATACAGATGGGTATGTGAACCACTTGAAGAGCA 1882
Db 11850 CCAATCTCAATGAGAGGCAATGCCAGGTGTGACAGAGAAATGTGTGATTACTGAAGAGCA 11909
Qy 1883 AGAAAGAGTGGGCTTTTAACTGCATCGCGGCTCATGAACCTCTGTCTGGTCTGCG 1942
Db 11910 AGAAGAGAGTGGGCTTCTTCAAGAGCATTCAGGCGCTGATGACAGACATGACGCTCGG 11969
Qy 1943 ATCTTGAACGCTTTCAGAGAGAACCAAGGCTGAAGGTCTGGGCGTGGGCTGTGAAGGTG 2002
Db 11970 ATCTCAATGTCTTTCAGAGAGACAGAACAGGACCTGGGCAATGTGTGAACGAGAGATG 12029

Qy 2003 CCGCG-----GAGAGAGAGACATGCAATGACGCCGAGTTCACTGCG 2044
Db 12030 GAACCGTCATCAATCCGACAGAAACGAGAGAGAGTATGTGCCATGTACGAATTCACACAA 12089
Qy 2045 CACTCTTCAGGTTCACTTCAAGCTCACTGTGAAAGAGACAACTTGGACTGGCAACATCAC 2104
Db 12090 ATCTGTTCATATTTTTCAGAGCTGCTGTGTAGGGGACCAACAGATTTTCAAAATCTACT 12149
Qy 2105 TGGAAATCAGCGCGGTAAACAGACAAAGTGAACGTGTGCATCTGCAACCGTGAATCAC 2164
Db 12150 TAGGACACAGAGAGGACACACACACATTAATCATTAATCTGACAGTGAATCAC 12209
Qy 2165 TGTGCGGCTGCAAGAGTTCATATGAACTTTTACTGTGCACTATCTGAAGAGAACTGA 2224
Db 12210 TCTGCGGCTGCAAGAGTTCATATGAGGACTTCTTACTGTATCTACTCCGGACAGATGTCA 12269
Qy 2225 TCGACCCGCGCGGCAAGAGAACTTTTCAAGGCCATTTGGCGTGTCTCCCAAGTATCA 2284
Db 12270 TTGAGAGACAGGCAAGAGAACTTCTCAAGGCCATGTCCGTGGCCAAACAGTGTCA 12329
Qy 2285 ACAACCTCACTGAAGTCAATACAGGACCTTGTACGAGAAATCAGAGGCTTTGGCTACT 2344
Db 12330 ACAGCTTCAACGAGTACATTCAGAGGCCCTGTGACCGGGAACGACAGAGCTTGGCCACA 12389
Qy 2345 CAGGTTGTGAGACGCTGTCCGATTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2404
Db 12390 GCCGCTCTGGAGCGCGGTGTGTGAGATTCCTGACGATGTTTGGCCATGATGATGAAG 12449
Qy 2405 TGTGAGAGACATCTGTGCGAGGTGTGACCTGTGAAGAACTTCTCAATCTGCAAGAGCA 2464
Db 12450 TCGCTCAGGACTTCGACACAGATTCGAGCTGTGAAGAGCTGTGCACTGTGCAAGAGCA 12509
Qy 2465 TGAATCCCATGATGCTGTCCATGCTTGAAGAGAAATGTGTAATGTATCAATAGGCAAG 2524
Db 12510 TGTGTGTATGTCTGTCTGTCTTCACTGAAAGAGAACTGTGTGAACGAGATGTGCCGCG 12569
Qy 2525 AAATGTGAGACACATGATGAATCGGCTTCCACGCTGGAACATGATCTTGAATTACTTG 2584
Db 12570 AGATGTGAGACATGCTGT 12629
Qy 2585 ACATGTCTTCAAGAGTGAAGAGACCTGACCTCCAGCGCCAGCTTCCAGAGATTTGATGCCA 2644
Db 12630 ACATGTCTTGAAGACCAAGAGATCTGTGGGCTCCAGGCGCTTCCAGAGCTACGTGACCG 12689
Qy 2645 ATTAACAGCGCTGGGCTGTGCCAAGAGACTTCAAGAGAAATGGAACCAAGAGAGTT 2704
Db 12690 ATCCCGTGGCTCATCTCAAAAGAGACTTCCAGAGGCGCATGTGACAGCAGAGAGAGT 12749
Qy 2705 ATACTCCGAAAGAAATGAGTTCTTCTAGCTTGTGCGAGAGAGCAACGACGCAAGT 2764
Db 12750 TCACTGGGCGGAAATTCAGATTTCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 12809
Qy 2765 TAGACTACATCGGTTTCTGCGACCGTTTCCAGAGGCTTCCAGAGAGATCGGTTTAATC 2824
Db 12810 TCAACTTCAGAGAGTTTCGCAACCGCTTCCAGAGAGCAGCCCGGAGCATTCGCTTCAAG 12869
Qy 2825 TGGCGGTGTATGACTTAACTTGTGACATATGCGCAATATGCGCAAGGCTTGAATTTGACGTT 2884
Db 12870 TGGCGGTGTGTGACCACTGTGAGACAGTGTGCCAGACACCTGCGCTGCGCACT 12929
Qy 2885 TCTGAGAGACGCGAGGTTCACTGTAATCTTGAACCAATTCCTGGCGGTATGAGAG 2944
Db 12930 TCTGAGAGCTGTGTGAGACATCTTGAATTAATTCCTGCGCTTACCTGCGCGCGATGAGAG 12989
Qy 2945 TCAATGCGGCTTCAAGGCAATGAGGCTGTCTTCAATCTTGAAGATCAAAGAGTCTAA 2999
Db 12990 TCAATGCGGCTTCCGCGCATGAGGCGATCACTTCAAGATTCAGAGACCAA 13044

RESULT 12
AAS69156
ID AAS69156 standard; cDNA; 15359 BP.

QY 1286 GCTTCCGACAACTTCACTACATTTCTGCGGAGACATCGAGCGGTGATCACTTGCCTC 1345
 Db 11034 GTTTCGGATGACCGCCCTGTATCAACCTGCCACGCAACCGGCGATGTAACTATGTTCCCTCG 11093
 QY 1346 GCAGCTACTAGAGCTCTG---TTGGAAGAGAGAACATTGACACAGAAAGTATGTATG 1402
 Db 11094 AGAGCTACAGGCTGCATGATCTTACTGAAAGCACAGTTTGAAGACCGCATGTATG 11153
 QY 1403 AAGATCTTACTCAATTCATTTCGAGACGACAGCTGGAAGAGATGACGTGTGAGAGAG 1462
 Db 11154 ATGACCTT-----TCAAAAGCTGGGAGGACAGAGAGAGAGAGAGAGAGAGAGAG 11204
 QY 1463 GTGGAAGGCTGACCCCTCAACGAGCTGTCAACAACCTTGTGTGCGGTGCCATGACTG 1522
 Db 11205 AGAAGAGCCAGACCCCTGACACAGTTGTCTGTGCACTTCAGCCGCACTGCCCTGACGG 11264
 QY 1523 AGAGCTCCGCGCTTTGACAGAGGATTCCTATATCATGTCTTATGACACATCATATACGA 1582
 Db 11265 AAAAG---AGCAAACTGGATGAGATTAATCTGTACATGAGCTTATGTATCATATGACGA 11321
 QY 1583 AGTCTGTGAG 1642
 Db 11322 AGAGCT-----GCCACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 11354
 QY 1643 CAGAGGCTGAAAGACGAAAGGACAGATATACAGAAACAGAAATGAGAAACAAAGAGC 1702
 Db 11355 GTGAAGCTGAAAG 11414
 QY 1703 TCCCAATTCACAGAGCGGCGGTGCGAGACGCTGGGGGTTCGCGAAATGATGTGTGTGACA 1762
 Db 11415 TCTTGTACAGACAGACAGAGCTGTGACACCGCGGGGGCGCGAGATGTCTGTGACAGATGA 11474
 QY 1763 TCTCCGCGCTCAAGAGCGCTGCCAGAGATGTCTATGAAGACTTTACAGCTCGATATTA 1822
 Db 11475 TCAGTGTCTGAAAGAGAGAGAGAGAGAGATGTGTGTCTTCAACCTGTAACTGGGACTCT 11534
 QY 1823 GTATATCTGAGGGGCGGCAATATGTATATACAGATGGGTATGTGGAACCACTTGAAGACA 1882
 Db 11535 CCATCTCAATGAGGAGCAATGTGAGGTCCAGAGAAATGCTGAGATTAATCTTAAGAGACA 11594
 QY 1883 AGAAGAGCGTGGGCTTCTTATACGTCCATTCGCGGCTCATGAAGTCTGTGTCTGTGTG 1942
 Db 11595 AGAAGAGATGTGCTTCTTCCAGATTCAGAGCATGTATGCAAACTGACGAGTCTGTG 11654
 QY 1943 ATCTTGAAGCTTTCGAGAGAACACAGAGCTGAGAGTCTGGCGTGGGTCTGGAAGGTG 2002
 Db 11655 ATCTCATATGCTTTGAGAGACAAAGACAGCGGAGCTGGGCAATGTATGAGGATG 11714
 QY 2003 CGGCG-----GAGAGAGAAACATGATGACGCCGAGTTCACTGTGCG 2044
 Db 11715 GCACTGTCAATCAATCGCCAGAACGAGAGAGAGATGAGGAGATGATTAATTCACACAG 11774
 QY 2045 CACTCTTCAAGTTCACTTCACTCACTGTGAGAGACAACTTGGACTGGCAGAAATAC 2104
 Db 11775 ACCGTTCCTCAATTCCTCAATTCCTGTGTAGGGGCGCAATTAATGATTTTCCAAAGCTAC 11834
 QY 2105 TGGCAATCTAGAGCGGAGTAACAGCAACAGTGAACGTGTATCTGTGACCGGTGACCTAC 2164
 Db 11835 TACGGACACAGACAGGAGACACACATTAATCATCATATTTGCACTGTGTGACTAC 11894
 QY 2165 TGTGTGCGGTGACAGAGATCATCATGAGCTTCTTACTGTGCACTCAAGCAAGAACTGA 2224
 Db 11895 TCTGTGCGGTGACAGAGATCATCATGAGCTTCTTACTGTGTACTGTGCGGAGAGATGTC 11954
 QY 2225 TCGACCGGCGCGGCAAGGCAATTTCTTCAAGGCAATGGCGGTGCTTCCAGATATTC 2284
 Db 11955 TTGAAGAGCAGGCGCAAGAGAACTTCCAAAGCAATGTGTGTGTCTAAGCAGATGTTC 12014
 QY 2285 ACACCTCACTGAAGTATATCAGGAGACCTTGTATCGAGAAATCAGCAGGCTTTGGCTCACT 2344
 Db 12015 ACAGCTCACTGAAGTATATCAGGATCTCTGTACCGGAGAACAGCAGAGGCTTGGCGAC 12074

QY 2345 CCAAGTTGTGGACCGCTGTGCGGTGTTTCTGTCTTCTATTTCTCCACATGACAGACAAGT 2404
 Db 12075 GTGCGCTATGAGGACGAGAGTGGAGTGGAGTTCCTGCACTGTGTGCGCCACATGATATGAAGC 12134
 QY 2405 TGTGGAAGCACTGTGCGAGAGTGGAGCTGTGGAAGAACTCCCTCAATCTGCAGAGAAGCA 2464
 Db 12135 TGTCTCAAGACTTAAGCCAGATGAGCTGTGGAAGAGCTGTGAGATCTGCAGAGAAGCA 12194
 QY 2465 TGATCCCATGATGTCTGTCACTGTGGAAGAAATGTGTATATGTATGATATCGGCAAGC 2524
 Db 12195 TGTGTGATATGT 12254
 QY 2525 AATGTGTGACACACTATGATGAATCGGCTCCAGCTGTGAACCTGATCTGAAATTAATCTTG 2584
 Db 12255 AGATGTGTGACATGTCTGTGGAATCTTCAATCCATATGTGAGATGATCTCAAGTTCTTG 12314
 QY 2585 ACATGTCTCTCAAGCTGGAAGAGACCTGCAAGCCAGCTTCCAGAGATTTGAAGCA 2644
 Db 12315 ACATGTCTCTGAACTCAAGACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 12374
 QY 2645 ATTAACAGCGAGTGGGTGTGCTGCCAAGGACTTCAAGAGAAATGGAACAAAGAGATG 2704
 Db 12375 ATCCCGTGTGCTCTCAATCTCCAGAGAGACTTCCAGAGAGCCATGACAGCCAGAGCACT 12434
 QY 2705 ATATCTCCAGAGAAATGAGATGATCTCTTACTGTGTGCGAGACGAACAGCGCAAGT 2764
 Db 12435 TCAGCGGTCCAGAAATCCAGATTCGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 12494
 QY 2765 TAGACTCAATCGGTTTCTGCGACCGTTTCAAGAGCTGTGCAAGAGAGATCGGTTTAAT 2824
 Db 12495 TCAATCTCCAGAGATGT 12554
 QY 2825 TGGCGGTGTACTGACTTAATCTGTGTGAACATATGCGGAGACGACTTGAATTTGCACTGT 2884
 Db 12555 TGGCGGT 12614
 QY 2885 TCTGTGAGACGCGAGGT 2944
 Db 12615 TCTGTGAGCTGTGCGGAGACATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 12674
 QY 2945 TCATGTGGGCGGCTCAAGCGCATGAGCGGTGTACTGTGAGATTCAGAGAGTCTAA 2999
 Db 12675 TCATGTGGGCGGCTCAAGCGCATGAGCGCATGTACTGTGAGATTCAGAGAGCA 12729

RESULT 13
 AD085750
 ID AD085750 standard; cDNA; 15359 BP.
 XX
 AC AD085750;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #2564.
 XX
 KW human; tumour-associated antigenic target; TAT; cytosolic; gene therapy;
 XX cancer; cell proliferative disorder; gene; ss.
 OS Homo sapiens.
 XX
 PN W02004060270-A2.
 XX
 PD 22-JUL-2004.
 XX
 PF 15-OCT-2003; 2003WO-US029126.
 XX
 PR 18-OCT-2002; 2002US-0418988P.
 XX
 PA (GENT) GENENTECH INC.
 PA (MUTD/) MU T D.
 PA (ZHOU/) ZHOU Y.
 XX
 WU WU TD, Zhou Y;
 PI

Db 11154 ATGACCTT-----TCAAAAGCTGGGAGCAGAGAGAGAGAGAGAGTGGAGG 11204
Qy 1463 GTGAGAAAGCTGAGACCCCTCTCAAGCAGCTGTCACCACTTCTGTGGGGTTCATGACTG 1522
Db 11205 AGAAGAAAGCAGACCCCTCTGACCAAGTTGTCTCTGACCTTCAAGCCGACCTCCGACG 11264
Qy 1523 AGAGGTCCGCGCTTTGACAGAGATCTCTATATCATGTCTTACGCAACATCATAGCGA 1582
Db 11265 AAAAG---AGCAAACTGGATAGAGATTACTGTACATGGCTTATGCTGATATCATGGCAA 11321
Qy 1583 AGTCTGTGGAGAAAGAGAGAGAGAGGGGGTGGGAGAGAGAGAGAGGGGGTGGAGAG 1642
Db 11322 AGAGCT-----GCCACCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 11354
Qy 1643 CAGAGGCTGAG 1702
Db 11355 GTGAGAGCTGAG 11414
Qy 1703 TCTTATTCACCAAGCGCGGCTGGCGGACCGGTGGGGTGGCCGAATGGTGTGCTGACA 1762
Db 11415 TCTTGTACAGCAAGCAGCGCTGCAACCGGGGGGGCGCGAGATGGTGTGCAAGATGA 11474
Qy 1763 TCTCCGGGTCCAAAGGCGCTGCCAGAGATGTCATGAGAGACTTTCACAGTCCGTATTTA 1822
Db 11475 TCAGTGCTGAAAG 11534
Qy 1823 GTATATGAG 1882
Db 11535 CCATCTCTCATGAG 11594
Qy 1883 AGAAGAGAGTGGGCTTTTATGTCATCGCGGCTCATGAGAGCTCTGCTCCGTGCTCG 1942
Db 11595 AGAAGAGAGTGGGCTTTTATGTCATCGAGAGTATCCAGAGACTGATGCAAAACATGACGCTCGG 11654
Qy 1943 ATCTTGAAGCGCTTGGAG 2002
Db 11655 ATCTCAATGCTTTGAG 11714
Qy 2003 CGGCG-----GGAG 2044
Db 11715 GCACTGTATCATACGCGAG 11774
Qy 2045 CACTTTCAGGTTCACTTCACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2104
Db 11775 ACCGTGTCCTCAATTCCTCAATTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 11834
Qy 2105 TGGGAACTCAGAGCGGAG 2164
Db 11835 TACGAGACAG 11894
Qy 2165 TGTGCGGCTGAG 2224
Db 11895 TCTGCGGCTGAG 11954
Qy 2225 TCGAACCCGCGCGAG 2284
Db 11955 TTGGAAG 12014
Qy 2285 AACCCCTCATGAG 2344
Db 12015 ACGAGCTCATGAG 12074
Qy 2345 CCAAGTTGTGGAG 2404
Db 12075 GTGCGCTATGAG 12134
Qy 2405 TGTGAG 2464
Db 12135 TCGCTCAG 12194
Qy 2465 TGATCCCATGATGCTCTCATGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2524

Db 12195 TGTGATGATGATGCTGCTGCTACTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 12254
Qy 2525 AAATGATGAGACACTAGTGAATCGGCTTCAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 2584
Db 12255 AGATGATGAG 12314
Qy 2585 ACATGTTCTCAAGCTGAG 2644
Db 12315 ACATGTTCTCAAGCTGAG 12374
Qy 2645 ATTAACGAGCGGCTGGGTGCTGCCAAGAGACTTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 2704
Db 12375 ATCCCGGTGCTCATCTTCCAG 12434
Qy 2705 ATATCCCGAG 2764
Db 12435 TCAAGCGGTCCAG 12494
Qy 2765 TGAATCATCGGTTTCTGAG 2824
Db 12495 TCAATGCGAG 12554
Qy 2825 TGGCGGTGTTACTGACTAATGTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2884
Db 12555 TGGCGGTGCTGAG 12614
Qy 2885 TCTTGAAG 2944
Db 12615 TCTTGAAG 12674
Qy 2945 TCAATGCGGCTTCAAGCGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2999
Db 12675 TCAATGCGGCTTCAAGCGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 12729
RESULT 14
AD084285
ID AD084285 standard; cDNA; 15359 BP.
XX
AC AD084285;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1099.
XX
KM human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW cancer; cell proliferative disorder; gene; ss.
XX
OS Homo sapiens.
XX
PN MO2004060270-A2.
XX
PD 22-JUL-2004.
XX
PF 15-OCT-2003; 2003WO-US029126.
XX
PR 18-OCT-2002; 2002US-0418988P.
XX
PA (GETH) GENENTECH INC.
PA (WU/) WU T D.
PA (ZHU/) ZHU Y.
XX
PI Wu TD, Zhou Y;
XX
DR WPI; 2004-534300/51.
XX
PT New nucleic acid molecule and encoded polypeptide, for diagnosing,
XX preventing or treating cell proliferative disorders such as cancer.
PS Claim 1; SEQ ID NO 1099; 5504bp; English.
XX
CC The present invention describes an isolated tumour-associated antigenic
target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide

OY	1593	AGTCTGTGAGAAAGAAAGAGAAAGAGGGGTGGCGAGAAAGAAAGGGCGGTGCGAAG	1642
Db	11332	AGAGCT-----GCCACTGGAGAGGAGGGGAGAGCG	11355
OY	1643	CAGAGGCTGAAGACGAAGGCGAGACCAATACAGAAACAAGAAATGAGAGAAACAAGC	1702
Db	11355	GTGAAGCTGAAGAGAGAGGTGAAGTCTCTTTGAGAGAGAAACAGATGAGAAACAGAGCG	11414
OY	1703	TCCTAATTCACCAAGCCGCGGTGGCGGACCGTGGGGTTGGCGAAATAGTGTCTGTGCACA	1762
Db	11415	TCCTGTACACAGCAACGCGTGCACACCGGGGGGGCGCGAGATAGTGTCTGCAGATGA	11474
OY	1763	TCTCCGCGCTCAAAAGGCGTGGCCCAAGCAGATGTGTCAAGAAAGACTTTTACAGTCTGATTTA	1822
Db	11475	TCAGTGCGCTGAAAGAGAGAGACAGGTGTGCATGTGTCTCCACCTCGAAGCTGGGACTCT	11534
OY	1823	GTATATCTGAGGGGGCGGCATATTGATATACAGATGGGTATGTTGAACCACTTGAAAGACA	1882
Db	11535	CCATCTCTCAATGAGAGGCAATGTCTAGGTTCACGCAAGAAATGCGATGTATCTTTAAGACA	11594
OY	1883	AGAAAGACGTGGGCTTCTTATACGTCAATGCGCGGCGCTCATGAATCTGTGTCGGTCTG	1942
Db	11555	AGAAAGAAATTTGGCTTTCTTCCAGATATCCAGGCACTGATGTCAAAATGCAAGCTCTTG	11654
OY	1943	AATCTGACGCGCTTCGAGAGGAACAACAAGGCTGAAGGTCTGGCGTGGGTCTGGAAAGTG	2002
Db	11655	ATCTCAATGCTTTGAGAGACAGAACAGGCGGAGGGGCTGGCGCATGTGAATGAGAGATG	11714
OY	2003	CGGG-----GGAGAGAAAGAAATGACATGACATGACGCGGAGTTCACTGTGG	2044
Db	11715	GCACTGTATCATATGCGACAGAACGAGAGAAAGGTCAATGGCGAGATGAAATTCACAGAG	11774
OY	2045	CACCTTTCAAGTTCAATTCAGTCACTGTGAGAGACAACAATTGACCTGGCAACTTACC	2104
Db	11775	ACTGTTCCTCAATTCCTCAATGTGCTGTGAGGGGGCAAAATATGATTTCCAGAACTTACC	11894
OY	2105	TGCGAATCTCAGGCGCGGTAAACACCAACAACATGAACGTGTATCTGCAACCGTGCATACC	2164
Db	11835	TACGGAACAACAACAGGGAACAACGACCACTTAAATCAATCAATTCACCTGTGGAACTTACC	11894
OY	2165	TGTCGCGGCTGCAAGAGATTCATCATATGACCTTTTAACTGCGCACTACTCAAGCAAGAACTGA	2224
Db	11895	TCTCTGCGGCTGCAAGAAATTCATTCAGGCACTTTCTACTGTACTCTGCGGCAAGATGTCA	11954
OY	2225	TCGACCCGCGCGGCAAGCAACTTCTTCAAGGCCAATTTGCGCTTCCAGATATTCAC	2284
Db	11955	TTGAAGAGCAAGGGCGAAGAGAACTTCTCAAAACCAATGTGCGGTGCTTAAGCAGTGTCTCA	12014
OY	2285	ACACCCCTCACTGAAGTGAATCAGGGAACCTTGTAACGAGAAATCAGAGGCGTTTGGCTCACT	2344
Db	12015	ACAGCTCTCACTGAATACATCCAGGATCTCTGCACCGGAAACCAAGACCTGGCGCACAC	12074
OY	2345	CCAGGTTGTGGGACGCTGTGCGTGGTTTCTGTCTTCTTATCTTCCACATGCAAGCAACAGT	2404
Db	12075	GTGCGCTATATGGGAAGCAGTGGTGGGAATTCCTGCACGCGTTTCGCCACATGATGATGAAGAC	12134
OY	2405	TGTGGAAGCACTGTCGCGCAGGTGACCTGCTGAAGGAATCTCTCAATCTGCAAGAGACA	2464
Db	12135	TCGCTCAAGAACTCAAGCCAAATCGATGTCTGAAGGAGCTGTGATCTGCAAGAAAGACA	12194
OY	2465	TGATCCCACTGATGCTGTGCATGCTTGAAGAAATGTTGTTATATGTTAACTCAATCCGCAAC	2524
Db	12195	TGTGTGTGTGATGTGTCTGTCTCTACTAGAAAGGAACGTGTGAACCGCAATGTCGCCGCG	12254
OY	2525	AAATGTGTGACACACTAGTGAATCGGCTTCCAACGTGAACCTGATCTTGAAATATCTTGG	2584
Db	12255	AGATGTGTGACATGTCTGTGTGAATCTCTATTCATGATGTGAGATGATCTCAAGTCTTTCG	12314
OY	2585	ACATGTTCTCTCAAGCTGAAGGACCTGACCTTCAGAGCGCAGCTTCAGAGGATTTGATGCCA	2644
Db	12315	ACATGTTCTCTGAACCTCAAGGCAATTTGTGGGCTCTGTAGCTTTCACAGACTACGTACCG	12374

Oy	2845	ATATACGCGGCTGGGGTGGTCCCAAGACTTTCAGAGGAAAAATGGACAAACGAAGAGTT	2704
Db	12375	ATCCCGGTGGCTCACTCCAGAGGACTTTCAGAGGCGCATGGACGCCAGAGCACT	12434
Oy	2705	ATACTCCCGAAGAAATCGAGTTCTCTCACTTGGCTGGAGACGAACCAACGACGGCAAGT	2764
Db	12435	TCAGCGGTCCAGAAATTCAGATTCTCTTCGTGGCTCCAAACGGATGAGAAACGAATGA	12494
Oy	2765	TAGACTCATCGGTTTCTGGACACGTTTCCACGAGCGCTCCAAAGAGATCGGGTTTAACT	2824
Db	12495	TCAACTCCGAAAGATTGCGCAACCGCTTTCAGAGGCGACGACACATCGGCTTCAACG	12554
Oy	2825	TGGCCGTTTACTGACTTAATTGTCTGAACATATGCCGACGAGCTAGATTGGCACGTT	2884
Db	12555	TGGGGGTGCTGACCAACCTGTCCGACATGTGCCGATACCTTCCTCCGACAACT	12614
Oy	2885	TCCGAGGACGGCAGGTTCAGTCTCTAACTACTTCGAACATTTCTGGGCGGTATCGAGA	2944
Db	12615	TCCGAGGACGGGCCGAGAGATCTTTGATGTACTTCGCCCTCACTCGGGCCGCATCGAGA	12674
Oy	2945	TCATGGGCGGCTCCAAAGCGATCGAGCGGTCTACTTCGAGATCAAGAGACTTAA	2999
Db	12675	TCATGGGCGGTCACCCGCACTCGAGCGGATCTTACTTCGAGATCTTCAGAGACCA	12729

RESULT 15
 ADQ83605
 ID AD083605 standard; cDNA, 15359 BP.
 XX
 AC AD083605;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #419.
 XX
 KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
 KW cancer; cell proliferative disorder; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN W02004060270-A2.
 XX
 PD 22-JUL-2004.
 XX
 PF 15-OCT-2003; 2003WO-US029126.
 XX
 PR 18-OCT-2002; 2002US-0418988P.
 XX
 PA (GETH) GENENTECH INC.
 PA (WUTD/) WU T D.
 PA (ZHOU/) ZHOU Y.
 XX
 PI Wu TD, Zhou Y;
 XX
 DR WPI; 2004-534300/51.
 XX
 PT New nucleic acid molecule and encoded polypeptide, for diagnosing,
 PT preventing or treating cell proliferative disorders such as cancer.
 XX
 PS Claim 1, SEQ ID NO 419, 5504bp; English.
 XX
 CC The present invention describes an isolated tumour-associated antigenic
 CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
 CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
 CC (a); (c) the complement of (a) or (b); (d) a sequence that hybridises to (a) -
 CC sequence identity to (a) - (c); or (e) a sequence that hybridises to (a) -
 CC (c). Also described: (1) an expression vector comprising the above
 CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
 CC a process for producing a polypeptide; (4) an isolated polypeptide
 CC comprising: (a) an amino acid sequence encoded by any of the above
 CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
 CC length coding region of the above nucleotide sequences; or (c) a sequence
 CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide

comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (9) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chemic) polypeptide, an antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth potentiating effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.

Sequence 15359 BP; 3251 A; 4580 C; 4717 G; 2811 T; 0 U; 0 Other;

Query Match 25.7%; Score 771.8; DB 13; Length 15359;

Best Local Similarity 56.5%; Pred. No. 5.8e-192; Matches 1591; Conservative 0; Mismatches 1187; Indels 117; Gaps 9;

38 TGAAGCCCAAGACATTAATGCAAAATGAAACATGCGACCTAGAGAGATCT 97
9819 TGGGGCTCCCAACAGTGTGAGAGATGTGTCCGAATCCGGTGTGAGCGGCTCA 9878
98 TAGCGAGGTGAGCAATTCGAGTGAAGCAAGACGACGACGAGCGGCGCATATCA 157
9879 TGGCAGACATTTGGGGGCTGCGGAGTCAAGTCCCGCTACAGAGATGCCGATGTCA 9938
158 TCGATGTGTGTGCTCTTACTCTGTTTATTTGCGTTTCTGTGTGGCAAGGGGCTG 217
9939 TCGAATACAGCTGCGCATGATGATGATGATGATGATGATGATGATGATGATGATG 9998
218 AATATGTTACT 265
9999 AGGCACCCCT 10058
266 AACACATGAACAGCTCTCTCAAGAAATGTTCTGAAGCTCATCAAAAGAAATCGGCANTG 325
10059 ACGACCTCAATCT 10118
326 AGAAGCGCGCTGTGATGACCGCATGCGCATGCGCATGCGCATGCGCATGCGCATG 385
10119 AGAAGCGCTCTGTGATGACCGCATGCGCATGCGCATGCGCATGCGCATGCGCATG 10178
386 CCGAAGAACTGCTGAGGAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 445
10179 GGCAGGAGCTCTGAGGAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 10238
446 ACAATATGTTCCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 505
10239 GGAAGATGTGTCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 10289
506 CATCCAGGTAGAGTCTCAGATATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 565
10290 CCCAGAGAGGCGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10349
566 CTTTCTACCGCTGTCTCATCAAGTACGTGACCTGACAGAGAACTGCTCTCAGAGACA 625
10350 CCTGTATCTCGCTCATCTCCCTACGTGAGACAAACAGAGCGGAGGTGAGAGAGC 10409

626 ATGTTCCAGAGCGGAAAGAGCTGTACACACAGCTGCTGAATTTTCAACATCTGTGCA 685
10410 GGAATCCAGAGCGGAAAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10469
686 AGACCGAGTACTTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 745
10470 AGTCCCAATTAAG 10529
746 TGTGTGATTAATCCAAACAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 805
10530 TGTCTCTCTGATCTGTGACAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 10583
806 AAGGTGTGAAAGAAAG 865
10584 AGTCCGAGGTCTCGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 10643
866 TCCAGAGTCTCTTAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 925
10644 TGCAGAGCTCATGT 10703
926 TCGCTGCGAGAGACAAAGAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 985
10704 GTGCGCCCAACGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 10763
986 CAGAACAGATGT 1045
10764 CAGATGAGAGAGTCCGGAATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10823
1046 CCGCAGACGAATGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1105
10824 GCTCCCGCTCTCTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10860
1106 GCAATATATATCTGT 1165
10861 GGGGCT 10913
1166 GAATGT 1225
10914 GAGT 10973
1226 TGAATGAAGAGT 1285
10974 CTAAGAGAGCGT 11033
1286 GCTTCCGAGCAATCTCACTATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1345
11034 GTTTCGT 11093
1346 GCAAGTACTAGAGCTGT 1402
11094 AGAGCTAAG 11153
1403 AAGATCTTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 1462
11154 ATGACCTT-----TCAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 11204
1463 GTGAG 1522
11205 AGAAG 11264
1523 AGAGGTCCGAGCTTTGTGAG 1582
11265 AAAAG---AGCAACTGT 11321
1583 AGTCTGT 1642
11322 AGAGCT-----GCCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 11354
1643 CAGAGGT 1702
11355 GTGAAGCTGT 11414
1703 TCTTATTCACCAAGCGGCTGT 1762

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OM nucleic - nucleic search, using sw model

Run on: April 14, 2006, 13:59:54 ; Search time 11349.5 Seconds

(without alignments)
12371.297 Million cell updates/sec

Title: US-10-668-767-127_COPY_10000_13000

Perfect score: 3001

Sequence: 1 cagctccctcgcgcgaacag.....cgagatcaaggagctcataa 3001

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0 .

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : Maximum Match 100%

Listing first 45 summaries

EST:*
1: gb_eest1:*
2: gb_eest2:*
3: gb_eest3:*
4: gb_eest4:*
5: gb_eest5:*
6: gb_eest6:*
7: gb_eest7:*
8: gb_eest8:*
9: gb_eest9:*
10: gb_eest10:*
11: gb_eest11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	642.6	21.4	14832	11	DQ052093 Homo sapi
2	500.2	16.7	14736	11	DQ052094 Pan trogl
3	479.8	16.0	3045	4	AK042482 Mus muscu
4	453.2	15.1	1042	5	BX402920 BX402920
5	429	14.3	605	2	BR488910 AT24194.5
6	392.6	13.1	601	3	BI502728 BBI700028
7	379.4	12.6	1169	6	CD509498 CDA96-F06
8	364.4	12.1	599	10	AG926182 Drosophila
9	325	10.8	842	8	CX784892 HESG3_40
10	320.8	10.7	781	8	CX784892 HESG3_40
11	319.6	10.6	684	2	BB619430 BB619430
12	317.6	10.6	964	2	BB619430 BB619430
13	287.8	9.6	813	8	DT063789 AGENCOURT
14	276.8	9.2	569	3	BM645859 170006873
15	276.2	9.2	887	10	C2533566 SRA-aac8
16	265.2	8.8	565	7	CO309773 EK219228
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18	249.2	8.3	620	7	CR757759 CR757759
19	246.2	8.2	626	8	DN416354 LIB4215-1
20	242	8.1	491	3	BI346800 376130 MA
21	239.2	8.0	531	1	AL916615 AL916615
22	238.4	7.9	556	6	CB359659 ZF001-P00

23	237.2	7.9	732	8	DN412056
24	235.4	7.8	582	7	CR757761
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28	230	7.7	588	7	CR757066
29	228.8	7.6	503	7	CN308890
30	228.2	7.6	575	7	CR757030
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34	216.6	7.2	645	8	DN375037
35	211.8	7.1	592	7	CR757028
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38	197	6.6	9562	11	DO034793
39	191.4	6.4	392	3	BI502873
40	191	6.4	864	7	CR991017
41	186.4	6.2	706	10	BX231389
42	181.6	6.1	1048	5	BU108104
43	178	5.9	643	10	CE473976
44	176.6	5.9	462	2	BG553101
45	170.6	5.7	642	8	DN428996

ALIGNMENTS

RESULT 1
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LOCUS Homo sapiens RYR1 gene, VIRTUAL TRANSCRIPT, partial sequence.
DEFINITION DQ052093.1 GI:66905537
ACCESSION DQ052093
VERSION DQ052093.1
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 14832)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civeille,D., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
A scan for positively selected genes in the genomes of humans and chimpanzees
Chimpanzees
JOURNAL (er) PLOS Biol. 3 (6), E170 (2005)
PUBMED 15869325
AUTHORS 2 (bases 1 to 14832)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civeille,D., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
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ORIGIN
Query Match 21.4%; Score 642.6; DB 11; Length 14832;
Best Local Similarity 49.1%; Pred. No. 1.4e-157;
Matches 1470; Conservative 0; Mismatches 1393; Indels 132; Gaps 9;

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DB TGGGGCTCCCAACAGTGTGAGAGAGATGTGTCCGACATCCCGGTGCTGGAGCGGCTCA 9478
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QY 218 AATAATTTATCTCTA-----GGCGAACAACGTAACAATGTTAAACGGCG 265
DB AGGCAACCCCTTCCGCTGCGCGCGGCGCCCCCAACCTGACAGCTGTCACTCTG 9658
QY 266 AACACATGAACCAAGCTCTCAAGAAATGTTCTGAAGCTCATCAAAAAGAAATCGCAATG 325
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QY 386 CCGAAGAACTGTGAGGATTCCTTCTGCGCGCTGCTGAACGTGTTCGCAACGCAAG 445
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QY 926 TCGTGTGAGAGAACAGAACTGTGTGAGCAATTTGAAGACAGGTTCCTGGAAGAAATGT 985
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DB CCATCTCATATGAG 11120
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DB ACCGTGTCCGATTTCTTACAAATTTGCTGTGAGAGAGAGAGAGAGAGAGAGAG 11360
QY 2105 TGGAACTCAAGCGCGGTATACAGAGCAACAGTGAACGTGATCTGACCGGTGACAC 2164
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Qy	2764	TTAGACTACATCGGTTTCTGCGACGCGTTTCCAGACCGCTGCCAAGAGATCGGGTTTAA	2823
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RESULT 3			
AKO42482			
LOCUS	AKO42482		
DEFINITION	3045 bp	mRNA	linear
VERSION	AKO42482.1	GI:26089063	
KEYWORDS	Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:R63095J05 product:RYANODINE RECEPTOR 1 (SKELETAL MUSCLE-TYPE RYANODINE RECEPTOR) (RR1) (RYR-1) (SKELETAL MUSCLE CALCIUM RELEASE CHANNEL) homolog (Homo sapiens), full insert sequence.		
ACCESSION	AKO42482		
VERSION	AKO42482.1	GI:26089063	
KEYWORDS	Mus musculus (house mouse)		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1	Carninci, P. and Hayashizaki, Y.	
AUTHORS	High-efficiency full-length cDNA cloning		
TITLE	Meth. Enzymol. 303, 19-44 (1999)		
JOURNAL	10349636		
PUBMED			
REFERENCE	2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	
AUTHORS	Normalization and subraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
TITLE	Genome Res. 10 (10), 1617-1630 (2000)		
JOURNAL	11042159		
PUBMED			
REFERENCE	3	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, S., Watanuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuyama, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	
AUTHORS	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer		
TITLE	Genome Res. 10 (11), 1757-1771 (2000)		
JOURNAL	11076861		
PUBMED			
REFERENCE	4	The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.	
AUTHORS	Functional annotation of a full-length mouse cDNA collection		
TITLE	Nature 409, 685-690 (2001)		
JOURNAL			
PUBMED	5		
REFERENCE			

AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3045)

Adachi, J., Aizawa, K., Akiyama, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hasehizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirose, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komori, H., Kouda, M., Koye, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsumi, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akihira, S., Tanaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/IRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers

FEATURES
Source

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/dev_stage="3 days neonate"
1..3045
/note="RYANODINE RECEPTOR 1 (SKELTAL MUSCLE TYPE RYANODINE RECEPTOR) (RYR1) (RIR-1) (SKELTAL MUSCLE CALCIUM RELEASE CHANNEL) homolog (Homo sapiens) (SWISSPROT|P21817, evidence: PASTY, 99.2%ID, 7.2%length, match=1092)"

ORIGIN

Query Match 16.0%; Score 479.8; DB 4; Length 3045;
Best Local Similarity 65.6%; Pred. No. 8.9e-115;
Matches 700; Conservative 0; Mismatches 367; Indels 0; Gaps 0;

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RESULT 4
BX402920
LOCUS BX402920 1042 bp mRNA linear EST 29-APR-2004
DEFINITION BX402920 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
CDNA clone CS0D0003YB21 5-PRIME, mRNA sequence.
VERSION BX402920
KEYWORDS BX402920.2 GI:46877799
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

estimated-cyto:44F1-45A7: 04/09/2001
Plate: AT.241 row: H Column: 10
High quality sequence stop: 572.

FEATURES

SOURCE

1. 605

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/lab_host="Plates AT.10-AT.120: DHS-alpha. Plates

AT.121-AT.319: DHS-alpha Tona"

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/note="Organ: ADULT testes; Vector: potB7; Site: 1: EcORI;

Site 2: XhoI; The mRNA for the testis library was made

from testes and seminal vesicles hand dissected from 0-3

day old Ore-R males. RNA kindly provided by the lab of

Margaret Fuller. Sized fractionated cDNAs were directly

ligated into potB7. Plasmid cDNA library."

ORIGIN

Query Match 14.3%; Score 429; DB 2; Length 605;

Best Local Similarity 81.8%; Pred. No. 1.4e-101;

Matches 495; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

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Db 1 CGCGAGTTCCAGCTGCGCTGCTTCCGTTCTATCCAGCTGAGCTGCGAGGCGCACACTT 60
Oy 2088 GAGCTGGAGAACTACTCTGCGAACTCAGGCGCGTAACAGCAACAGTGAAGTGGTCA 2147
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Oy 2388 CCAATGCAAGCAAGTGTGCAAGCACTGTCGAGGTGAGCTGCTGAAGAACTCTT 2447
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Oy 2448 CAATGCAAGCAAGTGTGCAAGCACTGTCGAGGTGAGCTGCTGAAGAACTGTTAA 2507
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Db 481 CGGACATATGGCAAGCAAGTGTGAGCACTAGTGAAGTGTGCAAGCAAGTGAAGCT 540
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Oy 2628 CCAAG 2632
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RESULT 6
B1502728/c

LOCUS B1502728 601 bp mRNA linear EST 08-APR-2002
DEFINITION B170002B00G11.5 Bee Brain Normalized/Subtracted Library, B17 Apis
mellifera cDNA clone B170002B0011 5', mRNA sequence.

ACCESSION

VERSION B1502728

KEYWORDS B1502728.1 GI:15353102

SOURCE EST.

ORGANISM Apis mellifera (honey bee)

Apis mellifera

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preyptera;

Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;

Apidae; Apis.

1 (bases 1 to 601)

Whitefield,C.W., Band,M.R., Bonaldo,M.F., Kumar,C.G., Liu,L.,

Pardinas,J., Robertson,H.M., Soares,B. and Robinson,G.E.

Annotated expressed sequence tags and cDNA microarrays for studies

of brain and behavior in the honey bee

Genome Res. 12 (4), 555-566 (2002)

11932240

Contact: Gene E. Robinson

Department of Entomology

University of Illinois

505 S. Goodwin Ave., Urbana, IL 61801, USA

Tel: 217 265 0309

Fax: 217 244 3499

Email: genec@life.uiuc.edu

This research was funded by the University of Illinois Critical

Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation

Award in Functional Genomics to G.E. Robinson and an NSF

Postdoctoral Fellowship in Bioinformatics to C.W. Whitefield.

PCR Primers

FORWARD: TAATACGACTCATATGAGG

BACKWARD: ATTACCTCCTACTAAG

Plate: B170002B20 row: G Column: 11

Seq primer: AGCGATTAACATTCACACAGGA

High quality sequence stop: 601.

Location/Qualifiers

1. 601

/organism="Apis mellifera"

/mol_type="mRNA"

/strain="mixed strains of European bees, predominantly

A.m. ligustica"

/db_xref="taxon:7460"

/clone="B170002B0011"

/sex="female"

/tissue_type="brain"

/dev_stage="adult worker honey bee"

/lab_host="DH10B"

/note="Organ: brain; Vector: pT73-Pac; Site 1: EcORI;

Site 2: NotI; This B17 cDNA library was generated by

subtraction of the B16 library with 4000 previously

sequenced clones. The B16 library was contributed by the

Soares laboratory and it was constructed and normalized

as described by Bonaldo, M.F., Lemmon, G. and Soares,

M.B. (1996). Genome Research 6(9): 791-806. RNA was

prepared from dissected brains of adult worker bees of

various ages and various behavioral groups."

ORIGIN

Query Match 13.1%; Score 392.6; DB 3; Length 601;

Best Local Similarity 78.2%; Pred. No. 5.9e-92;

Matches 470; Conservative 0; Mismatches 131; Indels 0; Gaps 0;

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Oy 2009 GAGGAAAGACATGACGAGCGAGTTCACTGCGCACTCTTCAAGTTCAATGACTCA 2068
Db 601 GAGGAAAGACATGACGAGCGAGTTCACTGCGCACTCTTCAATGACTCA 542
Oy 2069 CCTGTGAAGACAACTTGGACGAGAACTACCTGCAAGCTCAGGCGGTAAACGAG 2128
Db 541 CTTGCGAGGTCATTAATCTTGAATTCGAAATTAATTAAGAACGAGCTGGTAACGAA 482
Oy 2129 CAACAGTGAAGCTGTGATGCAACCGTGCAGTCACTGCTGCGGCTGCAAGAGTCAATCA 2188
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Qy 2970 GCGTGTACTTCGAGATCAAGAGTCTA 2398
 Db 783 GCGGGTGTACTTGAATCAAGAGTCCA 811

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 LOCUS AG926182
 DEFINITION Drosophila melanogaster DNA, clone: DME1-007J21.F.fa, genomic
 accession AG926182.1 GI:58447553
 VERSION AG926182.1 GI:58447553
 KEYWORDS
 SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
 AUTHORS Hattori, M., Toyoda, A., Murakami, K., Kuroki, Y., Fujiyama, A.,
 Tochio, T. K. and Sakaki, Y.
 TITLE BAC end sequences of library DME1
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 599)
 AUTHORS Hattori, M.
 TITLE Direct Substitution
 JOURNAL Submitted (19-JAN-2005) Masahira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
 (E-mail: hattori@gsc.riken.jp, URL: http://hsp.gsc.riken.jp/,
 Tel: 81-45-503-9111, Fax: 81-45-503-9170)
 Clones are derived from the BAC library DME1
 For BAC library availability, please contact Masa-Toshi Yamamoto
 (yamamoto@kit.jp).
 Submitted (30-11-2004) by Masahira Hattori,
 RIKEN, Genomic Sciences Center (GSC);
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail: hattori@gsc.riken.jp, Tel: 81-45-503-9111,
 Fax: 81-45-503-9170)
 This work was done in collaboration with Yamamoto, M-T. Drosophila
 Genetic Resource Center
 Saga Ippongi-cho, Ukyo-ku, Kyoto 616-8354, Japan
 Tel: 81-75-873-2660 FAX: 81-75-861-0881
 PRIMERS

COMMENT
 Sequencing : F
 LIBRARY
 Vector : pKS150
 R.Site 1 : SacI
 R.Site 2 : SacI.
 Location/Qualifiers
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 /mol_type="genomic DNA"
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 /clone_lib="DME1 Drosophila BAC library"

ORIGIN
 Query Match 12.1%; Score 364.4; DB 10; Length 599;
 Best Local Similarity 75.6%; Pred. No. 1.7e-84;
 Matches 452; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

Qy 50 ACATATGCAAAATGCAACATGATCGGACGCTAGAGACGATCTTAGCGGAGGTGG 109
 Db 599 ACATATGCTCAAGATGAGAGCTGTATCCAAATCTAAGACATTTCTCGCCGAGGTGG 540

Qy 110 ACCAATTCGTGAGTCAACAAGACGTAACAAGAGCGCGCATATCATGATGTGTGTC 169
 Db 539 ACCAATTCGTGAGTCAACAAGACGTAACAAGAGCGCGCATATCATGATGTGTGTC 480

Qy 170 TGCCTTACTCTGTCTTATTTGCGGTTCTGTGTGCGCAAGAGGCGCTGATTAATGTTACTC 229
 Db 479 TCCGCTGTGTTGCGGCTATCTACCGTTTGGTGTGCCAGGAGCGGATATGTCAATGC 420

Qy 230 CTACTGGCGGAAACCACTTAACAATGTAAAGCGGAAACATGATACCAGTCTCTCAAGA 289
 Db 419 CCAACAGTGGCAACCACTTGAACATGTGTCAAGCGGATCAATGATATCCGTTCGCGAAA 360

Qy 290 ATGTTCTGAAGCTCATCAAAAAGAACATCGGCATAGAGACGCGCGGTGATGACCCGCA 349
 Db 359 ATGTCCTTAATATGATCAAGAAACATTTGGCAACGATAGACGCCCTTGTATGATCCCA 300

Qy 350 TCGCCACTTAACAGAGAGATCATCATCAACAGTCCGAGAACTGTGAGGATTCCT 409
 Db 299 TTGCCGCTTATACGAGAGATTTATCATCAATACGTCGAGAGAGCTGTCAAGATTCGT 240

Qy 410 TCCTGCGCTGCTTAAAGTGTTCGCAAAACGCAAGCAATATGTTCCATTAAGAGAGAGA 469
 Db 239 TCTTCCGCTGCGGAGCGGATGAAAGAGCCCATGAGAACATGCTGACAGAGAGACA 180

Qy 470 GCTTAGAGGGGTTTATTAAGTCTGTCAACAGACACATCCAGGTAGATCTCAGATAC 529
 Db 179 GCATCGAGATTTATCATCAAGTCCGACAGACACATTCGACAGTGAAGACCGAGTGC 120

Qy 530 AAGAAATCTGCGAGTCTGTGTGACAGACATCTACTCTTTACCCGCTGCTCATCAAGT 589
 Db 119 AGAGAGACTGGAATCTGTGTGTGAGACATATCTCGTTTATCCCTGCTCATCAAGT 60

Qy 590 ACGTGACCTGCAAGAAACCACTGCTCAGAAACAATGTTCCAGAGCGGAGAGACT 647
 Db 59 AGTGATCTTCAAGAAACCACTGCTCAGAAACAATGTTCCAGAGCGGAGAGACT 2

RESULT 9
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 LOCUS CX784892
 DEFINITION HESC3_40.D03.g1.A036 NIH_MGC_260 Homo sapiens cDNA clone
 IMAGE:7479224 5', mRNA sequence.
 ACCESSION CX784892
 VERSION CX784892.1 GI:58301682
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 REFERENCE 1 (bases 1 to 842)
 AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cga@ds-remail.nih.gov
 Tissue Procurement: BresaGen, Inc.
 cDNA Library Preparation: Express Genomics, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLI)
 DNA Sequencing by: Laboratory for Genomics and Bioinformatics,
 University of Georgia
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNLI at:
 http://image.llnl.gov
 Plate: LHM15795 row: h column: 06
 Seq primer: JENREV (CAGGAACGCTATGAC)
 High quality sequence stop: 842.
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:7479224"
 /sex="male"
 /tissue_type="human embryonic stem cells"
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FEATURES
 source

/lab host="DH10B-T1 phage-resistant E. coli"
/clone lib="NIH_MGC_260"
/note="Vector: pExpress-1; Site 1: NotI; Site 2: EcoRV;
RNA obtained from human embryonic stem cells isolated from
the inner cell mass of blastocyst stage embryos. Cell line
id and NIH Registry designation is BG01. Positive for
SSEA3, SSEA4, Tra 1-60, Tra 1-81, CD9, Alk Phos, Oct4 and
Nanog expression; negative for SSEA1 expression. Passage
number 21. CDNA primed using oligo-dT primer:
5'-pGACTGATCTTCTAGTCGAGCGGCCCT(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. This primary library
is non-normalized (normalized primary library is
NIH_MGC_261). It was constructed by Express Genomics
(Frederick, MD). Sequence ends have been trimmed to
exclude vector and regions below phred quality 16. Note:
this is a Mammalian Gene Collection library."

ORIGIN

Query Match 10.8%; Score 325; DB 8; Length 842;
Best Local Similarity 69.8%; Pred. No. 4.7e-74;
Matches 439; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

2005 GCGGAGAGAAAGATGATGAGCGGAGTTACCTGCGCATCTTGAGTTCAATTCAG 2064
213 GAGGAGAGAGAGTATGATGCGGATGATGATTAATTCACACAAACCTGTTCCATCTTACAA 272
2065 CTCACCTGTGAGAGACACAACTTGAGCTGCGAGAACTACCTGCGAATCTAGCGCGTAAAC 2124
273 TTGCTCTGTAGAGGGGACAAATTAATGATTTCAGAACTACCTGAGAGACACAGACGAGAAC 332
2125 ACGACAAAGTGAAGTGTGATCTGCACCGTGCATCTGCTGCGGCTGCAGAGATCC 2184
333 ACGACCAATTAATCATCATCTTGGACCTGTGACCTACCTGCGGCTGCAGAGATCC 392
2185 ATCATGACCTTCTACTGACATCTCAAGCAAGAAAGTGAACCGCGCGGCAAGACG 2244
393 ATGACGACTTCTACTGATGATCTGACCTGCGCAAGAAAGTGAATTAAGACAGGCAAGAGG 452
2245 AACTTCTTCAAGGCAATGAGGCTGCGCTTCCCAAGTATTCACACCTCATCTGAAGTCA 2304
453 AACTTCTTCAAGGCAATGAGGCTGCGCTTCCCAAGTATTCACACCTCATCTGAAGTCA 512
2305 CAGGACCTTGTAGCAGAAATCAGAGGCTTTGCTCACTCCAGGTTGTGAGACGCTGTC 2364
513 CAGGATCCCTGCACCGGGAACAGCAGAGCCTGCGGCAACATGCGCTATGAGACGCAAGTG 572
2365 GATGATTCCTGTTCTTCTTCTCCCAATGACAGCAAGTGTGAGAGCACTTCGCGCAG 2424
573 GTGGATTCCTGCACAGTGTTCGCCCAATGATGATGAAGCTCGCTCAGAGACTCAAGCCAG 632
2425 GTGACCTGTGAGAGAACTCCTCAATCTGAGAGAGACATGATCCCATGATGCTGTCC 2484
633 ATGACAGCTGTGAGAGAGACCTGCGATCTGCGAAGAGACATGATGATGATGATGATGATG 692
2485 ATGCTTGAAGAAATGTTGTTAATGTAATTCGCGCAAGCAATGATGATGATGATGATGATG 2544
693 CTACTAGAGAGAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 752
2545 GAATCGGCTGCGAAGTGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 2604
753 GAATCTCTATCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 812
2605 GACCTGACCTTCAGAGCCAGCTTCCAGGA 2633
813 GACATTTGGGGCTCTGAAGCCTTCCAGGA 841

RESULT 10
CX786866 781 bp mRNA linear EST 02-MAR-2005
LOCUS CX786866
DEFINITION HESG3.65 H01.g1 A036 NIH_MGC_260 Homo sapiens cDNA clone
IMAGE17482075 5', mRNA sequence.
ACCESSION CX786866

VERSION CX786866.1 GI:58303656
KEYWORDS Est.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 781)

REFERENCE NIH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-remail.nih.gov
Tissue Procurement: Bresagen, Inc.
CDNA Library Preparation: Express Genomics, Inc.
CDNA Library Arrayed by: The I.M.A.G.E.B. Consortium (LNL)
DNA Sequencing by: Laboratory for Genomics and Bioinformatics,
University of Georgia
Cloned through the I.M.A.G.E.B. Consortium/LNL at:
http://image.llnl.gov
Plate: LHAM15802 Row: O Column: 01
Seq primer: JENREV (CAGGAACAGCTATGACC)
High quality sequence stop: 781.
Location/Qualifiers
1..781

FEATURES

source

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/mol_type="mRNA"
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/clone="IMAGE:7482075"
/sex="male"
/tissue_type="human embryonic stem cells"
/cell_type="human embryonic stem cells"
/cell_line="BG01"
/lab host="DH10B-T1 phage-resistant E. coli"
/clone lib="NIH_MGC_260"
/note="Vector: pExpress-1; Site 1: NotI; Site 2: EcoRV;
RNA obtained from human embryonic stem cells isolated from
the inner cell mass of blastocyst stage embryos. Cell line
id and NIH Registry designation is BG01. Positive for
SSEA3, SSEA4, Tra 1-60, Tra 1-81, CD9, Alk Phos, Oct4 and
Nanog expression; negative for SSEA1 expression. Passage
number 21. CDNA primed using oligo-dT primer:
5'-pGACTGATCTTCTAGTCGAGCGGCCCT(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. This primary library
is non-normalized (normalized primary library is
NIH_MGC_261). It was constructed by Express Genomics
(Frederick, MD). Sequence ends have been trimmed to
exclude vector and regions below phred quality 16. Note:
this is a Mammalian Gene Collection library."

ORIGIN

Query Match 10.7%; Score 320.8; DB 8; Length 781;
Best Local Similarity 70.6%; Pred. No. 6e-73;
Matches 427; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

2005 GCGGAGAGAAAGATGATGAGCGGAGTTACCTGCGCATCTTGAGTTCAATTCAG 2064
165 GAGGAGAGAGAGTATGATGCGGATGATGATTAATTCACACAAACCTGTTCCATCTTACAA 224
2065 CTCACCTGTGAGAGACAACTTGAGCTGCGAGAACTACCTGCGAATCTAGCGCGTAAAC 2124
225 TTGCTCTGTAGAGGGGACAAATTAATGATTTCAGAACTACCTGAGAGACACAGACGAGAAC 284
2125 ACGACAAAGTGAAGTGTGATCTGCACCGTGCATCTGCTGCGGCTGCAGAGATCC 2184
285 ACGACCAATTAATCATCATCTTGGACCTGTGACCTACCTGCGGCTGCAGAGATCC 344
2185 ATCATGACCTTCTACTGACATCTCAAGCAAGAAAGTGAACCGCGCGGCAAGACG 2244

Db 345 ATCAGCGACTTCTACTGTACTACTCGGCGAAGATGTCTTGAAGACGCGCAAGG 404

Qy 2245 AACTCTTCAAGGCGCATTTGGGCTTCCCAAGTATCAACACCTCACTGAAGTCATA 2304

Db 405 AACTTCTCAAGGCGCATTTGGGCTTCCCAAGTATCAACACCTCACTGAAGTCATA 464

Qy 2305 CAGGAGCTTGTACGACAGATGAGGAGGCTTGGCTCACTCCAGGTTGTGGACGCTGTC 2364

Db 465 CAGGAGCTTGTACGACAGATGAGGAGGCTTGGCTCACTCCAGGTTGTGGACGCTGTC 524

Qy 2365 GGTGTTTCTGTCTTCTTATTTCTCCACATGACGACAAAGTTTCAAGACCTGTCGAG 2424

Db 525 GTGGATTTCTGTACGATGTTTCCCAATGATGATGAAGCTGCTCAGACCTCAAGCCAG 584

Qy 2425 GTGAGCTGTGGAAGAACTCTCAATCTGACAGAGACATGATCCCATGATGCTGTC 2484

Db 585 ATCGAGCTGTGGAAGAACTCTCAATCTGACAGAGACATGATCCCATGATGCTGTC 644

Qy 2485 ATGCTTGAAGAAATGTTTGTATATGTAATCGCAAGCAATGATGAGACACTAGTA 2544

Db 645 CTACTAGAAGGGAAGTGTGTGAAGCGCATGATGCGCGGACATGATGATGCTGTCG 704

Qy 2545 GAATGGGCTTCCACAGTGAAGTGAATCTGAAATCTTGCATGATGTTCTCAAGCTGAG 2604

Db 705 GAATCTCATCAATGTGAGATGATGATCTCTCAAGTCTTCTCAAGCTGAG 764

Qy 2605 GACCT 2609

Db 765 GACAT 769

RESULT 11

BB639430 684 bp mRNA linear EST 26-OCT-2001

LOCUS BB639430 RIKEN full-length enriched, 3 days neonate thymus Mus

DEFINITION musculus cDNA clone A630095L05 5', mRNA sequence.

ACCESSION BB639430

VERSION BB639430.1 GI:16474825

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

1 (bases 1 to 684)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Kono, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

Unpublished (2001)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@res.riken.jp URL: http://genome.gsc.riken.jp/

Carninci, P., Shibata, K., Hayashizaki, N., Suganuma, A., Hayashizaki, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuyama, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Suganuma, A., and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shingawa, A., Saito, T., Kiyosawa, H., Yamashita, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., and Hayashizaki, Y.

Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

e mouse tissues.

Location/Qualifiers

1..684

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="A630095L05"

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/dev_stage="3 days neonate"

/lab_host="DH10B"

/clone_lib="RIKEN full-length enriched, 3 days neonate thymus"

/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGATCCAGAGAGCTTTTATTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATTCGAGTTATTAATTAATCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified Bluescript KS(+) after bulk excision from Lambda FliC I."

ORIGIN

Query Match 10.6%; Score 319.6; DB 2; Length 684;

Best Local Similarity 68.8%; Pred. No. 1.2e-72;

Matches 439; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

Qy 1933 TCCGTGCTGATCTTGAAGCGCTTGAAGAGAACCAAGCTGAAGTCTGGCGTGGGT 1992

Db 47 TTGCTCTGAGCTTCATGCTTTCGAGAGGAGAACAGAGGCGCTGGCATGGTG 106

Qy 1993 CTGAAGGTGCGCGGAGAGAGAAATGATGACGCCGATTCACCTGGCACTTTC 2052

Db 107 AACAGAGCGGAATCTGAGAGAAAGATGCGGATGACGATTCACAGAGACTGTC 166

Qy 2053 AGCTTCATTCAGCTCACTGTGAGAGACACAACTTGATCTGGAGAACTACCTGGAACT 2112

Db 167 CGTCTCTGAGCTGCTCTTGAGGCGGACAAATGATTTCCAAATACCTACCGGACA 226

Qy 2113 CAGGCGGTAACAGACAAAGTGAACGTTGATCTGACAGCTGATCACTGTCGGG 2172

Db 227 CAGACTGGGAACAGACCAATCATATATCTTATCTGACAGTGGATCACTCTGGG 286

Qy 2173 CTGACAGATCATCATGAGTCTTACTGCACTTCAAGCAAGAACTGATGACCCG 2232

Db 287 CTGACAGATCATCATGAGTCTTACTGCACTTCAAGCAAGAACTGATGACCCG 346

Qy 2233 GCCGCAAGGAACTTCTTAAAGGCAATGCGCTTCCCAAGTATCAACACCTC 2292

Db 347 CAGGGAAGAGAACTTCTTCAAGCCATGTCGATGAATTAACAAGTCTTCAACAGCTTC 406

Qy 2293 ACTGAAGTCATACAGGAGCTTGTACGAGATGACAGGCTTGGCTCACTCAGGTTG 2352

[illegible]

RESULT 12	
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DEFINITION	964 bp mRNA
DESCRIPTION	1 linear EST 13-MAR-2003
ACCESSION	BC409436
VERSION	1
KEYWORDS	mus musculus
SOURCE	mus musculus (house mouse)
ORGANISM	mus musculus

REFERENCE	1 (pages 1 to 96)
AUTHORS	Woo, J. T., Asai, Y., Zhu, M., Moates, J. M. and Magnuson, M. A.
TITLE	Identification of thirty-six genes whose expression is markedly affected by beta cell differentiation and de-differentiation
JOURNAL	Unpublished (2001)
COMMENT	Contact: Magnuson, M. A.

Department Of Molecular Physiology and Biophysics
Vanderbilt University
747 LH, 21st Ave at Garland Ave. Nashville, TN 37232-0615, USA
Fax: 615 322 7236
Email: mark.magnuson@mcmail.vanderbilt.edu
similar to mouse ryanodine receptor cDNA sequences (GenBank
Accession No.: AF071003.1)
PCR Primers
FORWARD: M13 forward
BACKWARD: M13 reverse
Insert Length: 964 Std Error: 0.00
Seq Primer: T7, M13 reverse, custom
POLYA=No.

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FEATURES
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                /note="Organ: Pancreas; Vector: pCR 2.1-TOPO (Invitrogen, Carlsbad, CA); Site 1: EcoRI; Site 2: BamHI; mRNA from GKP2 and GKP4 cells was used to perform subtraction suppression hybridization. Genes that are more highly expressed in GKP2 cells (an insulinoma derived cell), compared to GKP4 cells (a precursor cell line) were cloned PCR 2.1-TOPO and transformed into TOP10 competent bacteria."

```

Query Match	10.6%;	Score 317.6;	DB 2;	Length 964;
Best Local Similarity	66.9%;	Pred. No. 4.5e-72;		
Matches 452; Conservative	0;	Mismatches 224;	Indels 0;	Gaps 0;

OY	2323	AATCAGCAGGCTTTGGCTCACTCCAGGTTGGGAGCGTGGCGGATGTTTCTGTCTCTA	2382
Db	7	AATCAGCAGAGCCTGGCACAACAGCAGGCTGTGGAGTGTCTTGTGGGGCTTCTTCATGTA	66
OY	2383	TTCTCCACATGCAGGACAAAGTTGTGCAGACACTGTCGACAGTGGACCTGCTGAAGAA	2442
Db	67	TTTGACACANTCGAATGAAAGCTGTCTCAGGATTTCCAGCCAGATTGAGGCTTTAAAAA	126
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Db	127	CTTATGATCTCCAGAAAGACATGTGTGTCATGCTGTCTATGCTTAAAGGTAAATGTG	186
OY	2503	GTTAATGTGTCAATCCGCGCAGCCAAATGTGTGACACACTAGTAAATATGGCCTCCAACTG	2562
Db	187	GTTGACCGGACAAATATGGCCAAACATATGTGTGGCCATGTTGTGGAGTGTCTCAACAAAGTG	246
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Db	247	GAGATGATCTCTCAAGTTCTTTGACATGTCTTGAAAGCTGAAGAGCTTAACTCTCTGAC	306
OY	2623	AGCTTCCAGAGATTTGATGCCAAATACAGACGCGCTGGGTGCTGCCCAAGACCTTCAAGAG	2682
Db	307	ACATTTCAAAGATATGACCCTGATGCGAAGAGGGGTATTTTCCAAAGAGACTTCCACAA	366
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Db	427	GAGACAGATGAAAACGAGACACTTGACTATAGAAAGTTGTCAAGAGTTCCATGACCT	486
OY	2803	GCCAGAGAGATCGGGTTTAATTGGCCGTTACTGACTAACTGTCTGAACATATGCCG	2862
Db	487	GCCAGAGACATCGGCTTCAACGTGGCTGTCTGTGACCAACCTCTCAGACACATGCC	546
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OY	2983	GAGATCAAGAGATCTA	2998
Db	667	GAGATCAGCCAAATCCA	682

RESULT	13
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LOCUS	
DEFINITION	DTO63789 813 bp mRNA linear EST 11-AUG-2005 ABENOURT_56115410 NIH_ZGC_10 Danio rerio cDNA clone IMAGE:8003748 5' , mRNA sequence.
ACCESSION	DTO63789
VERSION	DTO63789.1 GI:72363038
KEYWORDS	EST.
SOURCE	Danio rerio (zebrafish)
ORGANISM	Danio rerio
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio. 1 (bases 1 to 813) NIH-MGC http://mgc.ncl.nih.gov/ , National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cga@pds-remail.nih.gov
 Tissue Procurement: Len Zou, Harvard
 cDNA Library Preparation: Open Biosystems
 cDNA library Arrayed by: The I.M.A.G.E. Consortium (ILNI)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Cloned through the I.M.A.G.E. Consortium
 Information can be found through the I.M.A.G.E. Consortium/ILNI at:
<http://image.llnl.gov>
 Plate: LLAM17172 row: c column: 10
 High quality sequence stop: 680.

FEATURES

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from the Niehngun strain. 1st strand cDNA was primed with
a Not I - oligo(dT) primer, double-stranded cDNA was
cloned into the Not I and EcoRV sites of pExpress-1.
Library was size-selected for >1 kb fragments. A
normalized version of this library is also available
(NH_ZGC_7). Library was constructed by Open Biosystems
(Huntville, AL)."
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ORIGIN

Query Match	9.6%	Score 287.8;	DB 8;	Length 813;
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				Gaps 1;

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 |||||
 1 GCATTCATGTATGCGCAACACAGCTTTCACACTCTTTCACAGATACATTCAGGGTCCCTGC 60

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61 ACCGGGAATCAGCAGGCTGTGGCTCAACAGTCGCTGTGGAGATCGGTGTTCCTCG 120

2377 TTCTATTCTCCACATGCAAGCAAGTTGTGAGCACTCGTCGAGGTGACTGCTG 2436
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2437 AAGAACTCTCAATCTGAGAGGACATGATCCCATGATGCTGTCCATGCTTGAAGCA 2496

2497 AATGTTGTTAATGTCAAATCGGCAAGCAATGTTGACACACTAGTAAATCGGCTCC 2556

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361 TCGGACGCGCTTCAAGAGTACGACCCGATGCGAAGCGCGTCATTTCCAAACGAGATTTC 420

2677 AAGGAGAAANTGGAACAACAGAGAGTTATCTCCGAGAAATCGAGTTCTCTAGCT 2736

421 CACAAGCAATGGAGAGCCATTAAAGCACTACACCCAAATCCGAGACGAGATTCCGTCTTCC 480

481 TGTGCGGAAACAGATGAGAAATGAGCTCTTAAGCTACGAAGAGTTCTGCAACGATTTTCAC 540

Db 541 GACCGCGGAAGATATCGTGTTTAACTGGCTGTTCTTCTTCAACCAATCTCTCAAGGCAC 600

Qy 2857 ATGCGGAACGAGCCTAGATTGSCACGTTTCTCGAGAGAGGACGTTACGTCCTGAACCTAC 2911

Db 601 ATGCGCGATGATTTCTCGCCTCCACAGCTTCTCGAGTTGGCGAGAACGCTCTGATATAT 660

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RESULT 1

LOCUS	BM645859	569 bp	RNA	linear	EST 26-FEB-2002
DEFINITION	170060687217474 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone				
ACCESSION	19600449655747 5', mRNA sequence.				
VERSION	BM645859				
KEYWORDS	BM645859.1 GI:18945370				
SOURCE	EST.				
ORGANISM	Anopheles gambiae (African malaria mosquito)				
	Anopheles gambiae				
	BukariVola, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae; Anophelinae; Anopheles.				
REFERENCE	1 (bases 1 to 569)				
AUTHORS	Holt R.A., Iln J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab R., Collins, P.H., Venter, J.C. and Hoffman, S.L.				
TITLE	Caiera Anopheles gambiae EST project				
JOURNAL	unpublished (2002)				
COMMENT	Contact: Holt R.A.				

COMMENT

45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HO11PR@celera.com
Plate: NU010049T row: F column: 01
Seq primer: M13 Reverse.
Location/Qualifiers

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Query Match	9.2%	Score 276.8	DB 3	Length 569
ORIGIN				(www.malaria.mig.org)...

3596 CAGGTCCTCCCAAGCTGAAAGCACTGACGACCTCCAGCCGACCTGTCCTCCAGAGATATTCGACAA 3645
Best Local Similarity 79.1%; Pred. No. 2,3e-61;
Matches 329; Conservative 87; Indels 0; Gaps 0;

11 CGTGTTCCTGAGCTGAAGCATCTGACCTCCACGCCGACCTTCAATGAGATTATAGCAA 70

71 CGGGGACGGTTGATATGCGGAAAGATTTCCGCGAANAAGATGAAACGACGAGNAGCTA 130

QY 2706 TACTTCCGAGAAATCGACATCTCTCCAGCTTGGTGGAGAGATCATGATGCTCAAT 2783
 DB 131 CACGCCGGGAGAGATCGACTTCTGTGCTGGCTTGTCCGAGACCAACCATGACGCGAATGAT 130

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2006, 14:57:45 ; Search time 1272.5 Seconds
(without alignments)
9489.034 Million cell updates/sec

Title: US-10-668-767-127_COPY_10000_13000

Perfect score: 3001

Sequence: 1 cagtcctccctgcgcgaacag.....cgagctcaagagctcataa 3001

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9281099 seqs, 2013915447 residues

Total number of hits satisfying chosen parameters: 18562198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications NA_New:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	732.2	24.4	15564	14 US-11-000-688-1500	Sequence 1500, Ap
2	724.4	24.1	10129	14 US-11-044-111-21	Sequence 21, Appl
3	644	21.5	14620	14 US-11-044-111-17	Sequence 17, Appl
4	63.8	2.1	1786	6 US-09-925-065A-73529	Sequence 73529, A
5	63.8	2.1	1786	6 US-09-925-065A-73530	Sequence 73530, A
6	63.8	2.1	1786	6 US-09-925-065A-73531	Sequence 73531, A
7	63.8	2.1	1786	9 US-10-301-480-174768	Sequence 174768,
8	63.8	2.1	1786	9 US-10-301-480-174769	Sequence 174769,
9	63.8	2.1	1786	9 US-10-301-480-174770	Sequence 174770,
10	63.8	2.1	1786	10 US-10-301-480-788177	Sequence 788177,
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12	63.8	2.1	1786	10 US-10-301-480-788179	Sequence 788179,
13	61.8	2.1	578	10 US-10-301-480-550750	Sequence 550750,
14	61.8	2.1	578	10 US-10-301-480-1164159	Sequence 1164159,
15	55.4	1.8	1556	8 US-10-750-185-28292	Sequence 28292, A
16	55.4	1.8	1556	8 US-10-750-623-28292	Sequence 28292, A
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c	21	52.4	1.7	5940	9	US-10-893-483-106	Sequence 106, App
c	22	51.8	1.7	648	6	US-09-925-065A-712572	Sequence 712572,
c	23	51.8	1.7	208765	9	US-10-330-773-407	Sequence 407, App
c	24	50.2	1.7	2227	6	US-09-925-065A-720983	Sequence 720983,
c	25	50.2	1.7	2227	6	US-09-925-065A-720984	Sequence 720984,
c	26	50.2	1.7	2227	6	US-09-925-065A-720986	Sequence 720986,
c	27	49.8	1.7	640	10	US-10-301-480-574144	Sequence 574144,
c	28	49.8	1.7	640	10	US-10-301-480-1187553	Sequence 1187553,
c	29	49.8	1.7	971	10	US-10-301-480-579957	Sequence 579957,
c	30	49.8	1.7	971	10	US-10-301-480-1193366	Sequence 1193366,
c	31	49.6	1.7	372	9	US-10-932-182A-174580	Sequence 174580,
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c	40	49.2	1.6	640	10	US-10-301-480-1187550	Sequence 1187550,
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c	42	49.2	1.6	640	10	US-10-301-480-1187552	Sequence 1187552,
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ALIGNMENTS

RESULT 1

US-11-000-688-1500

Sequence 1500, Application US/11000688

Publication No. US20050287544A1

GENERAL INFORMATION:

APPLICANT: BERTUCCI, Francois

APPLICANT: HOUIGATTE, Remy

APPLICANT: BIRBAUM, Daniel

TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS

FILE REFERENCE: 1423-R-03

CURRENT APPLICATION NUMBER: US/11/000,688

CURRENT FILING DATE: 2004-12-01

PRIOR FILING DATE: 2003-12-01

NUMBER OF SEQ ID NOS: 1596

SOFTWARE: PatentIn version 3.2

SEQ ID NO 1500

LENGTH: 15564

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial sequences:primer

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)..(15564)

OTHER INFORMATION: tyrosine receptor 3 (TYR3) gene.

US-11-000-688-1500

Query Match

Best local similarity: 55.7%; Pred. No. 3.8e-199; Length 15564;

Matches 1661; Conservative 0; Mismatches 1206; Indels 114; Gaps 9;

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Db 11524 ATACATCCAGGCGCTTGTGATGTAATCAACAGAGCTGGCTTCACAGCGGCTGTGGGA 11583
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QY 2358 CGCTGTGGTGGTTTCTGTCTCTATTCTCCACATGACAGACAAGTTGTGGAAGCATCTC 2417
DB 11554 CGCAGTGGTGGCTTCTCTCCATGTCTTGTCTAAATGAGAGAACTCTCTCAGATTC 11663
QY 2418 GTCCAGGTGACCTGTGGAAGAACTCTCAATCTGCAAGAGACATGATCCCATGAT 2477
DB 11644 CAGTCAATCGAGCTGTGAAGAACTCTTGGATCTCTTCAAGACATGTGTGTATGCT 11703
QY 2478 GGTGTCCATGCTTGAAGAAATGTTGTTAAATGTTCAATCCGCAAGCAATGTTGACAC 2537
DB 11704 TCTGTCCCTCTGGAAGGAAATGTGTAAATGACACATTTGGCAAGCATGTTGACAC 11763
QY 2538 ACTAATGAAATCGGCTCCACATGTAATCTGTAATCTTCAATCTTCTGCA 2597
DB 11764 ACTGTAAATCATCTACCAATGTAAATGATCTTGAATCTTGTACATCTTCTGAA 11823
QY 2598 GCTGAAGACCTGACCTCCAGCGCCAGCTTCCAGAGATTTGATGCAATMACAGCGCTG 2657
DB 11824 ACTTAAGACTTAAACAGCTCAGACCTTCAAGAAATGACCCAGATGTAAAGAT 11883
QY 2658 GGTGTGCCCAAGACTTCAAGAGAAATGGAACAAGAAAGTTATATCTCCGAAAG 2717
DB 11884 TATCTCCAAAAGAAATTCAGAGAGCCATGGAAGGCGCAAAAACAGTACAGCATGCA 11943
QY 2718 AATGAGTTCTCTAGCTTGTGCGAGAGCAACACAGCGCAAGTTAGATCATGCTG 2777
DB 11944 GATTAATCTTCTCTGTGTGTGCAAGAGCTGATGAAATGACATGTTAATTAAGCTTGA 12003
QY 2778 TTTCTGCAACCGTTTCAAGACCTGCAAGAGATCGGGTTTAACTTGGCGGTACT 2837
DB 12004 TTTTGTAAACCGGTTCATAGACCAAGCAAGATGAGGTTTAAATGTGGCTGTATAT 12063
QY 2838 GACTAATCTTGTGAACATATGCCGAAGACGCTTGAATGGACGTTTCTTGAAGACG 2897
DB 12064 GACAAATCTTCTGTGAACATATGCCGAAGATCCCGCTGAAATGTGTGTGACCGAC 12123
QY 2898 AGTTCAATCTGAACTTCTGAAACATCTCTGGGCGGTATGAGATCATGAGCGGCTC 2957
DB 12124 AAAAAATGCTTAAATTTATTTGAACCTTACCTAGACCATGAGATCATGAGTGGG 12183
QY 2958 CAAGGCAATCGACGCTGTCTACTTGAAGATCAAGAGTCTAAT 3000
DB 12184 CAAGAAATTTGACGCTTTATTTTGAATCATGTAATCAAT 12226

RESULT 2
US-11-044-111-21
; Sequence 21, Application US/11044111
; Publication No. US20050272362A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Wen
; APPLICANT: Straburg, Gale
; APPLICANT: Linz, John
; TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys
; FILE REFERENCE: MSU-09308
; CURRENT FILING DATE: 2005-01-27
; CURRENT APPLICATION NUMBER: US/11/044,111
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 10129
; TYPE: DNA
; ORGANISM: Meleagris gallopavo
US-11-044-111-21

Query Match 24.1%; Score 724.4; DB 14; Length 10129;
Best Local Similarity 56.1%; Pred. No. 4,7e-190;
Matches 1666; Conservative 0; Mismatches 1201; Indels 101; Gaps 12;
56 TGCAGAAATGGAACATGATGCGGACGCTAGAGACATCTTGAAGCGAGGTGACCAAT 115
DB 5519 TGGAGAGATGTGCCCCGACATCCCGAACCTGAGAGGCTGTATGAAGACATCGGGGGG 5578

QY 116 TGTGAGTCAAGAACAGATTAACAAGAGCGCGCATATCATGATGTGTGCTGCTT 175
DB 5579 TGGCGAGATCGGGCGCTCGCTACACAGAGATGCCCAAGTACATGAGGTGAAGCTGCCCA 5638
QY 176 TACTGTCTTATTTTGTGCTTGTGTGCGACAGGGGCTGTATATTTACTCTTACTG 235
DB 5639 TGTGTGCAATTAATTTGCCCCGTGTGTGTGAGCGGGGCGGACAGACGCCCC----- 5692
QY 226 GCGAAACCAAGTAAATATGTTAACAGGGAACAATGAACAAGTCT-CTCAAGAAATGT 294
DB 5693 AGGGGCGGTGGCCCGCGCCGTACCGGCAAGACCTTAAGCGCTGTGGGAAACATC 5752
QY 295 CTGAAGCTCATCAAAAAGAAATCGGCATGAGAAAGCGCGGTGATGACCGCATCGCC 354
DB 5753 CTGCGCATGTGTGTCAACAATCTGGGATTCACAGAGGCTGTGTGAATGAAGGCTGCA 5811
QY 355 ACTTACAGCAGCAGATCATCATCAAGCTCCAGAGAACTGTGAGGAATTCCTTCTG 414
DB 5812 GTGTTGTGCTCAGCCCATGTGTGAGCAAGCGGAGCTGTGCGCACCATTCATCATC 5871
QY 415 CCGCTGTGAAACGTGTTCGAAAGCGACGAACAATATGTTCCATTAAGAGAGAGCTTG 474
DB 5872 CCGCAGATGAGAAAGCTGAAAGAGGCGCAGGAAAGGTGTGTGAGAGAGAGAGAGCTG 5931
QY 475 AGGGGTTTATTAAGTGTGCAACAGACACATCCAGGTAGAGTCTCAAGTACAAAGA 534
DB 5932 CGCATGAGAGGGAAGGCGGAGCGGAGAC-----GCCAGCTGTATCCGCAAC 5982
QY 535 GACTGGCAGCTGTGTGTGAGAGACATCTACTCTTCTTACCGGTGTCTCATCAAGTACGT 594
DB 5983 GAGTTCTGT 6042
QY 555 GACTGTGAGAGAACCATGTGTGTGAGAACATATTTCAAGAGCGGAAAGAGTGTGTCAAC 654
DB 6043 GACAAACAGCGGCGCAAGT 6102
QY 655 CACGTGTGAAATCTTCAACATCTGTGTGAAAGACGATCTTGTGAAAGAGAGAG 714
DB 6103 ATGTGTGAGAGGTCTTATCTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6162
QY 715 AACTCATCTGTGCCAAGAAATGATTAACATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 774
DB 6163 AACTTGT 6222
QY 775 AGATGACAGCAGTAAAGATGT 834
DB 6223 AAGATGCGCAAGTCCGAGAGCGC-----CAGGGCGGTGTGTGTGTGTGTGTGTGTGT 6276
QY 835 CGTGTAAAGAAACGCGCAAGAGAGTCCAGGCGTCCCTAATGTGTGTGTGTGTGTGTGT 894
DB 6277 AAGAAAGAGCGCGCGGAGCGCTTATCTTCAATCCACATCTCTGTGTGTGTGTGTGTGT 6336
QY 895 AAGAGTTGTATTAACAGTTGT 954
DB 6337 AAGAAAGATGT 6396
QY 955 CATTTTAAAGACAGTTCTTGAAGAAATGTCAAGAAATGTGTGTGTGTGTGTGTGTGTGTGT 1014
DB 6397 CTGGCCAAAGACCGCTTACGCTGTGAAGACAGATGAAGGTGTGTGTGTGTGTGTGTGTGT 6456
QY 1015 ACCGAGTGAACATCTTCCAGATTAATAGATCCGAGAGCGAAATGTCTTGGCAACATTAAC 1074
DB 6457 AACAACTGTCACTGTGAGGAGAGTGTGAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6516
QY 1075 TTGTATAGCAAGTTAGTTTCAAGAGTAAAGACATATTAATCTGTGAAATCTGTGAAAT 1134
DB 6517 CTGTATGCGGCATGTGCGGAGGTGTGAAGACTGTGAACCCAGAGAA----- 6565
QY 1135 AAGGCAAGATTAATGATGATACGTGTGAGAGAAATGTGTGTGTGTGTGTGTGTGTGTGT 1194
DB 6566 -----AATGTGTGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6606

QY	1195	GGATTGCATATGATGCACCATATCCCAACAAATGATGAAGAAAGTGTACCCGGTGGGG	125
Db	6607	CACCTGGAGCAGACGGAGCACCCTTACAGAGTCCAGAGGCGGTGTGGCAAACTGCTC	6666
QY	1255	TGATATCAACGCAAGCGCGCGTCAATCGCTTCCTTCGACAACTTCACTATCTCTG	1314
Db	6667	TCCAAAGCAGCGCGCGCGCGGTGGTGGCTGTTCCTCGAATGACCGCGTCTAACAACTG	6722
QY	1315	CCGAGACATCGAGCGTGTAACTTCTTCGTGGCAGTACTACGAGCTCTGGTTGG--AA	1377
Db	6727	CCAGAGCAATCGCGCTCGCAATATGTTCTCGAGAGCGCTACAGCTCTGTGGTTGTGACG	6786
QY	1372	GAGGAGAACATTGGACAAAGATTAATGATAGAAAGATCTTAACATTCATTGGAACGCA	1433
Db	6787	GAGGAGACATCCCTTGGAGGACCGCATGATTTGACGACCTTGGCAAAATCA-----GGG	6833
QY	1432	GAGCTGAAGAAAGATGACGTGTGTGAGAGAGGTGTGAGAACTGACCCCTCAACGACGTG	1499
Db	6838	GAGGAGGAGGAGAGGAGGAGAAAGGAGAAAGCAAGAAAGCAGACCCCTGTGATCAGCTC	6897
QY	1492	GTCACCACTTCTGTGTGCGGTGCATGACTGAGAGGTCCGGCGCTTTGACAGAGATCTT	1551
Db	6898	ATCTGTGCACTTCAGCGCGCACGGCGCTGACCGGAGA--AAAGCAATTTGAGAGAGATCAC	6954
QY	1552	CTATACATGCTTTAGGACACATCAATAGCGAAGTCTGTGAGAGAGAGAGAGAGAGAGG	1611
Db	6955	CTGTACATGCGCTTACGCGGGGTATCATGCGCAAGCTGTCACTTTGAAAGAG--GGAATGA	7013
QY	1612	GGTGGGGAGAGAGAGAGAGGGGGGTGAGAGACAGAGGCTGAAAGCAGAGGCAAGCCAGT	1671
Db	7014	AG	7055
QY	1672	ATACACGAACAGAAATGAGAGAAACAAAGCTCTATTTCACCAAGCGCGTGGCGGAC	1731
Db	7060	TTTGGAGAGAGAGAGATGAGAGAGAGAGAGAGAGCTGTGTCACAGCACTCCGCGCTGCACA	7119
QY	1732	CGTGGGGTTGCCGAAATGGTGTGTCTGCACATCTCGCGTCCAAAGGCGTCCGACGAG	1791
Db	7120	AGGGGAGACGTGAATATGGTGTGTGACAGATGATCAACGCGCTGAAAGGGAGAGCGGGGGAG	7179
QY	1792	ATGTCATATGAAGACTTACAGCTCGGTATTAGTATATAGAGGGGCGGCAATTTGATATTA	1851
Db	7180	ATGCTTTTCCTCAACCTGTAAAGTTGGGGATCTCCATCTCTCAACGGGGGAAACCGCATGTG	7239
QY	1852	CAGATGGGTATGTTGAACCACTTGAAAGCAAGAAAGAGTGGGCTTTTAACTGCATC	1911
Db	7240	CAGCAGAAAAATGTTGAATTAACCTGAAGAGAGAAACGTGAGATCGGATTTCTCAAAAGCGTC	7289
QY	1912	GCGCGCTCAGTGAATCTCTGCTCGCTGCTCATTTTGAAGCTTGAAGAGAACACAGAG	1971
Db	7300	CAGGGCTGATGACAACTCTGCACGCTCTGTGACCTGAACCGCTTTGACCGGACAGAACAA	7359
QY	1972	GCTGAAGGCTTGGGGGTGGGTCTTGAAG-----GTGCGGGCGGAGAG	2033
Db	7360	GCGAGGGGCTGGGGATGGTGTACGAGAGAGAGAGAGAGAGATCATACGCGGTGAGAAACGGGAG	7419
QY	2014	AAGAACATGATGACGCGCGAGTTCACTTGCGCATCTTCAAGTTCAATTCACTCACTGT	2073
Db	7420	AAAGTGAATGTCCGATGATGATGATTTACGACGAGATCTGTTCCGGCTGTCAAGCTGTGTC	7479
QY	2074	GAGGAGACCAACTTGGACTGGGAGAACTACTCTGGCAATCAAGCGCGGTGAACAGACACA	2133
Db	7480	GAGGGGACCAACAGACCTTCCAGAAATTAACCTCCGACGCAAGACGGGACAAACCAACACC	7539
QY	2134	GTAACGATGATCTGACCGGTGACACTACGTGCGGGGTGCAAGGATCCATCATATGAGC	2193
Db	7540	ATCAACATCATATCATCTGACCGGTGAAATTAACCTGTGCGCTGTGCAAGGATCTCATACGCAAT	7599
QY	2194	TTCTACTGCACTACTCAAGCAAGAACTTATCGACCGCGCGGCAAGAGCAACTTCTTC	2253
Db	7600	TTCTATTGGTATTACTCGGGGAGAGAGCTGATTCGACGAGAGGAGAAACGGCACTTCTCC	7659
QY	2254	AAAGCCATTGGCGGTGCTTCCCAAGTATTTCAACCTCTCACTGAAGTCAATACAGGAGCTT	2313

Db	7650	AAAGCGATGCGTGTGGCCAAACGAGGTCTTCAACAGCTCCACCGAGTACATCTCAAGGCTCCG	77119
Qy	2314	TGTACGCAAAATCAGCAGGCTTTGGCTCCTCCAGTTGTGGACGCTGTCCGTTGGTTTC	23737
Db	7720	TGCACGGGGAAACGACAGAGGCTGGCTCCACAGCCGCGTGTGGGACGCGCTGTGTGGATTCC	77779
Qy	2374	CTGTTCCCAATCTCCCACTATGCAAGACAAAGTTTGTCAAGACCTAGTCGACAGGTGGACCTG	24333
Db	7780	CTGCACGCTCTTCGACACATATATAGAGATTGGCAGACAGCTCCAGCCAGATCGGCTGG	78339
Qy	2434	CTGAAGAACTCCTCAATCTTGCAGAGAGACATGATCCCAATGATGCTGTCCATGCTTGA	24933
Db	7840	CTGAAGAGCTGTGTGACCTTGCAGAGAGACATGTGTGGATGTGCTGTCTCTCTGGAA	78939
Qy	2494	GGAAATGTTTAAATGTGTACAAATGGCGAAGAAATGTGTGACACACTAGTAGAATCGGCGC	25533
Db	7900	GGCATGTGTGTGAACGGGACGATGTGACCGGAGGTGTGTGACATGACGGGTGAACTGTCC	79539
Qy	2554	TCCAAAGTGAACATGATCTCTGAAATTAATTGCACTGTTTCTCAAGCTGAAGGACCTGACC	26133
Db	7950	AGCAACGTCAACATGATCTGTGAATTTCTTGATATGTTCTCTGAAGCTGGCGGACATCGTG	80139
Qy	2614	TTCCAGCGCCAGCTTCCAGAGAGATTGATCCCAATACGACGGCTGGGTGGCTGCCAAGAAC	26733
Db	8020	GCTTCCGACGCTTCCCGCATTAAGTACGGAACCGCGGGGGCTCATCTCCAAAAGAAC	80739
Qy	2674	TTCAAGGAGAAATGGAACAACAAGAAGTATATCTCCGAAAGAAATCGAGTCTCTCTA	27333
Db	8080	TTCCAGAGGCGCATGTGACAGCCCAAGACGATGACAGCTGTCGAGGTGCAGTCTCTCTC	81339
Qy	2734	GCTTGTCTGCGAGCAAAACAAGACGGCAATTGACTACATCGGTTTTCTGCGACCGTTTC	27933
Db	8140	TCTGTCTCGAGGGCGGACGAGAAACGAGATGATCGACGTGGAGGGCTTCGTCTGGCGCTCC	81939
Qy	2794	CACGAGCTCTGCGAAGAGATGTGGGTTTAACTTGGCCGCTGTATCTGACTTAACTTGTCTGAA	28533
Db	8200	CAGAGGCGCGGTCTCGACATCTGGCTTAAAGTGGCGGTGTCTGTGACCAACTTGGCCGAG	82539
Qy	2854	CATATGCGGAACGAGCTTAGATTGGCACTTTCTGTGAGACGGGACGGTTTCAAGTCTGAAC	29133
Db	8250	CACGTCCCGCAAGACAGAGGGCTCGCACCTTTTGGAGCAGAGCGCGCCAGCATCTGGAG	83139
Qy	2914	TACTTCGAACCATTTCTGGGCGGTATGAGATCATGTGGCGGCTCCAAAGCGCATGACGCT	29733
Db	8320	TATTTCCGGCGCGTTTCTGGGCGCGATGAGATCATGTGGAGACGGCGCGCATGACGCGC	83739
Qy	2974	GTTACTTTCGAGATCAAGAGTCTAATA 3001	
Db	8380	CTTACTTCGAGATCAAGCGCGGCCAACAA 8407	

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RESULT 3
US-11-044-111-17
; Sequence 17, Application US/11/044,111
; Publication NO. US20050272362A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, wen
; APPLICANT: Strasburg, Gale
; APPLICANT: Linz, John
; TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys
; FILE REFERENCE: MSU-09308
; CURRENT FILING DATE: 2005-01-27
; CURRENT APPLICATION NUMBER: US/11/044,111
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 14620
; TYPE: DNA
; ORGANISM: Meleagris gallopavo
US-11-044-111-17

Query Match          21.5%; Score 644;  DB 14; Length 14620

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Query Match 21.5%; Score 644; DB 14; Length 14620;

Beet Local Similarity: 53.6%; Pred. No. 1.2e-167;
Matches 1600; Conservative 0; Mismatches 1270; Indels 114; Gaps 8;

QY 36 TTTGGAAACCCCAAGCATTAATGCAAGAAATGGAACAAATGCAATCCGACGCTGAGACAT 95
Db 9276 TTTAGATATGCTGTATACAGTAGAGAAATGTCTCAGAAATCCCTCAGCTGAGATGAC 9335
QY 96 CTTAGGACAGGTGACCAATTCGTGAGTCAGACAAGACGTACACAGAGCGCCGCATAT 155
Db 9336 AATTAAGAAATTAATTAATTAGCAGAGCTGAGACAGATATCTGAAATGCTCAAGT 9395
QY 156 CATCATGTGTGCTGCTTTACTCTGTTCTTAATTTGCGGTCTGTGAGGCAACAGGGCC 215
Db 9396 AATTGAGGTATCTTACCAATGCTGTGCAATTAATTGTCTTACTGTGAGGAAAGAGGCT 9455
QY 216 TGATAATGTACTCTTACTGCGGGAACCAAGTAACATGTTACAGCGGAACACATGAA 275
Db 9456 TGAAGGTCTCTGAAAGTGCTGGCCCTGTGTCGATGATGATCATCTGAGCATCTGAG 9515
QY 276 CCAGCTCCTCAAGAAATGTTCTGAGCTCATCAAAAAGAACATCGCAATGAGAACGCCGC 335
Db 9516 CATCATTTCTGGAAATATTTCTGAAATCATTAACCAATCTGGAAATGATGAGCATC 9575
QY 336 GTGATGACCCGCACTGCGCACTTACAGCAGCAGATCATCAACAGCTCCGAGAACT 395
Db 9576 TTGATGAAAAGAAATTGCAAGTTATGCTCAACCTATCATCAGCAAAAGCAAGCTGATCT 9635
QY 396 GCTGAGGATTCCTTCCTGCGCTGCTGAGACGTGTGGCAAAAGCAAGCAATATGTT 455
Db 9636 GCTGAAAATCACTTAATTTCCAACTGAGAAATTTGAAGAAAGCTATTAATATGTT 9695
QY 456 CCATTAAGGAGAGAGCTTGAAGGGGTTTATTAGTCGTCAACAGACACATCCAGGT 515
Db 9696 GATGAAAGAGAGCACTGAGGAGAGACATTA-----AATGACATCAAGAAAGC 9746
QY 516 AGAGTCTCAGATACAAAGACCTGCAAGCTGTGTCAGAGACATCTACTCTTACCC 575
Db 9747 TGAAGTACTTAATTCGATGAGTTGCTGTTCTTTGAGAGCCTTATGCTTATCC 9806
QY 576 GCTGCTCATCAAGTACGTGACCTGCAAGGAACCACTGCTCAGAAACATGTTCCGA 635
Db 9807 AATGCTGATACGTTACGTAGCAACACAGACCACTGCTTAAAGAAACCAAGTACGA 9866
QY 636 GGGGAGAGAGCTGTAACAACGTGCTGAATCTTCAACATCTGTGGAAGAGCCAGTA 695
Db 9867 TTTGATGATCTGTTTCGATGTAGCTGATGATTTTATCTGTGTGCAATCTCAATA 9926
QY 696 CTTCTTGAAGAGAACAGAACTTCACTCTGCAACAGAAATTTGAATCATGTGCTGAT 755
Db 9927 TTTCAAAAGAGAAAGCAAAATTTGTCTATACAGATGAATCAACAAATTTGGCATTTT 9986
QY 756 TATGCAACAGCAACAGAGAGTGAACAGAGTAACAGATGACTCTCTAAGGTGTGG 815
Db 9987 AACAGAGATACCAAAAGCAAAATGTCTAAAGCAATGCAATGAAAGTCTGAGGTCA 10046
QY 816 AAAAGAAAAGAGAGCAACCGTGAATAAGAAAGGCAAAAGCAAGAAAGTCCAGGCTC 875
Db 10047 TCAAGAGAGAAAGAA-----ATCAAAAGCAAGGGGGGATTTGTCTCCATACAAACATC 10100
QY 876 CTTAATGAGCTTGTCTGAAGAGGTGTATCAAGTTGCTTAACTAATTCGCTGGAG 935
Db 10101 CTTGATTTGATGCTGACTTTAAAGATGCTTCTATTTGGCTTGAATATGTATCTCAAG 10160
QY 936 AGAACAAGACTGTGTGACAGCATTTGAAAGACAGTTCTCTGAAGAAATGTCAAGACA 995
Db 10161 AGATCAAGGCTCATCTCATTTGGCTTAAGCTAGATATAGCCATAAGGACACTGAGAA 10220
QY 996 TGTGCAAGATTCGGGAAAGACCAGCTGACCTTCAGATTAATATGATCCGAGAGA 1055
Db 10221 AGTCAAAAGGATATATGTAATTAATTAATCTGCAAGAAAGTCTGATGATCCAGCTG- 10279
QY 1056 AATGCTTGGCAACATTACTTGTATAGCAAGTTAGGTTGAGAGATGAGCAATATATAC 1115

Db 10280 --TGAAATGCAAGTAAATCTATATATAAGACATTTCTGAAGATGATGAGCTCTGACCC 10337
QY 1116 TGTGAAACCTGTGAAATATAGGCCAGATTAATGATGATACCGTCGAGAGAAATCGTGC 1175
Db 10338 TGAAGAAATATGGAACGTGTGCAAGAGATATCAGCTGCT----- 10377
QY 1176 TATGATTAAGTGTCTTTTCGATTTGCAATGATGATGACCATCCCAAAATAGATAAGA 1235
Db 10378 -----CTGATATCATCTGACACAGGTTGAACCAACACTGATGATCAAGAAAGC 10424
QY 1236 GGTGTACCGGTGCGTGTGTGTGATACACGACAGCGCGCTCATTCGCTCTCCACA 1295
Db 10425 TGTTTGGCAAACTTCTGTCTCAAAACACGAAAAGCTGTGTGTGTTGTTTAAAT 10484
QY 1296 AACTTCACTACATTTCTGCGCAGACATCGAGCGGTGTAACATCTTGTGTCACGTA 1355
Db 10485 GGGCGCTTAATACACTTACCAGACCGTTTATTAATCTTCTCCATGCTATCA 10544
QY 1356 CGAGCTGTGTGAGAGAGAAACATTTGACAAAGATATGATAGAAATCTTACTCA 1415
Db 10545 GAACTATTTGATAGAAACAGAGAAATTTCAATTTGAGAGAAACTAGTTGAGATTTGGC 10604
QY 1416 ATCATTTGAGACGCAAGCTGAAGAAAGATGACGTGTGAGAGAGGTGAAAGCTGTA 1475
Db 10605 TACGTCTCCAAAAAGAGAGAAAGAAAGAGAAATACAGAGAA---GAACAACTGA 10661
QY 1476 CCCCCTACGAGCTGTGACACCTTCTGTGCGGTGTCATGACTGAGAGGTCCGCGC 1535
Db 10662 CCACTTCATCATGATATCTCTATTTTATGCGAAATGCTTCAAGAGAG---AGCA 10718
QY 1536 TTTGACAGAGATCTCTATATCATGTCTTACGCAACATCATACGAATGCTGTGAGA 1595
Db 10719 ACTGAAGATGATCCCTTATATATTTGCTATATGCTGATGATGCAAAAGACTGTACAGA 10778
QY 1596 AGAAGAGAGAGAGGGGTGGAGAGAAAGAGAAAGGGGTGAGAGACAGCTGAA 1655
Db 10779 AGAAGAGAGAGAGAGAGAGAGAAAGAGAAACATTTG----- 10819
QY 1656 CGAAGGACAGACGATATACAGAAATGAGAAACAAAGCTCTATTTCAACA 1715
Db 10820 -----AGAGAAAGAAATGAAAGCAAGAACTTTTATCAACA 10859
QY 1716 AGCGGCTGCGGACCGTGTGGGTTGCGGAATGTGTGTCACATCTCCGCTCA 1775
Db 10860 AGCTGCTTATCATGATGTGTGAGAGCTGTGAGATGCTCTTCAAGTATGATGCAAGCA 10919
QY 1776 AGGCTGCGCAGAGATGTCATGAAGACTTAAAGCTGATATAGTATCTGAGGG 1835
Db 10920 AGGTCAATCAAGAGCCCAATGTTGTTGAACATTAACCTTGTATTTCTTAATATG 10979
QY 1836 CGGCAATTTGATATACAGATGGGTATGTTGAACCACTTGAAGAAGAAAGAGCTGG 1895
Db 10980 TGGGAATACATTAATTTCAAGAAATGCTAGACTTGAAGAGAAAGAGAGCTGG 11039
QY 1896 CTTCTTAATGCTCATTCGCGGCTCATGAATCTCTGCTCGTGTCTGATCTTGAAGCTT 1955
Db 11040 ATTCTTCAAGTCTTCTGTGTTGATGACGTCTGTGAGTCTTGAATGAGCTT 11099
QY 1956 CGAAGAGAACCAAGCTGAAGGTGTGGGCTGTGAG----- 1999
Db 11100 TGAAGACAAATATTAAGCAGAAAGCTGGGAAATGTTACTGAAGAGAACTCATATCT 11159
QY 2000 --GTGCGCGGGAAGAGAAACATGCAATGACCGGAGTTTCACTGCGCACTCAAGTT 2057
Db 11160 ACGTAGCGTGTAAAGAGTGTGACAGATGATGAATTTACTGAGATCTATTTAGATT 11219
QY 2058 CATTCAGCTCACTGTGAGAGACAACTTGAATGCAAGAACTTACCTGCGACTCAAGC 2117
Db 11220 TTTTCAACTGCTCTGTGAAGGCAATTAAGATTTTCAAAATATATGACACTCAAGAT 11279
QY 2118 CGGTAAACAGCAACAGTGAACGTGTGATCTGCAACGTGTGATCACTGCTGCGGCTGCA 2177
Db 11280 GGGCAACACCAACAGTGAATATTAATCAATTAAGTGAAGTGAACCTTGTGCGCTTCA 11339

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OY 2178 GGAGTCCATCATGACCTTCTACGTGCACTACCAAGCAAGGAATGATCGACCCGGCCGG 2237
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DB 11340 GGAATCAATCAAGTGAATCTTATGTTAGTACTATTCAGAGAAAAGAGTTATGATGAAATCAGG 11399
OY 2238 CAAAGCGAATCTCTCAAGGCGCAATGGGGTGGCTCCCAAGATTCACACCCCTCACTGA 2297
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 11400 ACAAGCTAATCTCTTAAAGCTCTGCTGTCAACAAACAAATATTCATTCCTTACCGA 11459
OY 2298 AGTCATACAGGAGACCTTGTACGCAAGATCAGAGGCTTGTGCTCACTCCAGGTTGTGGGA 2357
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 11460 ATATATACAGGAGACCTTGTATGAGTACCAACAGAGTCTGGCTCATATGATGAGCTGTGGGA 11519
OY 2358 CGCTGTGAGTGTTCCTGTTCTTATTCCTCCACATGCAAGCAAGTTGTGCAAGCACTC 2417
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 11520 TGCAGTGTGTGATTTCTTCAATGATTTTGGCCAAATATGCAAGATGAACCTTTCACAGGACTC 11579
OY 2418 GTCCGAGGTGACCCGCTGAAAGGAATCTCCTCAATCTGCAAGAGGACATGATCCCATAT 2477
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 11580 TGCTCAGATGAACTGCTTAAAGAACTGCTAGATCTGCTAAAGGATGTTGTGATGTT 11639
OY 2478 GCTGTCCATGCTTGAAGAAATGTGTAAATGTTAAATCCGCAAGCAAAATGTTGACAC 2537
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DB 11640 GTTGTCAATTAATCTTGAAGGTAAGTTGTAAATGGAACAATGGAACAAATGCTGTGATAC 11699
OY 2538 ACTAGTAAGATCGGCTCCAAAGTGAACCTGATCTCTGAATATCTTGCACATGTTCTCA 2597
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 11700 ACTGTAGAAATCATCTAGCAACGTAGAAATTAATCTTGAAGTTTGTGACATGTTCTCAA 11759
OY 2598 GCTGAAGAACCTGACCTCCAGCGCCAGCTTCCAGAGATGATGCAATTAACAGAGGCTG 2657
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DB 11760 ATTAAGAAATTTAACTAACTCGGATGCTTTCAAGAGAGATGACCCAGATGTTAAGGCGAT 11819
OY 2658 GGTGCTGCCCAAGACCTTCAAGAGAAATGGAACAAAGAGTTTACTCCGGAAGA 2717
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 11820 CATTTCAAGAAAGATTTTCCAGAGTCAATGGAAGCTCAAAAACAATTAATACATCGA 11879
OY 2718 AATGAGTTCTCTGAGTTGCTGCGAGACGAACCAACGAGCAAGTTAGACTACATCGG 2777
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 11880 GATTGAATTCCTGTTGATCATGATACGGAAGCTGATGAATAATATATGTTCACTCATGGA 11939
OY 2778 TTTTCGGGACGGTTTCCAGAGCCCTGCAAGAGAGATGAGGTTTAACTTGGGCGGTTACT 2837
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 11940 TTTTGTAGAAAGATTTCAATGAAACAGCCAAAGATATTTGGCTTAAATGAGCAAGTTTGTCT 11999
OY 2838 GACTAATCTTCTGAAACATATGCGCAAGAGGCTAGATTGGACGTTTCTTGGAGACGGC 2897
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 12000 AACAAACCTTTCAAGAGCATATGCCATAAGCTCAGGCTTCAGAGCTTACTTGAACCTGC 12059
OY 2898 AGGTTCACTCTGAACTAATTGAAACATTTCTGGGCGGTATCGAGATCATGGGCGGCTC 2957
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 12060 AGAAAGTGTCTTAAATTAATCTTGAACCAATACCTTGGCCGTATGAAATTAATGAGGTGAGC 12119
OY 2958 CAAGGCGATCGAGCGTGTCTACTTTCGAGATCAAGAGATCTAATA 3001
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 12120 CAAAGAAATGAAGAGTTTACTTGAATCAAGTAATCCAGTA 12163

RESULT 4
US-09-925-065A-73529
; Sequence 73529, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
```

```
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73529
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-73529

Query Match      2.1%; Score 63.8; DB 6; Length 1786;
Best Local Similarity 72.2%; Pred. No. 7.7e-07;
Matches 83; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

OY 2085 CTGGAAGTGGAGAACTTACTGCGAACTCAGGCGGTAAACAGCAACAGTGAACGTGGT 2144
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1561 CTGAGACTTTCAGAACTTCTGCGGACTCAGATGGGCAACACCAACCGTGAATGCAT 1620
OY 2145 CATCTGACCGTGGACTGACTGCTGCGGCTGCGAGAGTCCATCATGAGACTTCTAC 2199
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1621 CATGACGACTGTGACTTCTGCGCTGTGCAAGTGAAGTGGAGGCGCTTGAC 1675

RESULT 5
US-09-925-065A-73530
; Sequence 73530, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-73530

Query Match      2.1%; Score 63.8; DB 6; Length 1786;
Best Local Similarity 72.2%; Pred. No. 7.7e-07;
Matches 83; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

OY 2085 CTGGAAGTGGAGAACTTACTGCGAACTCAGGCGGTAAACAGCAACAGTGAACGTGGT 2144
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1561 CTGAGACTTTCAGAACTTCTGCGGACTCAGATGGGCAACACCAACCGTGAATGCAT 1620
OY 2145 CATCTGACCGTGGACTGACTGCTGCGGCTGCGAGAGTCCATCATGAGACTTCTAC 2199
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1621 CATGACGACTGTGACTTCTGCGCTGTGCAAGTGAAGTGGAGGCGCTTGAC 1675

RESULT 6
US-09-925-065A-73531
; Sequence 73531, Application US/09925065A
; Publication No. US20040181048A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ PRIOR FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 73531
/ LENGTH: 1786
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-73531

Query Match      2.1%; Score 63.8; DB 9; Length 1786;
Best Local Similarity 72.2%; Pred. No. 7.7e-07;
Matches 83; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
```

```
QY 2085 CTTGAGCTGGCAGAACTACTGCGAACTCAGCCCGGTAAACAGCAACAGTGAACGTGCT 2144
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1561 CTCAGACTTTGAGAACTTCTCGGAGCTCAGATGGGCAACACACCGTGAATGTGAT 1620
QY 2145 CATCTGCACCGTGCAGTACTCTGCGGCTGCAGAGATCCATCATGACTTCTAC 2199
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1621 CATCAGCACTGTGAGTACTCTTCTGCGCTGTGCAAGGTGAGTGGAGGGCCTTGAC 1675
```

```
RESULT 7
US-10-301-480-174768
/ Sequence 174768, Application US/10301480
/ Publication No. US20060057564A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
/ FILE OF INVENTION: In the Human Genome
/ FILE REFERENCE: 108827.137
/ CURRENT APPLICATION NUMBER: US/10/301,480
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 10/215,598
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: US 60/311,695
/ PRIOR FILING DATE: 2001-08-10
/ NUMBER OF SEQ ID NOS: 1226818
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 174768
/ LENGTH: 1786
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-301-480-174768
```

```
Query Match      2.1%; Score 63.8; DB 9; Length 1786;
Best Local Similarity 72.2%; Pred. No. 7.7e-07;
Matches 83; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
```

```
RESULT 8
US-10-301-480-174769
/ Sequence 174769, Application US/10301480
/ Publication No. US20060057564A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
/ FILE OF INVENTION: In the Human Genome
/ FILE REFERENCE: 108827.137
/ CURRENT APPLICATION NUMBER: US/10/301,480
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 10/215,598
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: US 60/311,695
/ PRIOR FILING DATE: 2001-08-10
/ NUMBER OF SEQ ID NOS: 1226818
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 174769
/ LENGTH: 1786
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-301-480-174769
```

```
Query Match      2.1%; Score 63.8; DB 9; Length 1786;
Best Local Similarity 72.2%; Pred. No. 7.7e-07;
Matches 83; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
```

```
QY 2085 CTTGAGCTGGCAGAACTACTGCGAACTCAGCCCGGTAAACAGCAACAGTGAACGTGCT 2144
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1561 CTCAGACTTTGAGAACTTCTCGGAGCTCAGATGGGCAACACACCGTGAATGTGAT 1620
QY 2145 CATCTGCACCGTGCAGTACTCTGCGGCTGCAGAGATCCATCATGACTTCTAC 2199
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1621 CATCAGCACTGTGAGTACTCTTCTGCGCTGTGCAAGGTGAGTGGAGGGCCTTGAC 1675
```

```
RESULT 9
US-10-301-480-174770
/ Sequence 174770, Application US/10301480
/ Publication No. US20060057564A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
/ FILE OF INVENTION: In the Human Genome
/ FILE REFERENCE: 108827.137
/ CURRENT APPLICATION NUMBER: US/10/301,480
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 10/215,598
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: US 60/311,695
/ PRIOR FILING DATE: 2001-08-10
/ NUMBER OF SEQ ID NOS: 1226818
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 174770
/ LENGTH: 1786
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-301-480-174770
```

```
Query Match      2.1%; Score 63.8; DB 9; Length 1786;
Best Local Similarity 72.2%; Pred. No. 7.7e-07;
Matches 83; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
```

```
RESULT 10
US-10-301-480-788177
; Sequence 788177, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 788177
; LENGTH: 1786
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-788177
```

```
Query Match      2.1%; Score 63.8; DB 10; Length 1786;
Best Local Similarity 72.2%; Pred. No. 7.7e-07;
Matches 83; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 2085 CTTGAGCTGGCAGAACTACCTGCGAACTCAGGCGGCTAACAAGCAAGTGAACGTGGT 2144
Db 1561 CTGAGACTTTTCAAGAACTTCTGCGGACTCAGATGGGCAACACCAACCGTGAATGTCAT 1620

Qy 2145 CATCTGACCGGTGACCTACCTGCTGCGGCTGCAAGAGTCCATCATGACTTTTAC 2199
Db 1621 CATCAGCACTGTGACCTACTTCTGCTGTGCAAGTGAAGGAGGCGCTTGAGAC 1675
```

```
RESULT 11
US-10-301-480-788178
; Sequence 788178, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 788178
; LENGTH: 1786
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-788178
```

```
Query Match      2.1%; Score 63.8; DB 10; Length 1786;
Best Local Similarity 72.2%; Pred. No. 7.7e-07;
Matches 83; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 2085 CTTGAGCTGGCAGAACTACCTGCGAACTCAGGCGGCTAACAAGCAAGTGAACGTGGT 2144
Db 1561 CTGAGACTTTTCAAGAACTTCTGCGGACTCAGATGGGCAACACCAACCGTGAATGTCAT 1620

Qy 2145 CATCTGACCGGTGACCTACCTGCTGCGGCTGCAAGAGTCCATCATGACTTTTAC 2199
Db 1621 CATCAGCACTGTGACCTACTTCTGCTGTGCAAGTGAAGGAGGCGCTTGAGAC 1675
```

RESULT 12

```
US-10-301-480-788179
; Sequence 788179, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 788179
; LENGTH: 1786
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-788179
```

```
Query Match      2.1%; Score 63.8; DB 10; Length 1786;
Best Local Similarity 72.2%; Pred. No. 7.7e-07;
Matches 83; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 2085 CTTGAGCTGGCAGAACTACCTGCGAACTCAGGCGGCTAACAAGCAAGTGAACGTGGT 2144
Db 1561 CTGAGACTTTTCAAGAACTTCTGCGGACTCAGATGGGCAACACCAACCGTGAATGTCAT 1620

Qy 2145 CATCTGACCGGTGACCTACCTGCTGCGGCTGCAAGAGTCCATCATGACTTTTAC 2199
Db 1621 CATCAGCACTGTGACCTACTTCTGCTGTGCAAGTGAAGGAGGCGCTTGAGAC 1675
```

```
RESULT 13
US-10-301-480-550750
; Sequence 550750, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 550750
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-550750
```

```
Query Match      2.1%; Score 61.8; DB 10; Length 578;
Best Local Similarity 77.3%; Pred. No. 1.7e-06;
Matches 75; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 2085 CTTGAGCTGGCAGAACTACCTGCGAACTCAGGCGGCTAACAAGCAAGTGAACGTGGT 2144
Db 481 CTGAGACTTTTCAAGAACTTCTGCGGACTCAGATGGGCAACACCAACCGTGAATGTCAT 540

Qy 2145 CATCTGACCGGTGACCTACCTGCTGCGGCTGCAAGAG 2181
Db 541 CATCAGCACTGTGACCTACTTCTGCTGTGCAAGTGAAGGAGGCGCTTGAGAC 577
```

RESULT 14
US-10-301-480-1164159

/ Sequence 1164159, Application US/10301480
/ Publication No. US20060057564A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
/ FILE OF INVENTION: In the Human Genome
/ FILE REFERENCE: 108827.137
/ CURRENT APPLICATION NUMBER: US/10/301,480
/ CURRENT FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 10/215,598
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: US 60/311,695
/ PRIOR FILING DATE: 2001-08-10
/ NUMBER OF SEQ ID NOS: 1226818
/ SOFTWARE: PatSeq for Windows Version 4.0
/ SEQ ID NO 1164159
/ LENGTH: 578
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-301-480-1164159

Query Match 2.1%; Score 61.8; DB 10; Length 578;
Best Local Similarity 77.3%; Pred. No. 1.7e-06;
Matches 75; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 2085 CTTGAGCTGGCAGACTACCTGCGAAGTCCGCGTAAACAGACAGATGAGCTGGT 2144
DB 481 CTCAGACTTTGAGACTTCTCGGAGCTGAGATGGGCAACACCAACCGTAAATGTCAT 540
QY 2145 CATCTGACCGTGCATCACTGCTGCGGCTGCAGAG 2181
DB 541 CATCAGCACTGTGACTACTTCTGCGTCTGCAGG 577

RESULT 15
US-10-750-185-28292/c
/ Sequence 28292, Application US/10750185
/ Publication No. US20050260603A1
/ GENERAL INFORMATION:
/ APPLICANT: MMT GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: FANTIN, Dennis
/ TITLE OF INVENTION: COMPOSITIONS FOR IMPROVING BOVINE TRAITS
/ FILE REFERENCE: MM1100-2
/ CURRENT APPLICATION NUMBER: US/10/750,185
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 28292
/ LENGTH: 1556
/ TYPE: DNA
/ ORGANISM: Bovine
US-10-750-185-28292

Query Match 1.8%; Score 55.4; DB 8; Length 1556;
Best Local Similarity 62.8%; Pred. No. 0.00016;
Matches 86; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 2174 TGCAGAGTGCATCATGACTTCTACTGCACTACTCAAGCAAGAACTGATGACCCGG 2233
DB 1165 TTCAGGAATCAATAGATTTCTATTGGATTAATCTCGAAAAGATGTCATTGATGAAC 1106
QY 2234 CCGGCAAGCGAAGTCTTCAAGGCAATGGCGTGGCTTCCCAAGTATCAACACCTCA 2293
DB 1105 AAGGACAAAGAAATTTCTCCAAAGCTATTCAAGTGCACAAACAAAGCTTTAACAATCTTA 1046
QY 2294 CTGAAGTCATACAGGA 2310

DB 1045 CAGATATATTCAGGTA 1029

Search completed: April 14, 2006, 15:56:45
Job time : 1276.5 secs

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; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: Porcine RYR1 Gene
; POSITION IN GENOME:
; UNITS: bp
US-08-785-420-1

Query Match 24.1%; Score 722.6; DB 3; Length 15378;
Best Local Similarity 55.6%; Pred. No. 1.1e-182;
Matches 1664; Conservative 0; Mismatches 1199; Indels 132; Gaps 9;

QY 38 TGGAAACCCCAAGACATTAATGCAAGAAATGGAACATGATGATCCGACGTTAGAGCAATCT 97
DB TGGGGCTCCCAACAGCGTGGAGAGATGTGCCGAAATATTCGCGATGTGAGGCGGCTCA 9880
QY 98 TAGCGAGAGTGGACCAATTGCTGGAGTCAGACAGAGCTACAGAGGCGCGGATATCA 157
DB TGGCAGACATCGGGGGGCTGGCCAGATGCGGGGGCGCCCTACACGAGATGCCACACGTCA 9940
QY 158 TCGATGTGTGCTGCTCTTACTCTGTCTTATTTTGCCTGTCTGTGGGCAACAGGGGCTG 217
DB TTTGATGACACTGCTCCCATGCTGTGACAGCTACCTGCCCGCTGGTGGGAAACGGGGCCG 10000
QY 218 ATTAATGTTACTCTACT-----GGCGAAACACAGTAAAGATGTAAACAGCG 265
DB AGGCGCCCAACCGCCCTGCGCGGAGGCCCTCGCGCTTGCAAGCTGTCACTTCG 10060
QY 266 AACACATGAACAGAGCTCTCAAGATGTTCTGAAGCTCATCAAAAGAACATGGGCAATG 325
DB ACCACCTCAATCTCCTGTGGGAAACATCTCGGATCATGTACACATCTGGGCAATCG 10120
QY 326 AGAACGCGCGCTGGATGACCCGCACTGCGCACTCAACAGCAGATCATCATCAACAGCT 385
DB ACGAGGCTCATGTGATGAAGCGGCTGGCGGTGTTCGCCACAGCCCATGTGAGCGGGCC 10180
QY 386 CCGAGAACTGCTGAGGATTCCTTCTGCGGCTGCTGAACGTGTTCGAAAGCAACGG 445
DB GGGCGAGCTCTCTCACTCACTTCATCCCACTCGGGCGCTCGCAACAGGGCGG 10240
QY 446 ACAATATGTTCCATTAAGAGAGAGAGCTTGAAGGGGTTTATTAAGTGTCAACAGACGA 505
DB GGAAGGTGTGTGGCGAGAGAGAGAGAGCTGCGCTGAGAGCCGAGGAGAGCGAGG--- 10297
QY 506 CATCCAGATGAGTCTCAGTATACAGAGAGCTGAGCTGTGTGAGAGACATCTACT 565
DB AAGGGAGCTCTGTGTGCGGATGAGTTCTGTGTCTGCGCGGAGCTGTATG 10351
QY 566 CTTTCTACCGCTGCTCATTAAGTATGCACTGTGACAGAGAACCACTGGCTCAGAGAAC 625
DB CCCCTACCACTGCTCATTCGCTACGTGACAAACAGGGGCACTGGCTGACGGAAC 10411
QY 626 ATGTTCCAGAGGCGGAGAGAGCTGTACACACAGTGTGCTGAATCTTCAACATCGGTGA 685
DB CCAATCCAGCGCGAGAGAGAGTGTTCGAGATGTGGGCGAGATTTCACTACTGTGCTCA 10471
QY 686 AGACCCAGTACTTCTTGAAG 745
DB AGTCCCAACTTCAAGCGGAG 10531
QY 746 TGTGTCTGATTTATGCCAAG 805
DB TGTATTTTGTGACGCGAGCAACAGAGCAAAATGCGC-----A 10570
QY 806 AAGGTGTGAGAAAGAAAG 865
DB AGTGGGTGTCTCAGACAG 10630
QY 866 TCCAAAGGCTCCCTATGTGATGCTGTGAGAGAGTGTTAACAGTGTGCTTAACCTAT 925
DB TGCAGATATGCTGATGTGTGCGACACTCAAGAGAGATGTGCTCATGTGAGAGAGATGT 10690
QY 926 TCGCTGCGAG 985

DB 10691 GTGCGCCCAACGACAG 10750
QY 986 CAGAAACAGATGTGGAGAGATTCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1045
DB 10751 CAGATGAG 10810
QY 1046 CCGGAG 1105
DB 10811 GTTCCCGCTGTGCGCTGACAGATGAGCCCTGTACCG----- 10847
QY 1106 GCAATATATCTGTGAGAACTGCTGAAGAAATAGGCGCAAGATTAATGATACCGTCGAG 1165
DB 10848 -----GGGCTCCCGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 10900
QY 1166 GAATCGTGTATGATGATTAAGTCTTTCGATGATGATGATGATGATGATGATGATGATGAT 1225
DB 10901 GAGTCCAG 10960
QY 1226 TGAATGAAG 1285
DB 10961 CCAAG 11020
QY 1286 GCTTCGAG 1345
DB 11021 GTTCCGATGAG 11080
QY 1346 GCACTACTACAG 1402
DB 11081 AAGCTTCAAG 11140
QY 1403 AAGATCTTACTCAATCATATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1462
DB 11141 ATGACCTTTCAG 11191
QY 1463 GTGAG 1522
DB 11192 AGAAG 11251
QY 1523 AGAGGTCCGCGCTTTCGAG 1582
DB 11252 AAGAG---AGCAAG 11308
QY 1583 AGTCTGTGAG 1642
DB 11309 AGAGCTGCCACTGTGAG 11368
QY 1643 CAGAGGCTGAAG 1702
DB 11369 C-----CTTGAAG 11401
QY 1703 TCCATATTCACAG 1762
DB 11402 TCCATATTCACAG 11461
QY 1763 TCTCCGCTCCAAAGGCTGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1822
DB 11462 TCAGTCTCTGCAAG 11521
QY 1823 GTATATGAG 1882
DB 11522 CCAATCTGAACGAG 11581
QY 1883 AGAAG 1942
DB 11582 AGAAG 11641
QY 1943 ATCTTGAAG 2002
DB 11642 ATCTCAATGCTTTGAG 11701
QY 2003 -----CGGCGGAG 2044
DB 11702 GAAAGGTATCAACCGCAG 11761

QY 816 AAAGAAAAGAAAGCAACCGTATTAAGAAACGCGAACAAAGACAAAGAAATCCAAAGCTC 875
DB 10109 ACAAGACCAAGGACGCGAAGAAACAAAGCGCGGAGACCTTGATTCATCCAGACTC 10168
QY 876 CCTATGCTAGCTGTCTGAAGAGGTGTGTAACAGTTGSCCTTAACCTATCCGTCGAG 935
DB 10169 CCTATGCTAGCTGTCTGAAGAGGTGTGTAACAGTTGSCCTTAACCTATCCGTCGAG 10228
QY 936 AGAACAAAGACTGTGACAGCAATTTGAAGACAGTTTCTGAAGAAATGTGACAAAG 995
DB 10229 GACACAGAGCTGATCTCCCTCGAAATTCGAGATACGCCATAGGGACACAGATGAAGA 10288
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DB 10289 GGTCAAGAAACATCTGCGAAACAACTTGACCTTGACGAAAGCTGATGACCCAGCTGT 10348
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QY 1296 AACTTCACTAATTTCTGCGGAGACATCGACGCTGTAACATCTTCCCTGACGTA 1355
DB 10553 GGGCCCTCTCAACAACCTGCCAGGACCGCTCTATTTACCTTTCTCCATGCTATCA 10612
QY 1356 CGAGCTCTGTTGAAGAGAGAAACATTGACAAAGAAATGATGATGAAGATCTTACTCA 1415
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QY 1416 ATCATTTGAAAGACCAAGCTGAAGAAAGTGAAGTGTGTGAGAGAAAGTGAAGACCTTGA 1475
DB 10668 -TTGGCTTAATCTTCAAAAGGTAAGAGAGAGAGAGAGAGAGACAAAGAAACAACCTGA 10726
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DB 10727 CCCACTACATCAATCTATTTCTATTTTAAAGCCGACAGCTCTCAAGAGAGGA---GCAA 10783
QY 1536 TTTGACAGAGATCTCTATACATGTCTTACGACACATCATATGAGAAAGTCTGTGAGA 1595
DB 10784 ATTGAAGACGACCTTTGTACCTCTATTTCCAGCATGATGACCAAGATTTGTCAAG 10843
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QY 1836 CGGCAATATTGATATACAGATGGGTATGTTGAACCACTTGAAAGACAAAGAAAGCGTGG 1895
DB 11048 AGGCAATGCTGTGTGCAAGAAATGTATGATTAACCTTAAGAGAAAGATGCTGG 11107

QY 1896 CTTCTTTACGTCATGCGCGGCTCATGAATCTCTGCTCCGTGCTGATCTTGAACGCTT 1955
DB 11108 ATTCTTCAAGCCTTCTGTGTCTTATGACAGTCTTGACAGGTCTCTGATTTGAATGATC 11167
QY 1956 CGAAGGACAAACCAAGCTGAAGGTCTGGGCGTGTGAAG----- 1999
DB 11168 TGAAGGCAATTAAGCTGAAGCCCTGGGAGATGTGAATGAAGAAAGCACTATTT 11227
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QY 2298 AGTCAATACAGGACCTTTGATCGAGATCAGAGGCTTTGGCTCACTCCAGGTTTGGGA 2357
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QY 2898 AGGTCACTCTGAACCTTGAACCAATTCCTGAGCGCTATTCGAGATCATGAGCGGCTC 2957
DB 12128 AGAAATGTGTCTTAATTTACTTGGACCTTACTTGAACGCACTGAGATCATGAGTGGG 12187
QY 2958 CAAGCGCATGAGCGTGTCTACTTGAAGATCAAGAGTCTAAT 3000


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; SOFTWARE: PABSTEQ for Windows Version 4.0
; SMO ID NO 16775
; SMO ID NO 16775
; LENGTH: 12695
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16775

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Query Match	1.6%;	Score 49.4;	DB 3;	length 12655;
Best Local Similarity	46.8%;	Pred. No. 0.03;		
Matches 155; Conservative	0;	Mismatches 176;	Indels	0;

[illegible]

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RESULT 6
US-09-949-016-13727
; Sequence 13727, Application US/09949016
; Patent No. 681339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13727
; LENGTH: 49931
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(49931)
; OTHER INFORMATION: n = A,T,C or G
; US-09-949-016-13727

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Query Match	1.64;	Score 48.6;	DB 3;	Length 49931;
Best Local Similarity	57.64;	Pred. No. 0.097;		
Matches 87; Conservative	0;	Mismatches 64;	Indels 0;	

Qy	1591	GAGAGAAGGAGGAAGACGGCGTGGGAGGAAGAAAGGCGGTGGAGGAAGCAGAGGCCT	1650
Dδ	33552	GAAAGAAAAGAGAGATGTGAGGANGAGAGCAAGAGAGAGAGAGAGAAAAAAGAGAGAG	32611

[illegible]

RESULT 7
US-09-949-016-13728
; Sequence 13728, Application US/09949016
; Patent No. 6813228

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? TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
? TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
? FILE REFERENCE: CL001307
? CURRENT APPLICATION NUMBER: US/09/949,016
? CURRENT FILING DATE: 2000-04-14
? PRIOR APPLICATION NUMBER: 60/241,755
? PRIOR FILING DATE: 2000-10-20
? PRIOR APPLICATION NUMBER: 60/237,768
? PRIOR FILING DATE: 2000-10-03
? PRIOR APPLICATION NUMBER: 60/231,498
? PRIOR FILING DATE: 2000-09-08
? NUMBER OF SEQ ID NOS: 207012
? SOFTWARE: FaastSeq for Windows Version 4.0
? SEQ ID NO 13728
? LENGTH: 49931
? TYPE: DNA
? ORGANISM: Human
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1)...(49931)
? OTHER INFORMATION: n = A,T,C or G
? US-09-949-016-13728

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Query Match	1.6%	Score 48.6	DB 3	Length 49931
Best Local Similarity	57.6%	Pred. No. 0.097		
Matches 87	Conservative 0	Mismatches 64	Indels 0	Gaps 0
QY	1591	GGAGAGAGAGAGAGAGAGGGGCTGGCGAGAGAGAGAGGGGCTGGAGAACAGAGCCT	1650	
Db	32552	GAGGAAAAAGAGAGAGTGTGAGGAGGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	32611	
QY	1651	GAGAGCGAAGGCGAGGCCAGTTCACGACCAAGAAATGAGAAACAAAGCTCCATTC	1710	
Db	32612	GAG	32671	
QY	1711	CACCAAGCGCGGCTGGCGGAGCGTGGCGATTG	1741	
Db	32672	CCCTGAGAGCAGGCCAGATCTGGGGCTCG	32702	

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RESULT 8
US-09-949-016-13729
; Sequence 13729, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,458
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

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? ZIP: 02109-1875
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/574,959A
? FILING DATE: 19-DEC-95
? ATTORNEY/AGENT INFORMATION:
? NAME: Mandragouras, Amy E.
? REGISTRATION NUMBER: 36,207
? REFERENCE/DOCKET NUMBER: DFN-008
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (617)227-7400
? TELEFAX: (617)227-5941
? INFORMATION FOR SEQ ID NO: 8:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 3211 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 439..3157
? OS-08-574-959A-8

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Query Match      1.6%; Score 47.2; DB 2; Length 3211;
Best Local Similarity 62.9%; Pred. No. 0.059;
Matches 73; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

OY 1582 AAGTCTGTGAGAGAAGAAAGAGAGCGGGCTGGAGAGAGGAAGCGGGCTGAGAA 1641
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DB 2386 AACGCAGTAGTGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 2445
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 1642 GCAGAGGCTGAAGCGAAGCGAGGCCAGTTACGCAACAAGAAATGAGAACCA 1697
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2446 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGACTT 2501
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RESULT 12
; Sequence US-09-357-014--B
; Patent No. 6291645
GENERAL INFORMATION:
APPLICANT: Jaekyoon Shin, Ineill Young, Ratna K. Vadiamudi
            and Jack L. Strominger
TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
                    AND USES THEREFOR
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/357_014
FILING DATE: 19-Jul-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/574,959
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-008

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RESULT 13
 US-08-574-959A-6
 Sequence 6, Application US/08574959A
 Patent No. 5962224
 GENERAL INFORMATION:
 APPLICANT: Jaekyoon Shin, Insil Young, Ratna K. Vadiamdi
 APPLICANT: and Jack L. Strominger
 TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
 TITLE OF INVENTION: AND USES THEREFOR
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street, Suite 510
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/574,959A
 FILING DATE: 19-DEC-95
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: DFN-008
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)227-5941
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3901 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 435..3847
 US-08-574-959A-6

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